

# Ege Journal of Fisheries and Aquatic Sciences

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## EgeJFAS

# Su Ürünleri Dergisi



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**Ege University Faculty of Fisheries**



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# Authors Guidelines

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Thank you for deciding to submit your article to the Ege Journal of Fisheries and Aquatic Sciences (EgeJFAS). The journal welcomes the submission of articles that are of interest and high scientific quality. Authors should check the "Author Guidelines" very carefully before submitting their manuscripts. The instructions given here will ensure that your article's evaluation process (referee, publication, etc.) can proceed smoothly. Make sure your article is prepared and submitted in accordance with journal rules.

Submitted manuscripts will be checked primarily for compliance with journal subjects and rules. Manuscripts not complying with required formatting will be returned for correction. Papers outside the scope of the journal will be rejected.

## GENERAL INFORMATION

### Aim & Scope

Ege Journal of Fisheries and Aquatic Sciences (EgeJFAS) is open access, international, double-blind peer-reviewed journal publishing original research articles, short communications, technical notes, reports, and reviews in all aspects of fisheries and aquatic sciences.

The journal does not charge any submission and publication fees.

All articles receive DOI, are citable, published in PDF format.

The journal focuses on interdisciplinary studies that present new and useful information to the international scientific community/readership, and contribute to scientific progress. Before submitting your article, make sure it is suitable for the journal scopes.

The main functional areas accepted into the journal are listed as follows:

Marine and freshwater fisheries, Aquaculture, Vertebrate and invertebrate aquaculture (marine/freshwater), Planktonology and plankton culture, Living resources, Management and economics, Aquaponic, Seafood processing technology, Feeding and feed technologies, Fishing technology, Fisheries management, Population dynamics, Disease and treatment, Aquatic microbiology, Biology, physiology, Macroalgae, Biotechnology, Conservation and sustainability, Environments and ecology, Biogeography, Biodiversity, Climate effects, Pollution studies.

Ege Journal of Fisheries and Aquatic Sciences (EgeJFAS) (Su Ürünleri Dergisi) published quarterly (March, June, September, December) by Ege University Faculty of Fisheries since 1984.

The journal is published only as an e-journal since the 1st issue of 2020.

### Language

Although articles in English and Turkish are accepted, priority is given to articles prepared in English in order to increase international readability and citation. Limited Turkish articles are published in each issue.

Manuscripts should comply with the standard rules of grammar and style of the language (English or Turkish) with appropriate spelling and punctuation in which they are written.

### Editorial Policy and Referee Process

Manuscripts should not be copied elsewhere or submitted to another journal for parallel evaluation. Only original manuscripts are considered. It is evaluated with the understanding that the content is approved by all co-authors. Submitted manuscripts are first checked in terms of journal scope, language, presentation, and style. Manuscripts that are not suitable for these aspects will be returned without review.

In order to evaluate the appropriate articles, at least 2 or 3 external and independent referees who are experts in their fields are appointed by a member of the editorial board/section editor. Each manuscript is reviewed through a double-blind peer-review process (identities of neither authors nor peer reviewers are disclosed). Manuscripts returned to authors with referee reports should be revised and sent back to the editor as soon as possible.

Editor-in-chief/editors take the final decision (Accept, Reject) of the manuscript in line with the reviewer's opinions. All responsibility for the scientific content and expressions in the published article belongs to the authors. In accordance with the publication policies of EgeJFAS, the plagiarism report for the relevant manuscript is requested to be uploaded to the submission system by the responsible author.

### Article Types

The types of articles accepted include original research articles (priority), short communications, reviews, reports, and technical notes in all aspects, focusing on interdisciplinary studies in the field of fisheries and aquatic sciences.

**Original research papers:** These are the article type that the Journal gives the most importance and priority. Should contain data obtained from original studies such as experimental results, field data, and/or theoretical studies.

**Short communication:** It should include original results and headings, like research papers. Articles provide important new research results/methods or discoveries that do not possible to publish as a full research paper. These articles that are narrowly focused deserve to be published faster than other articles.

**Review:** Reviews may summarize current research areas of broad importance or provide the readers with an insightful introduction to new and groundbreaking areas of research. It should be examined and discussed in-depth and comprehensively written by the author(s) who have expertise in the subject area, not just the literature surveys. Only invited reviews (in English) are considered for publication. If you would like to submit an invited review, please contact the editor-in-chief (editor@egejfas.org) and upload a review cover letter containing the requested information. As of 2023, reviews in Turkish will not be accepted. Publication of those accepted in the previous year will be completed in 2023.

### Reports

**Case reports** encourage the submission of reports containing feature novel findings or new management strategies. Well-written and illustrated reports are taken into account.

**Brief reports** are short, observational studies that report the initial results or completion of a study or protocol.

**Technical notes:** They are short articles that focus on a new technique, method or procedure. It should identify significant changes or unique applications for the method described.

## MANUSCRIPT SUBMISSION

The manuscript, when submitted together with the Cover Letter (Submission declaration and verification) and Copyright Form signed by the corresponding author on behalf of all authors,

warrants (confirms) that it is original and has not been published elsewhere, has been approved - tacitly or expressly - by all co-authors and the responsible authorities at the institute where the work was carried out. The publisher will not be held legally responsible in case of any claim for compensation.

Before you start submitting an article, please ensure that the article complies with the journal guidelines (instructions) and that you are ready to upload all requested documents (Article File, Similarity Report, Cover Letter, Copyright Release Form, Ethics Committee Approval (if necessary)). Please note that submissions that do not contain the required documents/statements will be returned incomplete.

Authorship Contributions, Conflict of Interest Statement, Ethics Approval, Data Availability should be written in the article after Acknowledgements and Funding section.

### While starting

For submission of your manuscript prepared in accordance with the guideline to EGEJFAS please click here and after logging into your account (if you don't have an account please register at <https://dergipark.org.tr/en/> . Your default login ID is your email address. Use your existing account; do not create new accounts with new submissions) use the "Submit Article" button on the home page of the journal to start submission. Before submitting a manuscript, do not forget to check the Submission Checklist.

After log in, the article submission process is completed in 5 steps. Upload your article information, article file, and other necessary documents step by step correctly. There is no transition to the next step until a step is completed.

To follow the status of the article;

When log into the system (Dergipark) with user information, the related journal appears when the dashboard is clicked. By clicking on the journal, the status of the article can be followed.

After you submit your article via the online system, you will be able to follow the status of your article and you will be automatically notified by e-mail when there is any action.

### Similarity Report

To verify the authenticity of the submitted article, a similarity report should be obtained by using the services of plagiarism detection software (Crossref Similarity Check, iThenticate: Plagiarism Detection Software). This report should be uploaded as a separate file named "similarity report".

Although a similarity report is requested for all submitted articles, a second check will be made with the plagiarism detection software.

### Cover Letter

When submitting a manuscript, Cover Letter should be uploaded under the subheading "Cover Letter". Cover letter should be prepared separately from the manuscript file.

### Ethics in Publishing

Please see our information on Ethical Principles and Publication Policy. Before submission, do not forget to read the "Ethical Responsibilities of the Authors".

Please ensure that any manuscript you submit to this Journal conforms to the Committee on Publication Ethics (COPE) recommendations for ethics, Best Practice Guidelines and as well as to the rules of Egejfas.

## PREPARATION OF MANUSCRIPTS

Papers must be clearly written in Turkish or English. Manuscripts should be typed double spaced on A4 size paper in 12-point Times New Roman font including the references, table headings and figure captions with standard margins (25 mm) all around. The author's name should appear centered under the title. Numbered (1) note should give the author's institutional address and an asterisked (\*) note should indicate the corresponding author's e-mail address. Degrees and qualifications should not be included.

Line and page numbers should be given from the first page of the manuscript.

Please prepare your typescript text using a word-processing package (save in .doc or .docx).

The complete manuscript should be in a single file containing full text, references, figures and tables. Figures and tables should be inside the manuscript placed properly (not at the end of manuscript). The line number should be given to the whole manuscript.

- Research papers and reviews must not exceed 25 manuscript pages including tables and figures (except systematic checklists).
- Short communications, technical notes, and reports which are results of brief but significant work, must not exceed 10 manuscript pages including tables and figures.

Papers must be clearly written in Turkish or English. Manuscripts should be typed double spaced on A4 size paper in 12-point Times New Roman font including the references, table headings and figure captions with standard margins (25 mm) all around. The author's name should appear centered under the title. Numbered (1) note should give the author's institutional address and an asterisked (\*) note should indicate the correspondence author's e-mail address. Degrees and qualifications should not be included.

Please prepare your typescript text using a word-processing package (save in .doc or .docx).

The complete manuscript should be in a single file containing full text, references, figures and tables. Figures and tables should be at the end of the manuscript file and the locations should be indicated in the text.

- Research papers and reviews must not exceed 25 manuscript pages including tables and figures (except checklists).
- Short communications, technical notes and reports which are results of brief but significant work, must not exceed 10 manuscript pages including tables and figures.

### First Page

The title should be short concise and informative, and be a statement of the main result/conclusion presented in the manuscript. The title should not contain abbreviations. Do not forget to add English title for Turkish article. The title should be written in sentence order.

### Author Names and Affiliation

The first name and surname of each author should be clearly listed together and separated by commas. Provide exact and correct author names (forenames-surnames) as these will be indexed in official archives. Occasionally, the distinction between surnames and forenames can be ambiguous, and this is to ensure that the authors' full surnames and forenames are tagged correctly, for accurate indexing online.

Present the authors' affiliation addresses should be indicated at the author's name with superscript numbers immediately after the author's name. The full postal address of each

affiliation at the time of research should be listed in order: Department, institution, city with postcode, and country name.

Please clearly indicate who will handle correspondence at all stages of refereeing and publication, also post-publication. Provide an active e-mail address of the corresponding author. It is editorial policy to list only one author for correspondence.

ORCID numbers of all authors should be listed on the article title page as of June 2017. Authors who do not have an ORCID number are required to register their number at [www.orcid.org](http://www.orcid.org). The orcid number is mandatory. Articles that do not have an ORCID number or are incorrect will not be evaluated.

Please refer to the journal's "Ethical Responsibilities of Authors" policy in the Ethical Principles and Publication Policy section for details on eligibility for author listing.

## Abstract

English and Turkish abstracts (contributors who are not native Turkish speakers may submit their manuscripts with an English abstract only) of a maximum of 300 words should be included in all submissions. The abstract should be comprehensible to readers before they have read the full paper, and reference citations must be avoided. In the abstract, the importance of the work should be clearly stated; what, why, how it was done should be answered and the contribution of the results to the scientific world should be expressed. It should not contain undefined abbreviations.

Abstract should clearly the importance of the work described in the paper and reflect what was done, why it was done and what important results were achieved. It should not contain any undefined abbreviations and not be written in the first person.

## Keywords

Below the abstract, please provide 4-6 keywords related to the study that will help to increase the discoverability of your manuscript. It is especially important to include words that are fundamental to your manuscript but are not included in the manuscript title or abstract to increase discoverability by indexing services.

## Following pages

Following pages should contain the rest of the paper and should be organized into an Introduction, Material and Methods, Results, Discussion, Conclusion(s), Acknowledgements and Funding, Authorship Contributions, Conflict of Interest Statement, Ethics Approval, Data Availability, References. These should be capitalized. Please note that submissions without required documents/statements will not be accepted.

## Introduction

Provide clearly and an adequate background, avoiding a detailed literature survey or a summary of the results. State the specific objective or hypothesis of the study.

## Material and Methods

Provide adequate detail to allow the work/experiment to be reproduced. Methods already published should be mentioned by references. Significant modifications of published methods and new methods should be described in detail.

If the study requires "Ethics Committee Permission Certificate", be sure to report after the "Acknowledgements" section that permission has been obtained from the relevant institution. A copy of the "Ethics Committee Permission Documents" should be uploaded to the system. A detailed explanation on this subject has been made in the "Ethics Approval" heading above.

## Results

Results should be clear and concise. Results for different parameters should be described under subheadings or in separate paragraph. Present your results in a logical sequence in the text, tables, and figures.

## Discussion

The discussion should not repeat the results, but should provide a detailed interpretation of the data. The discussion should highlight the importance of the work and the resulting new insights. Only in exceptional cases may the results and discussion be combined with the editor's consent. Avoid extensive citations and discussion of published literature.

## Conclusions

This should briefly state the major findings of the study.

## Acknowledgements and Funding

Acknowledgements including people, grants, funds, projects, etc. should be kept brief and placed after conclusion section. Names of contributing people should be written clearly and fully.

Examples:

"The authors are grateful to John Nare, for his friendly collaboration and hospitality during the lipid analysis."

"The authors would like to thank Ken More for language revision."

Please clearly and fully specify the relevant funding information (name) with the grant number or codes.

Financial support acknowledgment should be written like the example given:

"This study was supported by the Turkish Scientific and Technological Research Institution (Grant number: .....)."

"This work was supported by Ege University Scientific Research Projects Coordination Unit. Project Number: ....."

"Author Mary Lee has received research support from Company A."

If the research has no specific financial support, please include the following statement:

"This research has not received a specific grant, fund or other support from any funding agency in the public, commercial, or not-for-profit sectors."

## Authorship Contributions

Identifying individual author contributions (CRediT - Contributor Roles Taxonomy, ICMJE-Defining the Role of Authors and Contributors, Transparency in authors' contributions) is important to reduce authorship disputes and facilitate collaboration. The publisher recommends that authors include statements of contribution stating each author's contribution to the work to promote transparency. This gives authors the opportunity to share an accurate and detailed description of their various contributions to the work. The corresponding author is responsible for ensuring that the disclosures are correct and accepted by all authors.

The roles of all authors should be listed. Authors may have contributed to more than one role. These contributions should be placed in the text with the heading of "Authorship Contributions", after the "Acknowledgements" section of the article. See below examples:

Example: All authors contributed to the idea and design of the study. Material preparation and investigation were performed by [full name], [full name] and [full name]. The writing/editing was carried out by [full name] and all authors have read and approved the article.

Example: CRediT author statement (Click for more information about CRediT)

Full name/s: Conceptualization, Methodology, Software

Full name: Data curation, Writing- Original draft preparation

Full name/s: Visualization, Investigation

Full name/s: Supervision

Full name/s: Software, Validation

Full name/s: Project administration, Resources, Funding acquisition

Full name/s: Writing- Reviewing and Editing

For review article; it should be stated whose idea, who did the literature survey and data analysis, who wrote the draft, and who revised the criticisms.

For articles produced from student's dissertations or thesis, it is generally recommended that the student is listed as the principal author (A Graduate Student's Guide-APA Science Student Council 2006).

## Changes to Authorship

At the time of submission, the author (s) information, the corresponding author and the order of the authors must be correct. Changing the author order, adding/deleting are not allowed during the revision phases. However, in rare cases, it can be applied when detailed and acceptable reasons are presented. All authors must agree with any addition, removal or rearrangement and the reasons for changes should be explained in detail. After the article is accepted, no changes can be made to the authorships.

## Conflict of Interest Statement

Authors should declare if they have any financial or personal relationships with any institution/organization or person that may adversely affect their work. Conflict of interest statement should be attached to the article after the Acknowledgements section.

If the authors have financial or personal relationships with any institution/organization or person that may adversely affect their work, they should declare within a separate file by selecting the 'conflict of interest' subheading as the file type when submitting the manuscript. Conflict of interest statement should also be attached to the article after the Acknowledgements section of the article.

In the event of a potential conflict of interest, the authors must state: "The following financial interests / personal relationships may be potential competitive interests."

Conflict of interest statement should be provided even if the authors have no competition or conflict of interest.

If there is no conflict of interest; "The authors declare that there is no known financial or personal conflict that may affect the research (article)" or "The authors declare that there are no conflicts of interest or competing interests".

## Ethics Approval

All animal and human experiments conducted in the manuscript research should comply with the ARRIVE guidelines, EU Directive 2010/63/EU, The Code of Ethics of the World Medical Association (Declaration of Helsinki), and National Ethics Committee for Animal Experiments (HADMEK, HADYEK). If there is a human study in the article, it must comply with The Code of Ethics of the World Medical Association (Declaration of Helsinki).

If the submitted article involves the use of animal (vertebrate) and human subjects, authors should prove that they have carried out the manuscript studies in accordance with the relevant laws and regulations and they have received the approval of the authorized institutional committee (s) (including the ethics committee name and reference number, if possible). If a study was granted exemption or did not require ethics approval, this should also be detailed in the manuscript.

Copies of approval should be uploaded to the system under the subheading "Ethics Committee Approval". In addition, an explanation should be added to the article with the title of "Ethics Approval" after the Acknowledgements section.

Examples:

"Approval was granted by the Ethics Committee of University B (Date.../No...)."

"This is an observational study. The ABC Research Ethics Committee has confirmed that no ethical approval is required."

"This article does not contain any human or animal studies performed by any authors."

"The authors declare that all applicable guidelines for sampling, care, and experimental use of animals in this study have been followed."

"Sampling and handling procedures of the fish were in accordance with an ..... protocol approved by University of ....."

"No specific ethical approval was necessary for this study."

## Retrospective Ethics Approval

If necessary, an application should be made to the ethics committee and approval should be obtained before starting a study. Generally, retrospective ethical approval cannot be obtained. It may not be possible to consider such articles for peer review. In such cases, it is at the Editor's discretion to decide whether to proceed with the peer review.

## Data Availability

Articles are open access and free to use. Published articles are archived permanently. Proper citation is required when using an article published in a journal.

In order for the datasets reflecting the results of the article should be accessible to the readers; the journal encourages that datasets may be stored in public repositories (where available and appropriate) and addressed in the article, provided in the article, or in supplementary files whenever possible, or available from the corresponding author upon request. Regarding data availability, authors can follow one of the ways described. Enquiries about data availability should be directed to the authors. This information should be placed in the text with the heading "Data Availability" after the "Acknowledgements" section of the article. See examples below:

Examples:

Data availability: All of the data summarized in the study are available in the (name) Data Repository, (link address).

Data availability: The data sets generated during and/or analysed during the current study will be provided by the corresponding author upon the request of the editor or reviewers.

Data availability: For questions regarding datasets, the corresponding author should be contacted.

Data availability: All relevant data is in the article.

## Scientific Style

In writing of systematic /biological papers, international terminology such as "International Codes of Zoological Nomenclature (ICZN), and International Code of Nomenclature for Algae Fungi and Plants (ICNAFF)(Formerly known as the International Code of Botanical Nomenclature - CBN) International Code of Botanical Nomenclature (ICBN)" must be strictly followed. The first mention in the text of any taxon must be followed by its authority including the year. The names of genera and species should be given in italics. Clearly write the full genus name at the first occurrence in the text, and abbreviate it when it occurs again. When

referring to a species, do not use the genus name alone; Be careful when using 'sp' (singular) or 'spp.' (plural).

## Equations and units

Please ensure that equations are editable. Leave a space on both sides of the <, ±, =, etc. equations used in the text. For units and symbols, the SI system should be used.

## Abbreviations

Please define non-standard abbreviations at first use in the text with full form followed by the acronym in parentheses. Use only the acronym for subsequent explanations.

## Footnotes

Footnotes should be numbered consecutively. Those in tables or figures should be indicated by superscript lower-case letters. Asterisks should be used for significance values and other statistical data. Footnotes should never include the bibliographic details of a reference.

## References

Full references should be provided in accordance with the APA style. The usage of reference managers as Mendeley® or Endnote® or an online reference manager as Citefast with the output style of APA 7th edition is advised in organizing the reference list.

Please ensure that every reference cited in the text is also present in the reference list (and vice versa) and avoid excessive referencing.

## In-Text Citation

In-text citation to the references should be formatted as surname(s) of the author(s) and the year of publication (also known as the author-date system).

If a specific part of a source (book, article, etc) is cited directly, a page number should also be included after the date. If the full source is used, the citation page number is not displayed.

For example: Kocataş, 1978, p. 3

Citation can be shown in two ways: Parenthetical Citation or Narrative Citation.

References to be made at the end of the sentence should be shown in parentheses. If the cited reference is the subject of a sentence, only the date should be given in parentheses. There should be no parentheses for the citations that the year of the citation is given in the beginning of the sentence.

Citation examples according to the number of authors are given below.

### One author:

Consider the following examples:

.....(Kocataş, 1978)

- Kocataş (1978) states.....

- In 1978, Kocataş's study of freshwater ecology showed that....

### Two authors:

If there are two authors, the surnames of both authors should be indicated and separated from each other by "and", (Geldiy and Ergen, 1972).

Consider the following examples:

.....(Geldiy and Ergen, 1972)

- Geldiy and Ergen (1972) states.....

- Similar results were expressed by Geldiy and Ergen (1972), Kocataş (1978).

### More than two authors:

For citations with more than two authors, only the first author's surname should be given, followed by "et al." –in Turkish article 'vd.'- and the date (Geldiy et al.,1971; Geldiy vd., 1971).

See below examples:

-Geldiy et al. (1971) state.....

.....( Geldiy et al., 1971).

There are few studies on this subject (Geldiy et al.,1971).

### Two or more works by different author:

When its needed to cite two or more works together, in-text citations should be arranged alphabetically in the same order in which they appear in the reference list and used semicolons to separate citations.

For example: Several studies have reported similar results (Geldiy and Ergen, 1972; Kocataş 1978; Thury 1987).

### Two or more works by the same author:

If there are two or more works by the same author, list the years of publication in order, earliest first. For example: (Kocataş, 1978, 1979, 1981) or Kocataş (1978, 1979, 1981)

### Citation to authors with more than one work in the same year:

The works should be cited as a, b, c, etc. after the date. These letters must be listed alphabetically according to the surname of the first author in the bibliography list.

For Example:

-Geldiy and Ergen, 1972a

-Geldiy and Ergen, 1972a, b

### No authors:

If the author is unknown, the first few words of the source should be used and dated.

For example: (A guide to citation, 2017).

In some cases, "Anonymous" is used for the author, accept this as the name of the author (Anonymous, 2001). Use the name Anonymous as the author in the reference list.

### No publication date:

If the publication date is unknown, write "n.d." (no date) in the in-text citation.

Example: (Geldiy, n.d.).

### Citation to secondary sources:

In scientific studies, citation should be made to the original primary sources. Cite secondary sources when the original work is out of print, not available, or only available in a language you do not understand. If you want to cite a work that you can't find yourself, through a citation from another source, using the phrase ".....as cited in".

For Example:

(Geldiy and Ergen 1972, as cited in Kocataş, 1978)

### Personal communication and unpublished results:

Personal communications, such as phone calls, emails, and interviews, are not included in the reference list because readers can't access them. The in-text citation is also formatted slightly differently as follow:

Example:

- Demands have been increasing lately. (A. Kale, personal communication, May 10, 2021).

### General use of websites and software:

It should be showed as below.

-The website of Egejfas ([www.egejfas.org](http://www.egejfas.org)) includes author guidelines.

-Statistical software SPSS (version 25) was used to analyze the data.

## In References

All citations should be listed in the reference list, with the exception of personal communications and unpublished results.

All references must be written in English. If an article is written in a language other than English, give the title in English and indicate the language in which the article is in parentheses at the end of the source. Example: (in Turkish)

If the article has only an English abstract, indicate it in parentheses (English abstract) or (only English abstract)

References should be listed alphabetically ordered by the author's surname, or first author's surname if there is more than one author.

Hanging indent paragraph style should be used.

The year of the reference should be in parentheses after the author name(s).

The correct arrangement of the reference list elements should be in order as "Author surname, first letter of the name(s). (publication date). Title of work. Publication data. DOI

Article title should be in sentence case and the journal title should be in title case. Journal titles in the Reference List must be italicized and spelled out fully; do not abbreviate titles (For example: *Ege Journal of Fisheries and Aquatic Sciences*, not *Ege J Fish Aqua Sci*). Article titles are not italicized. If the journal is paginated by issue the issue number should be in parentheses.

DOI (Digital Object Identifier) information (if available) should be placed at the end of the reference as in the example. After added DOI information, "dot" should not be put. The DOI information for the reference list can be retrieved from CrossRef © Simple Text Query Form (<https://doi.crossref.org/simpleTextQuery>) by just pasting the reference list into the query box. After copying and pasting all the references of your article in the query box on this page, the DOI information is listed as added to the relevant reference. It is strongly recommended to provide DOI information of the references.

- For a reference with up to 20 authors, ALL authors (up to 20) are spelled in the reference list. When the number of authors is more than 21, "....." is used between the 19th author and the last author (APA 7th edition).

For example:

Bolotov, I.N., Kondakov, A.V., Konopleva, E.S., Vikhrev, I. V., Aksenova, O. A, Aksenov, A. S., Bespalaya, Y. V., Borovskoy, A. V., Danilov, P. P., Dvoryankin, G. A. Gofarov, M. Y., Kabakov, M. B., Klishko, O. K., Kolosova, Y. S., Lyubas, A. A., Novoselov, A. P., Palatov, D. M., Savvinov, G. N., Solomonov, N. M., .....& Vinarski, M. M., (2020). Integrative taxonomy, biogeography and conservation of freshwater mussels (Unionidae) in Russia. *Scientific Reports*, 10, 3072. <https://doi.org/10.1038/s41598-020-59867-7>

- In the reference list starting with the same surname and names (initials), works with a single author are put in chronological order first, Then, two-author works are taken into account in alphabetical order of the second author. Multi-author works are listed only chronologically.

For example:

Kocataş, A. (1978)

Kocataş, A., & Ergen, Z. (1972).

Kocataş, A., & Geldiy, R. (1972)

Kocataş, A., Ergen, Z., & Geldiy, R. (1980)

The citation of journals, books, multi-author books and articles published online etc. should conform to the following examples:

### Journal Articles

Öztürk, B. (2010). Scaphopod species (Mollusca) of the Turkish Levantine and Aegean seas. *Turkish Journal of Zoology*, 35(2), 199-211. DOI:10.3906/zoo-0904-23

Özbek, M., & Ulutürk, E. (2017). First record of *Spongilla lacustris* (Porifera: Demospongiae) from the Eastern Black Sea (Uzungöl Lake, Trabzon) (in Turkish with English abstract). *Ege Journal of Fisheries and Aquatic Sciences*, 34(3), 341-346. <https://doi.org/10.12714/egejfas.2017.34.3.14>

### Books

Parsons, T.R., Matia, Y., & Lalli, C.M. (1984). A manual of chemical and biological methods for seawater analysis. New York, Pergamon Press.

Kleiner, F.S., Mamiya, C.J., & Tansey, R.G. (2001). Gardner's art through the ages (11th ed.). Fort Worth, USA: Harcourt College Publishers.

### Chapter in books

Gollasch, S. (2007). Is ballast water a major dispersal mechanism for marine organisms? In W. Nentwig (Ed.), *Biological Invasions* (pp. 29-57). Berlin: Springer.

### E-books and chapter in e-books

Mitchell, J.A., Thomson, M., & Coyne, R.P. (2017). A guide to citation. Retrieved from <https://www.mendeley.com/reference-management/reference-manager>

Troy, B.N. (2015). APA citation rules. In S.T, Williams (Ed.). A guide to citation rules (2nd ed., pp. 50-95). Retrieved from <https://www.mendeley.com/reference-management/reference-manager>

### Proceedings

Soultos, N., Lossifidou, E., Lazou, T., & Sergedilis, D. (2010). Prevalence and antibiotic susceptibility of *Listeria monocytogenes* isolated from RTE seafoods in Thessaloniki (Northern Greece). In Ş. Çaklı, U. Çelik, C. Altınelatan (Eds.), *West European Fish Technologists Association Annual Meeting 2010* (pp. 94-98). Izmir, Turkey: Proceedings Book.

### Websites

Mitchell, J.A. (2017, May 21). How and when to reference. <https://www.howandwhentoreference.com>

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# Fish diversity and community structure of a wetland system of the western Mediterranean Basin of Türkiye: Lake Koca (Dalaman)

## Türkiye'nin Batı Akdeniz Havzası'ndaki bir sulak alan sisteminin balık çeşitliliği ve topluluk yapısı: Koca Göl (Dalaman)

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**Abstract:** Lake Koca (Dalaman), a wetland in the western Mediterranean basin of Türkiye, is an extraordinary lake with salty, fresh, and sulfurous waters and is home to high biodiversity. The present study examines the spatial and seasonal variation in fish communities and assesses the influence of environmental parameters on the community structure of Lake Koca. A total of 1.530 specimens were captured, representing seven families and 11 species (2 non-native, 1 introduced, and 8 native species). Total fish abundance and richness were higher at the littoral than at the limnetic zone, but no seasonal variation was observed. Non-native fish species, *Coptodon zillii*, was the most abundant in the littoral zone, followed by species of Mugilidae. The abundance of the two endemic fish species (*Capoeta aydinensis* and *Ladigesocypris irideus*) was relatively low in both habitats. Shannon-Wiener diversity index and evenness did not vary seasonally and spatially. Fish abundance and richness were significantly and positively correlated with chlorophyll-a and macrophyte coverage while negatively correlated with depth. Spearman's Correlation analysis revealed that native fish species show a relationship with the chemical parameters of the water, while *C. zillii* showed a distribution related to depth and macrophyte density. Both anthropogenic activities and the presence of non-native fish may affect the distribution and abundance of endemic fishes.

**Keywords:** Fish biodiversity, seasonal variation, assemblage structure, environmental parameters, non-native fish, Lake Koca

**Öz:** Türkiye'nin Batı Akdeniz havzasında bir sulak alan olan Koca Göl, tuzlu, tatlı ve kükürtlü suları ile sıradışı bir sistem olup, yüksek biyolojik çeşitliliğe ev sahipliği yapmaktadır. Bu çalışma, balık topluluklarındaki mekansal ve mevsimsel değişimi incelemekte ve çevresel parametrelerin Koca Gölü'nün balık toplulukları üzerindeki etkisini değerlendirmektedir. Çalışmada yedi familya ve 11 tür (2 yabancı, 1 taşınmış ve 8 yerli tür) temsil eden toplam 1.530 örnek yakalanmıştır. Toplam balık bolluğu ve zenginliği littoral bölgede limnetik bölgeye göre daha yüksek bulunmuş, ancak mevsimsel bir değişiklik göstermemiştir. Yabancı balık türlerinden, *Coptodon zillii*, littoral bölgede en bol bulunan türdür ve bunu Mugilidae'ye ait türler izlemiştir. İki endemik balık türünün (*Capoeta aydinensis* ve *Ladigesocypris irideus*) bolluğu her iki habitatta da nispeten düşük bulunmuştur. Shannon-Wiener çeşitlilik indeksi ve düzgünlüğü mevsimsel ve mekansal farklılık göstermemiştir. Balık bolluğu ve zenginliği, klorofil-a ve makrofit kapatıcılığı ile anlamlı ve pozitif bir şekilde ilişkilirken, derinlik ile negatif bir şekilde ilişkilidir. Spearman Korelasyon analizi, yerli balık türlerinin suyun kimyasal parametreleri ile ilişki olduğunu, *C. zillii*'nin ise derinlik ve makrofit yoğunluğuna bağlı bir dağılım gösterdiğini ortaya koymuştur. Bu sulak alanda hem antropojenik faaliyetler hem de yabancı balıkların varlığı, endemik balıkların dağılımını ve bolluğunu etkilemiş olabilir.

**Anahtar kelimeler:** Balık biyoçeşitliliği, mevsimsel varyasyon, topluluk yapısı, çevresel parametreler, yabancı balıklar, Koca Göl

## INTRODUCTION

Among ecosystems with high biodiversity, wetlands cover only about 1% of the Earth's surface but provide habitat for about 20% of the world's species (Cheng et al., 2012). Species community structures of highly biodiverse wetland lakes exhibit spatial and seasonal variations (Fitzgerald et al., 2017; Jin et al., 2019). Wetland hydrology affects organisms' population and community dynamics by affecting abiotic factors (Winemiller et al., 2000). In summer, when the depth of wetland is low, high temperature, hypoxia, and predation can cause a decrease in fish species diversity and abundance, while an increase in depth can increase fish diversity as it causes habitat stability (Cvetkovic et al., 2010; Grubh and Winemiller, 2018). In addition, most fish species in a wetland system use coastal areas as seasonal or ontogenetic stages of development (Westrelin et al., 2018) for

feeding, spawning, nursery, or shelter habitat (Lewin et al., 2004; Matern et al., 2021). The aquatic vegetation in wetlands increases the spatial complexity and heterogeneity of these ecosystems (Marin Avendaño and Aguirre Ramirez, 2017), supporting production, high species diversity (Dustin and Vondracek, 2017), and consequently, food web complexity (Carey et al., 2010; Ziegler et al., 2015).

Lake Koca is a wetland under a special environmental protection zone with 395.03 ha. It is located in the western Mediterranean basin of Türkiye, within the borders of the Dalaman district of Muğla in Türkiye (Ayaz et al., 2013). This area is surrounded by mountains and seas and is connected to the Mediterranean Sea by a natural channel covered with reeds. Lake water is slightly sulfurous due to the hot springs

around the lake (Ayaz et al., 2013). In the past, the lake was fed by floodwaters coming from Tersakan Stream. However, when the direction of the stream was changed due to flood prevention in 1974, it caused the natural seasonal hydrological cycles to change. In addition, the high reinforced concrete bridge built on the canal connecting the Tersakan stream channel and Lake Koca caused the reinforcement to narrow and shallow with reeds, and as a result, migrating fish species such as Mugilidae species and *Anguilla anguilla*, etc. were prevented easy entry and exit between the sea and the lake (Şahin, 2019a). Some practices such as tourism, agriculture, and animal husbandry are significant threats to the area. In addition, it has been reported that some parts of the area are dried due to the existing airport and the agricultural fields (Şahin 2019b), and invasive fish species (*Carassius gibelio*, *Gambusia* sp.) were introduced into the lake several times (Şahin, 2019b).

Koca Lake wetland is one of Türkiye's richest and most sensitive in terms of ecosystem and species diversity due to its geographical location. Because it is an essential habitat for two endemic freshwater fish, *Capoeta aydinensis*, *Ladigesocypris irideus*, a butterfly species called Ottoman fire (*Lycaena ottomana*), Mediterranean monk seal (*Monachus monachus*), otter (*Lutra lutra*), the sea turtle (*Caretta caretta*), and many aquatic avian species, which are endangered on a world scale (Kıraç and Suseven, 2021), despite its national and global importance as a significant wetland supporting a wide diversity of animal taxa, but little information has been gathered about fish fauna. Yılmaz et al., (2006) conducted a taxonomic study on fish species in some inland waters of Muğla, including Lake Koca. There is no published article on the fish fauna of Lake Koca and its physicochemical properties. Research is urgently needed to understand sustaining biodiversity and ecosystem services and the value of floodplain lakes. The overall goal of this study is to describe spatial and seasonal variation in fish community structure (species richness, diversity, abundance, and evenness) in a wetland lake (Lake Koca) to investigate relationships between local environmental conditions and fish community structure. It is very important to reveal the current status of fish

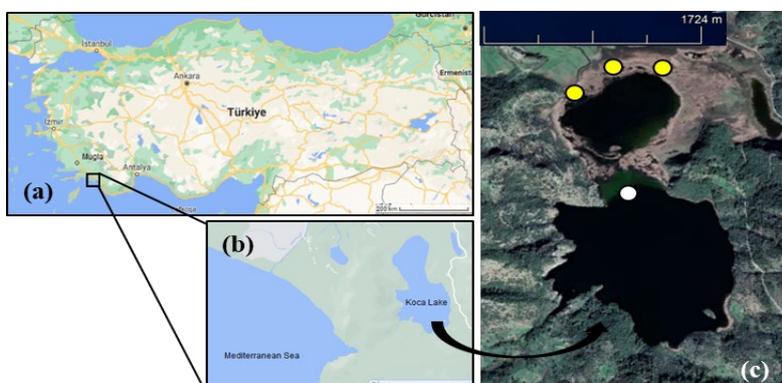
community in such a wetland system which is under anthropogenic pressure. This article presents the first detailed study of fish community structure in the Koca Lake.

## MATERIALS AND METHODS

### Study site

This study was carried out in the northwestern part of Lake Koca, a wetland lake in Türkiye. The lake is located within the borders of Kapukargın Village in southwest Türkiye and has hydrological connections to the Tersakan Stream and the Mediterranean Sea (Figure 1). While Tersakan Stream had a direct connection with the sea in the past, but today this connection is provided by narrow drainage channels. The lake's depth varies between 1 to 20m (Ayaz et al., 2013). The northwestern area of the lake is flat, and its depth is less than the southeastern part of the lake. There are Kargın and Sulfur lakes around Lake Koca. The characteristic Mediterranean climate prevails, summers are hot and dry, and winters are cool and rainy. The average annual temperature in the region is 18.3 °C. The hottest month is July with an average of 27.8°C and the coldest month is January with 10.1°C (Çınar and Ardahanlıoğlu, 2015). The annual average total precipitation is relatively high with 853 mm, of which 55% in winter, 19% in spring, 25% in autumn, and 1% in summer.

The marsh vegetation is also well represented in the wetlands and marshy areas around the littoral zone of Lake Koca, which has extensive stands of aquatic emergent (*Schoenetum nigricantis*, *Phragmites australis*, *Juncus maritimus*, *Typha domingensis*), floating (*Lemna* sp., *Azolla* sp., etc.) and submerged aquatic macrophytes (*Ceratophyllum* sp., *Myriophyllum* sp., *Potamogeton* spp., etc.). The coverage percentage of littoral aquatic vegetation is 100% (Çınar and Ardahanlıoğlu, 2015). We determined two different regions in the lake: the first region was located in the littoral zone of the lake which had extensive and dense patches of submerged, floating, and emergent macrophytes; and the second was located in the limnetic zone of the lake which had characterized by mostly a mud bottom with little submerged vegetation, but no floating and emergent macrophytes (Figure 1).



**Figure 1.** Location of Lake Koca in the western Mediterranean basin in Türkiye (a) and Lake Koca (b) and four study sites (c) within the lake. The yellow circles indicate the littoral sampling zone, and the white one indicates the limnetic zone

### Sampling protocol

Two regions (littoral and limnetic sites) of Lake Koca were sampled for fish in winter, spring, summer, and autumn between February 2019 and December 2020. Three different locations were selected for fish sampling in the littoral site. The littoral site was sampled using overnight fyke-net sets with 17 mm mesh (mean soak time = 12 h/fyke net). Four traps for each littoral station were set as a pair with leads (15 m) facing each other and nets oriented parallel to the shoreline. Fish sampling was made from one station at the limnetic site (Figure 1). Fishes were caught using trammel nets with inner nets consisting of four 100 m long panels of 10, 25, 50, 80, and 100 -mm mesh. Trammel nets were set into the water at around 9:00 – 10:00 pm and retrieved at around 9:00 - 10:00 am the following day. After sampling, all fish individuals were treated in accordance with the guidelines of the local ethics committee (Reference number: 93773921). Captured fishes were anesthetized in MS-222 and then fixed in 4% formalin in the field. In the laboratory, samples were sorted, and identified into species (based on studies: Balik et al., 1992; Muus and Nielsen, 1999; Kottelat and Freyhof, 2007; Özuluğ and Freyhof, 2011; Güçlü et al., 2013; Turan et al., 2017; Güçlü et al., 2020), and counted.

Before trammel and fyke netting, temperature (T), dissolved oxygen concentration (DO), conductivity (Cond), and pH were measured at each survey site with a multiparameter probe (YSI Instruments). Depths (m) were measured with a meter stick at the mouth of each fyke and trammel net, and the percent macrophyte cover (MacCov) was assessed for the lead length between the wings for each net (Bhagat and Ruetz, 2011). Braun-Blanquet coverage categories were used to estimate densities from calculated percent macrophyte values (Barbour et al., 1987). For analysis of water quality parameters such as phosphate ( $\text{PO}_4^{3-}$ ), nitrate ( $\text{NO}_3^-$ ), nitrite ( $\text{NO}_2^-$ ), and ammonium ( $\text{NH}_4^+$ ), a one liter sample of surface water was collected within each study station and season. Water samples were immediately placed on ice. In the laboratory, each water sample was filtered through precombusted Whatman GF/F filters (Merck, Darmstadt, Germany). The filtrate was then used to measure soluble  $\text{PO}_4^{3-}$ ,  $\text{NO}_3^-$ ,  $\text{NO}_2^-$  and  $\text{NH}_4^+$  using calorimetric kits and the WTW model Photo Flex Turb (Xylem Analytics Germany Sales GmbH & Co. KG, Weilheim, Germany). To measure chlorophyll (Chl-a), 1 L of water was collected at each site and placed in polyethylene bottles. After the water samples had been filtered through a Whatman GF/F filter, the filters were placed in 90% acetone for 24 h and measured absorbance using a spectrophotometer (at 665, 664, and 750 nm) (Wetzel and Likens, 1991).

### Data analysis

Due to the different fishnets used in the lake, fish densities could not be calculated and compared in terms of catches per unit effort (CPUE). Instead, they were presented as the total number of fish obtained to indicate fish abundances roughly. Spatial (site with or without aquatic

vegetation) and seasonal changes in fish community metrics were analyzed. Different community metrics were determined for each site and season, including species richness (total number of species (S)), species diversity (Shannon diversity index ( $H'$ )), numerical abundance (N), species evenness index (E), and species richness index (D). Higher values represent greater diversity (Cheng et al., 2012). These standard indices for each survey were calculated using the following formula:

Shannon diversity indices ( $H'$ ) (Krebs, 1998):

$$H' = - \sum_{i=1}^S P_i \log_2 P_i$$

where  $P_i$  = the proportion of individuals belonging to the  $i$ th fish species in the data set. Species richness (S) is the absolute number of species captured in a given area and time. Evenness was calculated to estimate the equitability of species abundances within each community. Species evenness index (J) (Pielou, 1966):

$$J' = H' / \ln(S)$$

Where  $H'$  = Shannon-Wiener diversity index and S = total number of species. Species richness index (D) (Menhinick, 1964):

$$D = S / \sqrt{N}$$

Where S = number of different species in the sample, N = total number of individuals.

A one-way analysis of variance (ANOVA), and a student's t-test were used to compare fish community metrics and environmental parameters among seasons, and sites (littoral vs. limnetic), respectively. Before the analysis of variance, all variables were tested for normality (Shapiro Wilk test), and the homogeneity of variances (Cochran tests). After macrophyte coverage was arcsine-square-root transformed and all environmental data were transformed by  $\log_{10}(x+1)$ , data showed normal distribution. Principal components analysis (PCA) was used to examine spatial and seasonal relationships among environmental parameters. The Pearson correlation coefficient was used to investigate relationships between environmental parameters and fish community metrics. In addition, the degree of association between fish species and environmental parameters was calculated by applying Spearman's correlation since the abundance data of each fish species did not show normal distribution. All analyses were performed with SPSS version 23.

## RESULTS

### Spatial and temporal variation in environmental conditions

While seasonal variations in nitrite, nitrate, phosphate, temperature, and pH were statistically significant, depth, chlorophyll-a, and macrophyte cover were spatially different. Temperature was highest in summer ( $F_{3,7}=162.421$ ;  $p=0.000$ ), whereas pH and nitrite were in winter ( $F_{3,7}=17.66$ ;  $p=0.009$ ;

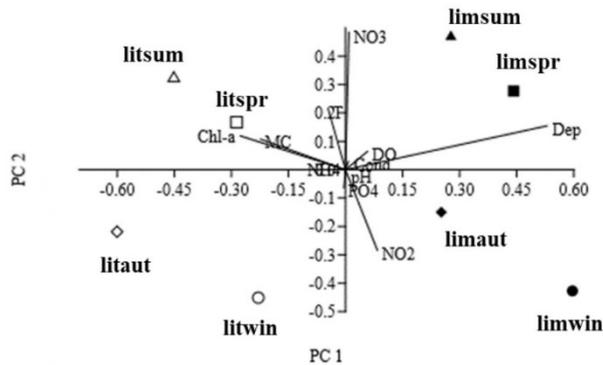
$F_{3,7}=124.169$ ,  $p=0.000$ , respectively) (Table 1). The nitrate was higher in summer but lower in winter and autumn ( $F_{3,7}=94.93$ ,  $p=0.000$ ). The phosphate concentration was the highest in autumn ( $F_{3,7}=21.86$ ,  $p=0.006$ ). The water depth was

higher in the limnetic than littoral site ( $t_6 = -9.727$ ,  $p=0.000$ ), while chl-a concentration and macrophyte cover were greater in the littoral site ( $t_6 = 2.936$ ,  $p=0.026$ ;  $t_6 = 3.347$ ,  $p=0.015$ , respectively) (Table 1, Figure 2).

**Table 1.** Seasonal and spatial variations in some environmental parameters of Lake Koca

	Winter		Spring		Summer		Autumn	
	Littoral	Limnetic	Littoral	Limnetic	Littoral	Limnetic	Littoral	Limnetic
NH <sub>4</sub> <sup>+</sup> (mg/l)	0.01	0.01	0.02	0.01	0.02	0.02	0.03	0.02
NO <sub>2</sub> <sup>-</sup> (mg/l)	1.53	0.97	-	-	0.03	0.02	0.11	0.06
NO <sub>3</sub> <sup>-</sup> (mg/l)	0.01	0.02	1.23	0.81	2.68	1.04	0.01	0.02
PO <sub>4</sub> <sup>3-</sup> (mg/l)	0.12	0.1	-	-	0.06	0.06	0.44	0.57
T (°C)	13.6	12.5	24.6	23.4	27.6	27	19.4	19
DO (mg/l)	9.01	9.96	10.14	11.16	9.89	10.32	6.18	8.21
pH	8.36	8.3	7.96	7.88	7.99	7.84	8	8.03
Cond (µS/cm)	418	425.63	401	419.87	448	487.6	410	400.65
Chl-a (µg/l)	3.04	1.01	5.81	2.31	6.74	3.01	7.23	3.21
MacCov	3	1	4	1	5	2	5	3
Depth (m)	3.25	11.54	1.8	9.22	1.05	6.45	2.6	10.15

The two PC axis explained 91.6% of the total variation in the season and site data (Table 2). The first PC axis described a gradient of decreasing macrophyte coverage and chlorophyll-a associated with increasing depth. The second PC axis was associated negatively with nitrite and positively with nitrate and temperature (Table 2; Figure 2).



**Figure 2.** PCA ordination of environmental parameters (Lim: Limnetic site, Lit: Littoral site, win: winter, spr: spring, sum: summer, aut: autumn)

**Table 2.** PCA eigenvalues (in parentheses) and major axis loadings of environmental parameters

Environmental Parameters	PC 1 (0.198)	PC 2 (0.128)
Ammonium	0.00	0.00
Nitrite	0.13	-0.44*
Nitrate	0.01	0.75*
Phosphate	-0.01	-0.10
Temperature	-0.07	0.33
DO	0.09	0.10
pH	0.00	-0.02
Conductivity	0.01	0.05
Depth	0.82*	0.24
Chl-a	-0.43*	0.18
MacCov	-0.34*	0.17

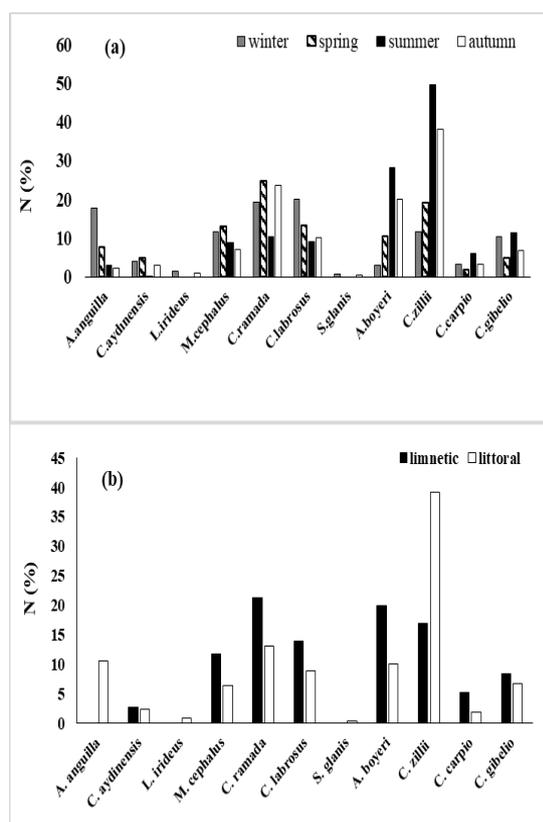
\*High correlation coefficients

### Fish Community Structure

A total of 12 fish taxa belonging to six families and 1.530 fish specimens were collected across four seasonal sampling events during the study. In general, the most dominant families, according to their numerical abundance, are Mugilidae (36.21%), Cichlidae (29.74%), Atherinidae (14.18%), and Cyprinidae (11.11%). Two fish species, *Capoeta aydinensis*, and *Ladigesocypris irideus* were endemic, and comprised 2.94%. In contrast, two non-native fish species (*Coptodon zillii* and *Carassius gibelio*) contributed 37.12% of the numerical abundance of the total catch. *Cyprinus carpio* comprised 3.27% of the total catch. The other fish species were the sole representatives of the Anguillidae: *Anguilla anguilla*, Siluridae: *Silurus glanis*, which comprised 6.08%, and 0.20% of the total catch, respectively.

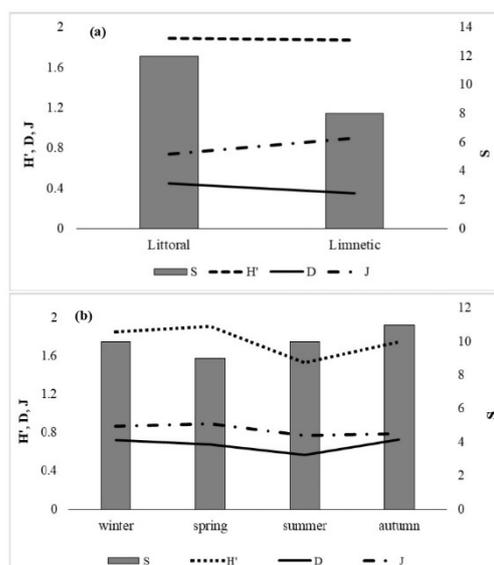
There was no seasonal variation in the total abundance of fishes when data were pooled across all habitats ( $F_{3,7}=0.064$ ,  $P=0.976$ ). It was determined that *C. zillii*, which was the most abundant fish species, had a very high abundance in the summer (49.61%) and autumn (38.10%) (Figure 3). When data were pooled across all seasons, the total abundance was higher in the littoral site compared to the limnetic site ( $t_6 = 7.132$ ,  $p=0.000$ ). Especially, *C. zillii* (39.1%) was the most abundant in the littoral site, followed by Mugilidae species (*Mugil cephalus*, *Chelon ramada* and *Chelon labrosus*) (28.4%). In the limnetic site, the most dominant species were Mugilidae species (48.98%), followed by *A. boyeri* (19.84%) and *C. zillii* (16.90%) (Figure 3).

During the study, species richness (S) and species richness index (D) varied from 6 (limnetic site during summer) to 11 (littoral site during autumn) and from 0.50 (limnetic site during summer) to 0.76 (littoral site during autumn), respectively (Figure 4). While there were no significant differences among seasons for species richness ( $F_{3,7}=0.194$ ,  $p=0.896$ ) and D ( $F_{3,7}=0.535$ ,  $p=0.683$ ), species richness showed significant differences between sites with the highest in littoral site ( $t_6 = 4.127$ ,  $p=0.006$ ).



**Figure 3.** The temporal (a) and spatial (b) variations in the total fish abundance

Shannon-Wiener diversity index ( $H'$ ) and Evenness ( $J$ ), which is a measure of whether the abundance of the species is evenly distributed, ranged from 1.34 (littoral, summer) to 1.98 (littoral, spring) and 0.58 (littoral, summer) to 0.96 (littoral, spring and limnetic, winter), respectively. Both  $H'$  and  $J$  did not vary seasonally ( $F_{3,7}=4.035$ ,  $p=0.106$ ;  $F_{3,7}=0.488$ ,  $p=0.709$ , respectively) and spatially ( $t_6=0.48$ ,  $p=0.964$ ;  $t_6=1.263$ ,  $p=0.253$ , respectively) (Figure 4).



**Figure 4.** The spatial (a) and temporal (b) variations in mean community metrics of fishes

Water depth was negative (-0.713), but macrophyte coverage was positively (0.731) associated with species richness, whereas the opposite was true for the evenness index (0.718, -0.714, respectively). Total abundance was negatively associated with depth (-0.794) and positively correlated with chlorophyll-a concentration (0.738) and macrophyte coverage (0.765).

Spearman Correlation analysis between abundance and environmental parameters showed that *A. anguilla* had a significant negative correlation with depth. Both *S. glanis* and *L. irideus* were negatively associated with nitrate. *M. cephalus* abundance was correlated with nitrite, phosphate, and dissolved oxygen, but *C. ramada* with conductivity, *C. labrosus* with ammonium. The non-native fish species, *C. zillii*, was negatively associated with water depth while positively with chl-a and macrophyte coverage (Table 3).

**Table 3.** Spearman correlation coefficient between fish species and environmental parameters (Aa: *A. anguilla*, Sg: *S. glanis*, Li: *L. irideus*, Ab: *A. boyeri*, Ca: *C. aydinensis*, Cc: *C. carpio*, Cg: *C. gibelio*, Cl: *C. labrosus*, Mc: *M. cephalus*, Cr: *C. ramada*, Cz: *C. zillii*)

Parameters	Aa	Sg	Li	Ab	Ca	Cc	Cg	Cl	Mc	Cr	Cz
Ammonium	0.063	0.031	0.031	0.611	-0.156	-0.036	-0.548	<b>-0.833*</b>	-0.419	0.419	0.405
Nitrite	0.254	0.655	0.655	-0.419	-0.228	-0.06	0.524	0.333	<b>-0.743*</b>	-0.443	0.19
Nitrate	0.025	<b>-0.733*</b>	<b>-0.733*</b>	0.359	-0.108	0.299	-0.571	-0.19	0.551	-0.144	0.095
Phosphate	-0.076	0.483	0.483	0.012	-0.359	0.144	0.238	-0.19	<b>-0.766*</b>	-0.108	0.095
T	0.101	-0.405	-0.405	<b>0.731*</b>	-0.275	0.252	-0.524	-0.524	0.192	0.012	0.429
DO	-0.304	-0.592	-0.592	0.024	0.192	0.168	0	0.333	<b>0.886**</b>	0.012	-0.429
pH	0.304	0.546	0.546	-0.611	0.024	-0.216	0.286	0.238	-0.575	-0.275	0.095
Cond	-0.228	-0.234	-0.234	0.311	-0.491	0.575	0.262	0.238	0.12	<b>-0.766*</b>	0.024
Depth	<b>-0.761*</b>	-0.234	-0.234	-0.24	0.012	0.335	0.429	0.429	0.323	0.036	<b>-0.881**</b>
Chl-a	0.545	0.312	0.312	0.347	-0.06	-0.311	-0.5	-0.69	-0.599	0.216	<b>0.762*</b>
MacCov	0.639	0.333	0.333	0.293	-0.11	-0.293	-0.473	-0.618	-0.64	0.073	<b>0.837**</b>

\*\*Correlation is significant at the 0.01 level (2-tailed).

\*Correlation is significant at the 0.05 level (2-tailed).

## DISCUSSION

The fish community structure of the Koca Lake wetland can be characterized by relatively low species richness but an overabundance of some species. The fish community in Lake Koca was dominated by *A. anguilla*, *A. boyeri*, *M. cephalus*, *Chelon ramada*, and *C. labrosus* (42.29%), characteristic of other coastal lakes of the western Mediterranean basin (Akin et al., 2005). Non-native fish species (*C. zillii*, and *C. gibelio*) were dominant in the Koca Lake wetland and represented 37.12% of the fish community. Although *C. carpio* is a native species for some regions of Türkiye (Atalay et al., 2017), it was not recorded in a previous study from Lake Koca (Yilmaz et al., 2006). Tarkan et al. (2015) has been reported as an introduced fish because this fish has been transported to almost all parts of Türkiye due to aquaculture production and stocking programs. Therefore *C. carpio* is an introduced fish species for this lake and contributed more to the fish community than endemic species. On the other hand, freshwater-dependent endemic species (*C. aydinensis* and *L. irideus*) were at a very low density (2.94%). The abundance of non-native species and the decline of native fishes could reflect the high degree of human influence on the wetland, leading to the current semi-replacement of native species. There is no study on the fish community composition or biodiversity of this wetland and only a study provides information on the fish fauna (Yilmaz et al., 2006), and reported that no non-native species, but only catadromous species were recorded between 1999 and 2003.

Our results showed that the non-native cichlid *Coptodon zillii* was the most abundant species of the Lake Koca fish community. This species is evaluated as the high invasiveness in the USA (U.S. Fish and Wildlife Service, 2014) and is generally considered to be a greedy herbivore that depends on aquatic plants for feeding, protection, or spawning (Nico et al., 2014). High fertility (developed gonads even in 0-year-old) and ecological plasticity may have contributed to successful populations of *C. zillii* (Gu et al., 2016; Çoban, 2018). We found a high abundance of *C. zillii* in the littoral site during summer and autumn. For example, the littoral site was characterized by higher chl-a and macrophyte coverage, and lower depth. However, abundance of other non-native (*C. gibelio*) and introduced fish species (*C. carpio*) did not correlate with any of the abiotic environmental parameters we identified. In fact, this result can be explained by the fact that both fish species are opportunistic generalists (Balik et al., 2003; Gül et al., 2010). Seasonal or daily habitat use preferences may vary in both fish. For example, *C. carpio* shows a significant preference for shallow, vegetated habitats during all seasons, but they migrate to deep water during the day (Zhang et al., 2020). *C. gibelio* prefers shallow waters with dense aquatic plants for feeding and spawning in spring and summer, and deep waters in autumn and winter (Giosa et al., 2014).

Species of the Mugilidae family, which are among the native catadromous species, are marine-estuarine dependent

and are commercially important fishes. These species are found in greater density in the limnetic site of Lake Koca in spring and summer. Similar results have been reported in other lagoon and wetland systems in the Mediterranean region (Akin et al., 2005; Franco et al., 2008; Scapin et al., 2018). The abundance and distribution of Mugilidae species were correlated with local abiotic factors. For example, *M. cephalus* and *C. labrosus* were negatively correlated with water nutrient parameters such as nitrite, phosphate, and ammonium, respectively. The abundance of *C. ramada* was negatively correlated with conductivity. It has been reported that *C. ramada* is more tolerant to organic pollution and eutrophication than *M. cephalus* (Bogliione et al., 2006). Besides, the three sympatric mullet species show interspecies differences in breeding period, habitat, and resource use to reduce competition, which may lead to differences in abundance and distribution (Cardona, 2006; Akin et al., 2005).

One of the endemic fish species, *L. irideus* has the lowest abundance (only 7 individuals) and was mainly caught in the marginal vegetation in the littoral site during winter and autumn. In addition, the abundance of *L. irideus* was found to be negatively associated with nitrate. *L. irideus* was assessed as "Near Threatened" according to the IUCN Red List 2014 (Freyhof, 2014). Although no precise data on population trends are available in the literature, the populations of this species are slowly declining due to the negative effects of anthropological activities (Yilmaz et al., 2015). Another endemic species, *C. aydinensis*, is a species that has a low tolerance to environmental changes and prefers specific habitats (Akbaş et al., 2019). *C. aydinensis* had a very low abundance and constituted 2.48% of the fish community of Lake Koca. It was determined that the abundance and distribution of this species were not correlated with the environmental variables of this wetland. Akbaş et al. (2019) also showed that this endemic fish from the Tersakan Stream which flows into the Lake Koca, was a slow-growing species, therefore the age of reaching sexual maturity is higher than other fish. The destruction of habitats by anthropogenic activities and the presence of non-native fish are critical to the survival of populations of such sensitive and slow-growing species.

Unlike species diversity, species abundance, richness, and evenness showed spatial patterns in Lake Koca. Fish sampling method and used fishing nets can explain spatial patterns (limnetic vs. littoral) in fish community structure. Besides, the fish community of Lake Koca is strongly associated with environmental parameters revealing spatial patterns. Evenness, richness, and abundance were highly correlated with macrophyte coverage and chlorophyll-a concentration. As a central component of the freshwater ecosystem, macrophytes are essential in providing resources and shelter to aquatic organisms (Silva et al., 2013). Aquatic macrophytes appear to play a powerful role in structuring the fish community in Lake Koca. Fish species richness and abundance were high in the littoral habitat, where macrophyte

coverage and chlorophyll-a concentration were high. Similar trends have been identified in many wetland and lake ecosystems (Pelicice et al., 2008; Cvetkovic et al., 2010; Thomaz and Cunha, 2010; Bhagat and Ruetz, 2011). Macrophytes increase habitat structural complexity and productivity for aquatic macroinvertebrates which are important food resources for fish. Additionally, the increase in habitat complexity provides an increase in fish species richness and associated fauna, due to the diversification of possibilities in exploring different habitats (Dias et al., 2017).

In this study, none of the fish community structure parameters showed seasonal variation. However, seasonal patterns are quite common in fish communities from estuarine and lagoon systems (Nsor and Obodai, 2016; Jin et al., 2019; Grubh and Winemiller, 2018). The seasonal variation of communities within these systems is often due to the reproductive biology of fish (reproductive migrations between marine and freshwater and seasonal dynamics) (Akin et al., 2003). Fish that spend their trophic life in fresh water and then migrate to the sea to spawn, such as eels (*A. anguilla*), and marine-estuarine opportunist fish such as Mugilidae (were commonly found in Lake Koca. Estuarine migrant Mugilidae members regularly enter the estuary, especially when juveniles, and use them as nurseries to take advantage of higher nutrient input and structured habitats to develop rapidly in their first years of life. After that, they migrate to coastal seas, where reproduction usually takes place (Rangely et al., 2023). These migratory species, albeit small in size (N. Kaymak personal observation), may have been sampled during four seasons and may have affected the species richness. In addition, some species (*C. zilli*, *M. cephalus*, *C. ramada*, etc.) that were abundant in all seasons may have affected the species diversity patterns.

## CONCLUSION

The contribution of non-native fish to the fish abundance of Lake Koca was quite high and the most dominant of non-native

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fish was *C. zilli*. Species diversity and abundance are higher in the littoral than in the limnetic habitat, and in the summer season. All biodiversity parameters showed correlations with environmental parameters such as chlorophyll-a and macrophyte density which are related to primary productivity in the lake. Water quality parameters such as nitrate, nitrite, and phosphate were negatively correlated with native fish distribution. The results of the analysis in this study showed that environmental parameters and non-native fish species in this wetland system affect both biodiversity and fish community structure.

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## AUTHOR CONTRIBUTION

Nehir Kaymak wrote the main manuscript text, Yılmaz Emre designed the project and study, Şenol Akin reviewed the draft, Nehir Kaymak and Nesrin Emre analyzed the data.

## CONFLICTS OF INTEREST

The authors declare that there is no known financial or personal conflict that may affect the research (article).

## ETHICS APPROVAL

Approval was granted by the Ethics Committee of Burdur Mehmet Akif Ersoy University (Date: 19.07.2018 / Approval Number: 93773921).

## DATA AVAILABILITY

For questions regarding datasets, the corresponding author should be contacted

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# Investigations on *Paradiplozoon bliccae* (Reichenbach-Klinke, 1961) (Monogenea: Diplozoidae) found in *Capoeta aydinensis*, an endemic fish in Türkiye, based on ecological, molecular and host related factor approaches

Türkiye'nin endemik balıklarından *Capoeta aydinensis*' ten *Paradiplozoon bliccae* (Reichenbach-Klinke, 1961) (Monogenea: Diplozoidae)'nin ekolojik, moleküler ve konak ilişkili faktör yaklaşımıyla araştırmalar

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**Abstract:** The present study investigated diplozoid parasites in an endemic species, *Capoeta aydinensis* Turan, Küçük, Kaya, Güçlü & Bektaş, 2017 in Köyceğiz Lake, near Muğla province (Türkiye). The aim of this research is to improve a record of diplozoid species occurrence in *C. aydinensis*, an endemic fish species by collecting data from a previously unexplored locality situated in a different geographical region of Türkiye. A total of 187 individuals of *C. aydinensis* were collected by using fishing nets from October 2019 to July 2020 and examined for the presence of diplozoid species. Only one species of diplozoid has been recorded, known as *Paradiplozoon bliccae* (Reichenbach-Klinke, 1961), which has been identified morphologically and confirmed through molecular analysis. The nucleotide sequences of the parasite's nuclear internal transcribed spacer (ITS2) gene marker were determined as well as phylogenetic analyses by using Bayesian inference (BI) analyses. On the basis of the molecular findings, the morphological identification of the diplozoid parasite species was confirmed. Of 187 fish sampled, 27 were infected with 117 *P. bliccae*, representing an abundance of 0.6, a mean intensity of 4.3 and a prevalence of 14.4%. The prevalence and mean intensity of infection were based on the season and sex of the host. The highest values of infection for prevalence, mean intensity and abundance were found in summer. Meanwhile, mean intensity and abundance of *P. bliccae* were higher in males, the prevalence was higher in females. To our knowledge, the present study is the first ichthyoparasitological study of *C. aydinensis* in Köyceğiz lake, near the province of Muğla in Türkiye. Furthermore, sequence data of *P. bliccae* from fish hosts in this locality were reported to GenBank for the first time as part of this study. Therefore, this study widens the host range of this parasite species in Türkiye.

**Keywords:** Köyceğiz lake- *Capoeta aydinensis*, *Paradiplozoon bliccae*, molecular approach, seasonal effects, host sex

**Öz:** Bu çalışma, Muğla (Türkiye) ili yakınlarındaki Köyceğiz Gölü'nde bulunan endemik *Capoeta aydinensis* Turan, Küçük, Kaya, Güçlü & Bektaş, 2017'in diplozoid parazitleri üzerine yapılmıştır. Araştırmanın amacı, Türkiye'nin farklı bir coğrafi bölgesinde daha önce keşfedilmemiş bir lokasyondaki endemik balık türü *C. aydinensis*'in diplozoid türlerinin varlığına ilişkin kayıtların geliştirilmesidir. Ekim 2019 – Temmuz 2020 tarihleri arasında araştırma alanından balık ağları kullanılarak toplam 187 *C. aydinensis* bireyi toplanmış ve diplozoid türlerinin varlığı açısından incelenmiştir. Ayrıntılı morfolojik tanımlamanın ardından yalnızca bir diplozoid türü, *Paradiplozoon bliccae* (Reichenbach-Klinke, 1961) tanımlanmıştır. Bu morfolojik tür tanımlamasını moleküler yöntemlerle doğrulamak için, konak balıktan alınan parazitlerin internal transcribed spacer 2 (ITS2) gen bölgelerinin nükleotid dizileri belirlenmiş ve Bayesian Inference (BI) algoritmaları kullanılarak filogenetik analizleri yapılmıştır. Elde edilen moleküler bulgulara göre diplozoid parazit türünün morfolojik olarak tanımlanması doğrulanmıştır. Diplozoid parazit dizileri ayrıca LT560257 erişim numarasıyla GenBank'ta saklanan *Paradiplozoon bliccae* dizileriyle de yüksek homoloji (%99.32) göstermiştir. İncelenen 187 balıktan 27'sinin toplam 117 *P. bliccae* ile 14.4%; 4.3; 0.6 sırasıyla enfeksiyon oranı, enfekte balık başına ortalama parazit sayısı ve incelenen balık başına ortalama parazit sayısı hesaplanmıştır. Enfeksiyon oranı, enfekte balık başına ortalama parazit sayısı ve incelenen balık başına ortalama parazit sayısı için en yüksek değerler yaz aylarında bulunmuştur. *P. bliccae*'nin enfekte balık başına ortalama parazit sayısı ve incelenen balık başına ortalama parazit sayısı erkeklerde daha yüksektir, enfeksiyon oranı dişilerde daha yüksek bulunmuştur. Bildiğimiz kadarıyla bu çalışma, Muğla ili Köyceğiz Gölü'nde *C. aydinensis*'in ilk ihtiyoparazitolojik araştırmasıdır. Ayrıca bu çalışma ile ilk kez bu lokalitedeki konak balıklardan elde edilen *P. bliccae*'nin sekans dizi verileri de GenBank'a raporlanmıştır. Böylece bu çalışma, bu parazit türünün Türkiye'deki konak yelpazesini üçe, yer sayısını ise ikiye çıkarmıştır.

**Anahtar kelimeler:** Köyceğiz Gölü, *Capoeta aydinensis*, *Paradiplozoon bliccae*, moleküler yaklaşım, mevsimsel etki, konak cinsiyeti

## INTRODUCTION

According to Froese and Pauly (2022), 409 species of freshwater fish have been reported from Türkiye's inland

waters so far. Endemic fish species represent 194 of these species (Çiçek et al., 2018). One of these endemic species,

*Capoeta aydinensis* Turan, Küçük, Kaya, Güçlü & Bektaş, 2017 is distributed in clear and moderately flowing waters with a substrate of stones and pebbles (Froese and Pauly, 2022). It occurs in the Büyük Menderes River as well as Dalaman, Namnam and Tersakan in the freshwater ecosystems (Froese and Pauly, 2022). Despite the increase in the number of studies on helminth parasites of endemic fish species in Türkiye in recent years, it is evident from current literature that comprehensive studies on the helminth parasites of endemic fish species are needed due to the determination of the helminth fauna of most endemic fish species distributed in Türkiye. In confirmation of the above information, there is only one ichthyo-helminthological record for *C. aydinensis* so far in Türkiye (Nejat et al., 2023). In addition to these, Diplozoid parasite species also appear to be very poorly represented in Türkiye fauna. Besides these studies, Özer (2021) found that the genus *Paradiplozoon* Akhmerov, 1974 is represented in Türkiye by six previously known species of parasites and one unspesies identified parasite plus that no previous study has found *Paradiplozoon* spp in this host fish in the locality. Moreover, *Paradiplozoon bliccae* has been recorded in only three studies in Türkiye so far (Innal et al., 2020; Unal et al., 2017; Nejat et al., 2023). Diplozoids are a unique family of Monogenea that are common and widespread gill parasites of cyprinid fishes (Pecínková et al., 2005). The frequency diplozoid parasite detections in host fish is not constant for all species, as is the case for other helminth parasites (Yunchis, 1988), and varies depending on season, host biology, host age, size, and salinity and temperature of the water of the location in the study area.

Therefore, the current study aims to: (i) Determine the *Paradiplozoon* species that infect *C. aydinensis* by collecting data from a previously unexplored location in a geographic region in Türkiye, which is different from the previous records. (ii) Increase the number of members within the Diplozoidae family documented in Türkiye. (iii) Expand our understanding of the geographical distribution and host range of Diplozoid parasite specimens in Türkiye's waters. (iv) Determine whether the influence of season and host sex on the occurrence of these parasites in *C. aydinensis*.

## MATERIALS AND METHODS

### Sampling and parasitological analysis

A total of 187 individuals of *Capoeta aydinensis* were caught by commercial fishermen in Köyceğiz lake, located in Muğla province. The collection was seasonal, from October 2019 to July 2020. The fish samples were placed in 12-liter cold chain plastic containers filled with ice molds on a fishing boat and were immediately transferred to the research laboratory. Then the fish were wrapped in aluminum foil to keep them separate and were placed in the freezer. On examination day, the fish were defrosted (in tap water) for approximately 20 minutes at room temperature. The remaining fish were defrosted one by one, following the completion of the previous examination. The sex of each fish was determined during dissection, and then the gills were examined for *Paradiplozoon*

specimens from newly defrosted fish individuals by using an Olympus stereomicroscope. The number of parasites was counted and preserved with a mixture of glycerin–ammonium picrate (Malmberg, 1957; Khotenovsky, 1974). The identification of *Paradiplozoon* specimens were performed according to morphological keys of Gussev (1985); Bychowskaya–Pavlovskaya (1962); Khotenovsky (1985) and other available references with an optical microscope. Finally, the collected diplozoid species were fixed and stored in absolute ethanol at +4 C° until DNA isolation and delivered to the Laboratory of Parasitology in Department of Public Health and Infection Diseases of “MS LAB (Eskişehir, Türkiye)”, for molecular identification. The photomicrographs of all parasite specimens were taken by using a photographic camera mounted Leica DMR microscope with phase contrast and an Olympus BX-50 research microscope.

### Molecular Analyses

Before DNA isolation, the samples fixed in alcohol were first centrifuged at 3000 RPM in 1.5 ml microcentrifuge tubes, noting that ethanol in the upper part was removed. The Genomic DNA of the parasites were extracted using the A.B.T.™ DNA Purification Kit (Qiagen, Hilden, Türkiye), by following the standard manufacturer-recommended protocol. The purity levels of the isolated DNA samples were measured first with the Maestrogen Nano (Maestrogen, Taiwan) spectrophotometer and then with the Qubit 4 fluorometer (Thermo Fisher Scientific, Waltham, MA, USA) systems. After isolation, DNA samples were amplified using Promega goTaq polymerase and buffers. A fragment of ITS2 rDNA was amplified by using primers:

D (5'GGCTYRYGGNGTCGATGAAGAACGCAG-3') and

B1 (5'GCCGGATCCGAATCCTGGTTAGTTTCTTTCT-3').

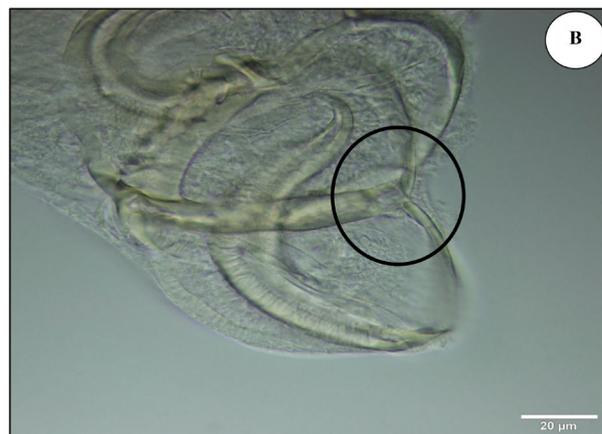
Polymerase chain reaction (PCR) was carried out according to the reaction conditions of Matejusová et al. (2001). PCR amplicons were sent to MS LAB (Eskisehir, Türkiye) for Sanger sequencing (Applied Biosystems, Forster City, CA). Post-PCR samples were verified using the Qiagen QIAxcel Advanced capillary electrophoresis system (Qiagen, Hilden, Germany) to 293 base pairs. The resulting sequencing was analyzed to distinguish species using NCBI blast program (Altschul et al., 1990). Sequence data was published to GenBank (GenBank accession number: OP723498, <http://www.ncbi.nlm.nih.gov>). The acquired nucleotide sequences were compared to *Paradiplozoon* spp. sequences supplied and found to be more than 95% identical in GenBank. A phylogram was generated using the MrBayes 3.1.2 (Huelsenbeck et al., 2001) program.

For phylogenetic analyses, the sequence obtained in this study was aligned with the data in the literature using the ClustalW algorithm in the MEGA-X (Kumar et al., 2018) program. As a result of the alignment, non-informative parts of the sequences were cut at the start and at the end. Then, the Modeltest v. 2.1.5 (Darriba et al., 2012) program was used to determine the mutation model that best matched the data

obtained. Among a total of 56 mutation models, it was determined that the most appropriate mutation model for the data set was the GTR model (general time reversible model) according to the Akaike information criterion (AIC). MrBayes 3.1.2 (Huelsenbeck et al., 2001) program was used to construct the phylogenetic tree. As an outgroup, *Sindiplozoon* spp. was used. Markov Chain Monte Carlo analysis was carried out over 4 chains. In addition, analyses were carried out for 10 million generations until the split frequency fell below 0.01. When the analysis reached saturation (ESS values), it was monitored using the Tracer v.1.7 (Rambaut et al., 2018) program. 25% of the trees obtained by sampling every 1000 generations were removed by burn-in. The consensus tree was obtained as a result of the analysis that was viewed and edited in the Figtree v1.4.2 (Rambaut 2014) program (Figure 2).

### Statistical analysis

Data on *Paradiplozoon* species was categorized according to the seasons and the sex of the host fish. The levels of prevalence, mean intensity and abundance of infection as defined by Bush et al. (1997) were calculated.



**Figure 1.** A clamp of *Paradiplozoon bliccae* isolated from *Capoeta aydinensis*; **A**-posterior view. - posterior end of median sclerite (circle indicates); **B**-anterior view. - anterior end of median sclerite. Detail of the trapeze spur and anterior joining sclerites forming a specific T-shape of the clamps (circle indicates)

Changes in infection parameters in relation with seasons are shown in Table 1. Seasonal prevalence, mean intensity and abundance of this parasite species differed between seasons. During spring, a total of 20 specimens of *P. bliccae* were found in 11 of 57 fish examined, yielding a prevalence of

Standard statistical computations (standard deviation) were carried out using Microsoft Excel (Office 2000). Kruskal-Wallis (more than two groups) tests were applied to find significant differences in the mean intensity of the parasite species for the size and seasons of host fish. The Mann-Whitney U test (two groups) was used to determine the correlation between the intensity of each helminth species infection and the host sex. The significance level of  $\alpha \leq 0.05$  was used. All statistics analyses were performed using SPSS v. 28 for Windows.

### RESULTS

On the gills of 187 *Capoeta aydinensis* individuals, one species of diplozoid was identified. Based on our detailed studies on haptor and attachment apparatuses morphology of the species, *Paradiplozoon bliccae* was identified (Figure 1A-B), and confirmed by molecular analysis. A total of 117 specimens of this parasite were found infecting 27 of the 187 fish examined, with prevalence (14.4%), a mean intensity (4.3 parasite/fish) and abundance (0.6). The seasonal variation of the infection of *P. bliccae* was also investigated in our study.

19.2%, a mean intensity of 1.8 parasites/fish, and an abundance of 0.3. For summer, 58 fish were caught and a total of 97 parasites were found in 16 of the 58 fish examined (prevalence 27.5%, mean intensity 6 parasite/fish and abundance 1.6).

**Table 1.** Prevalence and intensity values of *Paradiplozoon bliccae* in *Capoeta aydinensis* from Köyceğiz Lake according to seasons and host sex

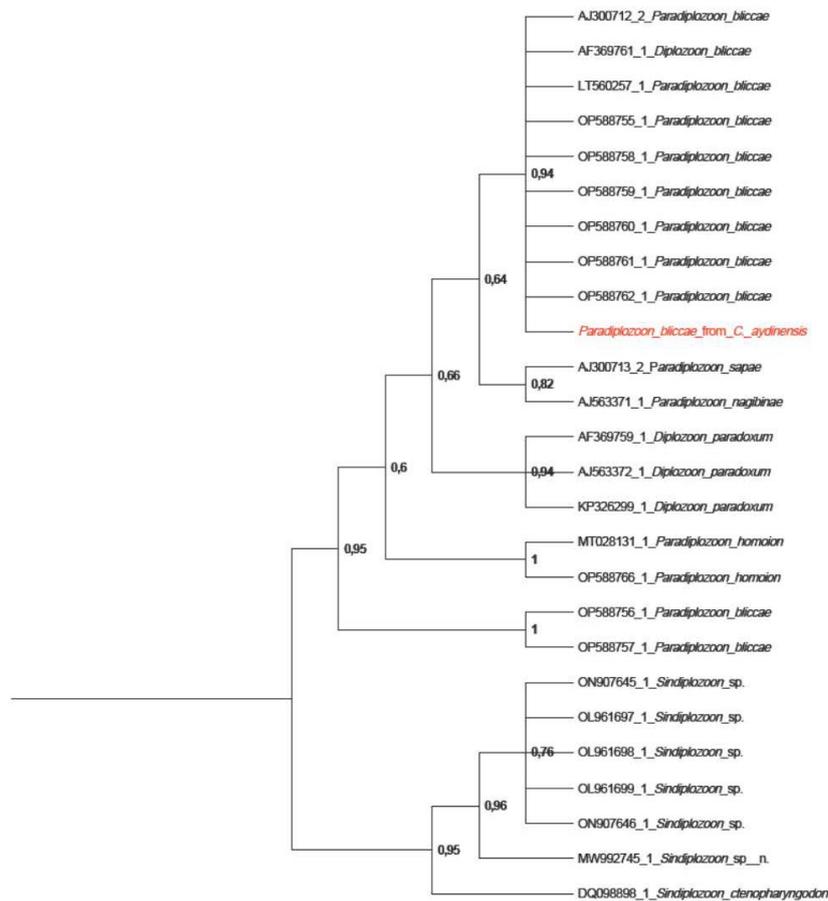
		Infection parameters			
		Prevalence (%)	Mean intensity $\pm$ SD	Abundance	Total parasite no
Seasons	Autumn (n=16)	-	-	-	-
	Winter (n=56)	-	-	-	-
	Spring (n=57)	19.2	1.8 $\pm$ 1.07	0.3	20
	Summer (n=58)	27.5	6 $\pm$ 3.15	1.6	97
Fish sex	Female (n=123)	16.2	3.3 $\pm$ 2.36	0.5	66
	Male (n=60)	11.6	7.2 $\pm$ 3.86	0.8	51

This species was not detected in the autumn and winter samples. Seasonal prevalence of infection was higher in summer, 27.5%, the highest mean intensity and abundance values were also found in summer (Table 1). According to Kruskal Wallis's-H test, there were statistically significant differences in number of parasites collected per season ( $p < 0.001$ ).

A total of 187 *C. aydinensis* individuals (123 females, 60 males, and 4 not identified) were examined for diplozoid parasites. *P. bliccae* was found in 7 of 60 male fish examined, with prevalence, mean intensity and abundance of infection of 11.6%, 7.2 parasite/fish and 0.8, respectively. A total of 66 specimens of this parasite species infected 20 of the 123 female examined fish (Table 1).

The prevalence of *P. bliccae* was higher in females (16.2%) when compared to males (11.6%) while the mean intensity and

abundance of this species was higher in males (Table 1). There was a statistically significant sex-related difference in the number of this species based on Mann-Whitney U test ( $p = 0.02$ ). The partial sequence of 293 nucleotides of the present diplozoid species was obtained in the present study and is represented in Figure 2. The BLAST analysis of these sequences revealed high homology (99.32%) and (99.32%) with *Paradiplozoon bliccae* sequences deposited by Unal et al. (2017) (GenBank LT560257), Matějusová et al. (2001) (GenBank AJ300712), respectively and high similarity (98.98%) with *P. bliccae* collected from *Squalius cii* published by Sicard et al., (2001) (GenBank AF369761) (Figure 2). The data sequence of this present diplozoid species was deposited in GenBank (accession number: OP723498). Multiple alignments were performed on *Paradiplozoon* specimens using sequencing data from NCBI GenBank and a phylogenetic tree was generated (Figure 2).



**Figure 2.** Phylogenetic tree for the relationships of *Paradiplozoon bliccae* *Paradiplozoon* spp., sequences supplied and found to be more than 95% identical in GenBank. Scale bar (=2) represents the expected number of substitutions per nucleotide

## DISCUSSION

*Capoeta aydinensis* is one of the endemic fish species that spread in the Büyük Menderes river drainages and Dalaman, Namnam and Tersakan in South-Western Türkiye (Turan et al., 2017). To our knowledge, there is only a single ichthyohelminthological data reported for *C. aydinensis* in Türkiye so far (Nejat et al., 2023).

In this study, the diplozoid parasites fauna was investigated in *C. aydinensis* from Köyceğiz Lake from Southwestern Anatolia, Türkiye. Only one diplozoid species was identified, namely *Paradiplozoon bliccae*. It was described based on the haptor and the attachments apparatus morphology. The identifying feature of *P. bliccae* is the typical shape of anterior

joining sclerites forming a specific T-shape and its trapeze spurs shapes, anterior joining of sclerites of the clamps and the size of the central hook sickle were distinguished it from other closely related species belonging to the genus *Paradiplozoon*. (Figure 1A-B, circle indicates). In addition to the morphological characters used to identify species belonging to the genus *Paradiplozoon* above, to our best knowledge, in identifying the morphological types of monogenic parasites belonging to the Diplozoidae family, the following characteristics are used; measurements and shapes of the clamps and central hook, anterior/posterior part ratios of the body, shape of the intestinal cecum ending at the back, etc. Structures selected according to taxonomic importance are used. Situations such as the continuous growth of these structures, which are important in species identification, and the change in metric measurements even within the species, make species identification of diplozoid parasites very difficult. Therefore, it is clear that it should be confirmed using molecular analysis as well as morphological characters. For these reasons, molecular analyses were carried out. And in our study, 293 bp of ITS2 gene region was replicated and compared with the data in GenBank. The molecular identification and DNA sequences using the ITS2 gene showed that the specimens from *C. aydinensis* in Köyceğiz Lake were identified as *Paradiplozoon bliccae* (Figure 2). Our samples were clustered into *Paradiplozoon* and into *Paradiplozoon bliccae* species in the BI phylogenetic tree (98- 99). For example, the sequences of *P. homoion* are 100% similar to accession number MT417728 sequences presented by Benovics et al., (2020). Several previous reports have indicated that in support of morphological data (Unal et al., 2017; İnnal et al., 2020; Nejat et al., 2023), they have used the ITS2 gene 5.8S rRNA gene to confirm the morphological identification of these diplozoid parasites.

In this aspect, the present study raises the number of reports on the molecular characterization of *Paradiplozoon* specimens collected from Türkiye. In addition, sequence data of *P. bliccae* from host fish in this locality were reported to GenBank for the first time with this study. In addition, this is the first survey on the ichthyo-helminthological data for this host fish in Köyceğiz Lake in Türkiye. Therefore, this study expands localities for *P. bliccae* in Türkiye.

In the present study, a total of 117 specimens of *P. bliccae* were found in 27 of 187 *C. aydinensis* examined with prevalence and mean intensity of 14.4% and 4.3 parasite/fish respectively. *P. bliccae* has been previously reported from only two fish species living in different habitats in Türkiye: *Pseudophoxinus burduricus* Küçük, Güllü, Güçlü, Çiftçi and Erdoğan, 2013 (Teleostei: Cyprinidae) and *Squalius fellowesii* Gunther, 1868 (Teleostei: Cypriniformes) both collected from Doğanbaba Creek with prevalence and mean intensity varying from 23.3% and 6.1 parasite/fish to 30.9% and 3 parasite/fish respectively (Unal et al., 2017; İnnal et al., 2020). These findings are inconsistent with ours. Considering the above records, this present study adds new data to the infection parameters of this diplozoid species. Furthermore, *Blicca*

*bjorkna* Linnaeus, 1758 (Cyprinidae) has been designated as a main host for this parasite, despite the fact that this diplozoid species has also been recorded in different studies from various freshwater fish species in Europe and Asia (Matějusková et al., 2001; Al-Nasiri, 2009; Sobecka et al., 2014). As for the infection results of this species in their study: infection prevalence value was 13.7%, 18.2% in *Cyprinion macrostomum*, *Cyprinus carpio* respectively from Tigris River (Al-Nasiri, 2009) 1.8% *Leuciscus idus* from Dabie Lake. Moreover, as far as we know up to now, different diplozoid specimens especially, *P. homoion* have been also recorded in previous studies in Türkiye (see, for example, Koyun, 2001; Öztürk, 2005; Soylu and Emre, 2007; Aydoğdu et al., 2020a,b). In the studies conducted on different fish species distributed in different localities in Türkiye, the prevalence levels of infection of parasite specimens belonging to the genus *Paradiplozoon* varied between 1.3% and 73.6%. However, as the authors, we suggest that the formation and distribution of diplozoid parasite specimens recorded above may be due to a combination of differences in biotic and abiotic ecological characteristics variables of the geographical location. While similarities in the prevalence level of diplozoid specimens in fish living in the same habitat can be explained by similarities in biotic and abiotic factors observed in the same locality. The differences can be attributed to the diversity of biotic and abiotic factors that vary from one aquatic ecosystem to the next.

The seasonal variation of the infection of *P. bliccae* was also investigated in our study. The prevalence and mean intensity levels of this species were both higher in summer (27.5%; 6 parasite/fish respectively) (Table 1). Seasonal variation of *P. bliccae* infection rates has also been studied in different fish species in Türkiye so far (Unal et al., 2017; İnnal et al., 2020). Seasonal variation in infection rates of Aegean chub (*Squalius fellowesii*) by Unal et al., (2017) and Burdur spring minnow (*Pseudophoxinus burduricus*) by İnnal et al., (2020) from Doğanbaba Creek, Burdur have studied. They recorded the highest infection prevalence value of *P. bliccae* in the summer (59% in *S. fellowesii*, 45.4% in *P. burduricus*). However, in both studies, the researchers recorded the highest intensity values of this species in different seasons. Unal et al. (2017) found the highest mean intensity values of this species in autumn samples (3.7 parasite/fish) while İnnal et al. (2020) recorded the highest intensity value of this species in winter samples (11.5 parasite/fish). The season with the highest infection prevalence values for this species recorded in this study was consistent with the above studies, but the season with the highest mean intensity values recorded is inconsistent.

The authors (Koyun, 2001; Öztürk, 2005; Soylu and Emre, 2007; Unal et al., 2017; Aydoğdu et al., 2020a,b; İnnal et al., 2020) studied the seasonal variability of *Paradiplozoon* spp. infection in different fish species in Türkiye and suggested that this might be due to a combination of differences in the parasite species, different rates of parasite development in different waters, the host and environmental conditions. We also support their suggestion.

In the present study, the mean intensity and abundance of *P. bliccae* infection were higher in male than female hosts (Table 1). However, the prevalence of this species was higher in females (16.2%) compared to males (11.6%). İnnal et al. (2020) recorded the highest prevalence levels of infection in female individuals of *P. burduricus*. The results of the present study also confirm the findings of İnnal et al., (2020). In contrast to our study, Unal et al., (2017) found the highest prevalence levels of this species in male fish in *S. fellowesii*. According to Rohde (1978) and Kennedy (1972), the parasites may infect both sexes differently. They suggested that this might be resulted to differences in colour, hormonal features, mucus, stress, the different feeding habits and habitat used between sexes. In our study, the host sex had a significant influence on *P. bliccae* infection parameters. The differences in these findings may be the result of the above-mentioned factors varying between sexes. This information may indicate that the female individuals of *P. burduricus* and *C. aydinensis* have similar behaviour or feeding habits.

## CONCLUSION

In this study, a total of 187 individuals of endemic fish species were examined for diplozoid parasites from October 2019 to July 2020 in Köyceğiz Lake from Southwestern Anatolia, Türkiye. By using morphological and anatomic assessment, only one diplozoid species, *Paradiplozoon bliccae*, was identified, it was confirmed by molecular characterization that these specimens recorded in the host fish are indeed *P. bliccae*. To the best of our knowledge, this is the second ichthyoparasitological study for *C. aydinensis* in Türkiye as well as the first record of *P. bliccae* from this previously unexplored host and region. It is, therefore, a new locality for the distribution of *P. bliccae*. Furthermore, this study adds new valuable information to the molecular characterization of this species collected from Türkiye. In addition, sequence data of *P. bliccae* from host fish was reported to GenBank for the first time from Köyceğiz Lake with this study. Additionally, this study provides further insight into how the infection parameters of this species vary with seasons and host fish sex.

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## AUTHOR CONTRIBUTION

Nurten Aydogdu, Nesrin Emre and Ali Aydogdu contributed to the conception, coordination and design of the study. Nesrin Emre collected the samples. Nurten Aydogdu, Nesrin Emre and Ali Aydogdu performed the laboratory activities and organized the database. Nurten Aydoğdu, Nesrin Emre and Ali Aydoğdu conducted on morphological analysis studies for the identification of diplozoid parasite species. Nurten Aydogdu, Ali Aydogdu and Özgür Emiroglu conceived of the study of diplozoid species by molecular analysis, and participated in its design and coordination and helped to confirm the morphological identity of diplozoid species by molecular analysis. Nurten Aydogdu and Ali Aydogdu participated in its design and coordination and helped to draft the manuscript. Nurten Aydogdu and Ali Aydogdu critically oversaw the substantial revisions of the manuscript.

## CONFLICT OF INTEREST STATEMENT

All authors have read and agreed to the published version of the manuscript. The authors declare that they have no conflicts of interest. The authors have also nothing to disclose

## ETHICAL APPROVAL

No ethical approval was required, as this study did not involve clinical trials or experimental procedures. During the study, no treatment/experiment was implemented on the live animal. All sampling and laboratory work on fish have complied with the Republic of Türkiye Ministry of Agriculture and Forestry Animal Welfare Laws.

## DATA AVAILABILITY

Data supporting the results are available in the manuscript.

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# Effects of different cooking methods on the proximate and fatty acid composition of Atlantic salmon (*Salmo salar*)

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**Abstract:** It is essential for human health to maintain a diet rich in unsaturated fatty acids, particularly polyunsaturated (PUFA), composed of omega-3. Atlantic salmon (*Salmo salar*), an important source of omega 3 long chain PUFAs, has a sizeable amount in international seafood trade because it is an abundant source of omega-3 long-chain PUFAs. Despite the fact that cooking fish to high temperatures alters its fat, protein, vitamin, and mineral content, cooked fish is preferred by consumers. The purpose of this research was to compare nutritional, physical and sensory properties of Atlantic salmon cooked in the oven, steamed and also a combination of the two cooking methods. Farmed Atlantic salmon was used to make steaks that were defrosted in the fridge the night before. Cooking methods applied were baking in the oven, steaming, and a combination of oven-baking and steaming. The results showed that the crude protein level of oven-baked salmon meat was greatest among all cooking methods. Heat treatment affected the fatty acid composition of Atlantic salmon flesh, as shown that the total saturated fatty acids of cooked fish groups were higher than those of raw salmon. It was determined that oven baking was the most effective heat treatment for maintaining all lipid characteristics of the meat, including the PUFA concentration and n-3/n-6 ratio. When EPA and DHA values of all cooking groups were compared, combination cooking group has lowest value than other cooking groups.

**Keywords:** Heat treatment, Atlantic salmon, omega-3, oven-baking, steaming

## INTRODUCTION

Individual diet has critical situation at prophylaxis and treatment processes, especially due to preventative medicine. Unsaturated fatty acids (UFA), which the body cannot synthesize on its own, are among the required dietary components for the human body but must be received through diet. The fatty acids, especially omega 3 and omega 6 polyunsaturated fatty acids (PUFA), were mentioned many studies on effects of them on health, and relationships between them and risk factors of the health. American Heart Association (AHA) has recommended enhancing consumption of omega-3 fatty acids for risk reduction of patients with cardiovascular diseases (CVD) (Smith Jr et al., 2011). Also, different studies have given countenance to consumption of PUFAs for the risk reduction in CVD (Wang, 2018; Jackson et al., 2019). Polyunsaturated fatty acids, especially omega 3, can protect against not only CVD also inflammatory diseases, cancer, obesity, diabetes (Gu et al., 2015; Nabavi et al., 2015; Saini and Keum, 2018), Alzheimer's disease (Song et al., 2016), kidney function (Xu et al., 2016) and major depressive disorder (Bigornia et al., 2016; Husted and Bouzinova, 2016). Alpha-Linolenic acid (ALA) (C18:3n3), Eicosapentaenoic acid (EPA) (C20:5) and Docosahexaenoic acid (DHA) (C22:6) are acceptable important omega 3 fatty acids.

One of the major sources of PUFAs is oily fish and/or fish oil. Naturally, fish and seafood consumption tend to increase a few decades. Global fisheries production has totally reached 177.8 million tonnes in 2019. Atlantic salmon (*Salmo salar*), that is a rich omega 3 long chain PUFAs resource, has a special place in the international seafood trade because of its

2.615 million tonnes production from aquaculture and 17.1 billion USD nominal value (FAO, 2021).

Fish meat is obtained by removing head, viscera, frame, fin, gill, and bone from fish. Consumers generally prefer cooked fish meat except non-heat treatment processed products for example pickled, dried and/or salted fish or some ethno-traditional products like sashimi. However, a high temperature has the potential to reduce the number of PUFAs in the flesh, particularly EPA and DHA, by destroying carbon double bonds. Additionally, the application of heat treatment results in a shift in the proportions of total fat, total protein, vitamins, and minerals found in fish meat. Fish cooking uses different techniques such as oven-baking, microwaving, frying (pan- or deep-), poaching, boiling, and grilling etc. These techniques are usually used as domestic cooking. During Covid19 pandemics, most of governments all on the world introduced restrictions for preventing spread of the disease such as closing up restaurants, diners, snack bars etc. Due to the influence of social media, many people have experimented with different culinary methods at home.

Oven-baking, which is a dry-heat cooking technique (Moradi et al., 2011; Sampels, 2015), is one of most used of them. Recent studies have reported that oven baking was best method for nutritional quality and PUFAs of cooked fish (Şengör et al., 2013; Hosseini et al., 2014; Vikøren et al., 2017). In addition, Erdem and Dinçer (2019) have informed that oven baking was optimal cooking technique for nutritional properties of flesh in their study.

Already, mild- and moist-heat treatments like steaming (Moradi et al., 2011; Sampels, 2015) are also popular in household. There are several studies reported that nutritional values of steamed fish meat have been closest those of raw fish meat (Choo et al., 2018; Cano-Estrada et al., 2018; Dong et al., 2018). Oven-baking and steaming are two cooking techniques with different characteristics. The study's objective is to examine the nutritional, sensory, and occasionally physical characteristics of oven-baked, steam-cooked and also combination these methods on Atlantic salmon (*Salmo salar*). In the experimental plan, two different cooking methods were used in combination in order to identify changes in the fatty acid composition and lipid index values of fish meat.

## MATERIALS AND METHODS

### Fish samples

Salmon steaks from farmed Atlantic salmon (*Salmo salar*) that were shipped from Norway as frozen were acquired from a global supplier and totalled 61 pieces each of  $113.89 \pm 3.31$  g. 10 pieces were used as raw material for proximate composition, fatty acids composition, lipid quality indices and colour measurement. Before cooking, each sample was defrosted overnight in a refrigerator at 4°C.

### Cooking methods

The cooking time of 18 minutes was determined based on the salmon meat's ability to maintain a consistent internal temperature of 63°C during the steaming process (USDA, 2023). Three different techniques were used. First batch used 17 Atlantic salmon pieces was cooked by using oven, second batch used 17 Atlantic salmon pieces was cooked by using water vapour and the last process used 17 Atlantic salmon pieces was the combination of both two cooking techniques. For oven baking, 18 minutes heating at 180°C were used within a conventional oven as preheated (Öztiryakiler Industrial Conventional Oven GN 1/1 Model, Turkey). The final internal temperature of oven-baked salmon meat was recorded at 70.8°C. For steaming, water (250 ml) was boiled in cooking pot (diameter: 20 cm; height: 12 cm) and a stainless-steel mesh strainer was placed in same pot. During steaming, salmon meat did not touch water just the vapour was used. Steaming occurred for 18 minutes at 100°C. For the combination method, steaming was firstly applied for 9 minutes, and then oven baking was performed for 9 minutes.

### Proximate composition

Atlantic salmon were homogenised using an electric chopper (Arzum AR1021, Turkey). Moisture and ash analyses were gravimetrically performed salmon pieces by placing into a glass petri dish at 105°C and a porcelain crucible at 550°C, respectively (Ludorf and Meyer, 1973). Sample and reagent for crude oil analysis (chloroform / methanol; 2/1) were mixed with a homogeniser, then solvents in permeate was evaporated (Bligh and Dyer, 1959). Crude oil percentage was calculated gravimetrically. Kjeldahl method was utilised for crude protein analysis (N×6.25) via Gerhardt Vapodest 40 according to

A.O.A.C. (1984) official method.

### Fatty acids analysis

Atlantic salmon steak oil that had been extracted from raw and cooked salmon steak was analysed using gas chromatography (GC) (Shimadzu Corp., Kyoto, Japan) to ascertain its fatty acids composition (FAC). Methyl esters were prepared by dissolving 10 mg of extracted oil in 2 mL of n-hexane and then adding 4 mL of (2 mol/L) KOH to methanol, as described by Ichihara et al. (1996). After centrifugation at 1792g, the N-hexane layer was separated out (Özogul and Özogul, 2007). Capillary column GC (HP-88; 100 m 0.25 mm i.d., 0.20 m film thickness; Agilent Technologies International Japan, Tokyo, Japan) equipped with a flame ionisation detector was used to identify fatty acid methyl esters. First, the column was heated from 120 to 170 °C at a rate of 10 °C/min, then it was heated to 250 °C at a rate of 4 °C/min, and finally it was maintained at 250 °C for 5 minutes. The flame ionisation detector was heated to a comfortable 260°C. A 1L sample was divided and injected at a 1:50 ratio. The concentration was determined by comparing the peak area of the samples to that of the mix standard. The average percentage of the overall FAME area was used to express the results of the three replicate GC analyses.

### Lipid quality

The atherogenic and thrombogenic indices (AI and TI, respectively) were derived using Ulbricht and Southgate equations (1991) to assess the likelihood that cooked samples would cause coronary heart disease. However, it is important to prioritise health while choosing a cooking method. Hypocholesterolemic/Hypercholesterolemic ratio (h/H) was calculated according to Santos-Silva et al. (2002). Flesh lipid quality index is calculated by relating the levels of the principal polyunsaturated fatty acids (PUFAs) n-3 eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) in the flesh to the overall lipid content of the flesh as a percentage (Abrami et al., 1992; Senso et al., 2007).

### Cooking loss

Using an equation inspired by Gluchowski et al. (2020), cooking loss was determined as a percentage from the difference in weights of the Atlantic salmon flesh before and after cooking.

### Colour measurement

The colour measurement method reported by Schubring (2003) was used.  $L^*$  (lightness),  $a^*$  (redness) and  $b^*$  (yellowness) values of CIElab colour space, were determined with measuring 10 times from the raw and cooked Atlantic salmon placed into a glass petri dish, after steaks mixed homogeneously by a chopper.

### Sensory evaluation

Seven assessors with experience in the sensory evaluation of fish products used a methodology described by Carbonell et

al. (2002). Odour, appearance, flavour, texture, and general acceptance were all rated as sensory criteria. The evaluation of attributes ranged from 1 (weak) to 5 (intense).

### Statistical analysis

The data was displayed as mean standard deviation. One-way ANOVA analysis was used to describe the variations in means. To examine for significant differences between the mean values of the various outcomes, the SPSS 25 program's Tukey test was utilised.  $P < 0.05$  was used as the significance level for all groups.

## RESULTS AND DISCUSSION

### Results of proximate analyses

Proximate compositional effects of different cooking techniques on salmon meat can be seen at Table 1.

**Table 1.** Proximate composition results (g/100 g)

Proximate composition	Raw salmon	Oven baking	Steaming	Combination cooking
Crude protein	19.33±0.44 <sup>a</sup>	19.90±0.76 <sup>ab</sup>	22.53±0.20 <sup>b</sup>	23.14±1.97 <sup>b</sup>
Crude fat	14.52±0.13 <sup>a</sup>	26.38±1.87 <sup>b</sup>	20.52±0.72 <sup>c</sup>	19.38±0.38 <sup>c</sup>
Moisture	63.00±0.42 <sup>a</sup>	51.26±0.54 <sup>b</sup>	53.74±0.60 <sup>c</sup>	54.53±0.59 <sup>c</sup>
Ash	1.24±0.17 <sup>a</sup>	1.14±0.01 <sup>a</sup>	1.24±0.08 <sup>a</sup>	1.08±0.02 <sup>a</sup>

At the level of  $P < 0.05$  significances, the same letter of meaning on the same line do not differ in any appreciable ways

In the study, the untreated group is defined as the raw salmon group (control group) to be used in comparisons to determine the effects of cooking techniques. As shown in Table 1 raw salmon steaks have the lowest crude fat percentage than those of cooked salmon groups (Table 1). The cooked groups demonstrated a significant increase in crude fat percentages as a result of water extraction in salmon meat, as anticipated due to the use of heat treatment. This situation depends on cooking time and temperature as mentioned before (Bastias et al., 2017). The findings indicate that the oven-baked salmon group exhibits the highest crude fat percentage, which aligns with the findings of previous studies (Şengör et al., 2013; Hosseini et al., 2014; Nieva-Echevarría et al., 2018). Oven-baking as a dry-heat cooking method may accelerates evaporation from salmon meat.

The moisture percentage of raw salmon is 1.23, 1.17 and 1.15 times more than oven-baking, steaming and combination cooking, respectively. Crude fat contents of oven-baking, steaming and combination cooking groups, are respectively approximately 1.82, 1.41 and 1.33 times more than uncooked salmon's. Although all cooking groups were used the same time (18 minutes), temperature used in oven-baking affected moisture and crude fat percentage. Therefore, crude fat and moisture contents of oven baking salmon meat have showed statistically significance ( $P < 0.05$ ). This result can be explained as the low amount of moisture in the oven environment and the high amount of evaporated water. There are studies informed that oven baked salmon meat has higher lipid percentage than

steamed salmon meat vice versa moisture percentage (Larsen et al., 2010; Şengör et al., 2013; Fomena Temgoua et al., 2022). There was no statistically significant difference observed in the ash contents among all groups ( $P < 0.05$ ).

Cooked salmon steaks by a combination method of steaming and oven baking has shown highest crude protein content. Although, crude protein values of oven-baked salmon is higher than those of steamed salmon in recent studies (Bastias et al., 2017; Gluchowski et al., 2020; Fomena Temgoua et al., 2022), steamed salmon's protein percentage is higher than that of oven-baked salmon in the present study. There was no statistically significant difference among the groups of cooked salmon in terms of crude protein content ( $P > 0.05$ ). Oven-baked salmon meat has shown the lowest protein value in all cooked groups. Protein denaturalization may be discussed for oven-baked salmon meat; as a consequence, it was exposed to higher temperatures for a longer time than the others.

### Fatty acids composition

Table 2 shows how different cooking techniques affect the fatty acid composition of Atlantic salmon meat. As a consequence of heat treatment, total saturated fatty acids ( $\sum$ SFA) of cooked salmon groups increased according to initial value of raw salmon in Table 2. While comparing the three prepared groups, it was observed that the steamed group had the lowest increase in  $\sum$ SFA. However, it was noted that the level of palmitic acid (C16:0) in the steamed salmon meat increased, but it reduced in both the oven-baked group and the combination cooking group. There was no statistically significant difference ( $P < 0.05$ ) observed in the value of C16:0 between steaming salmon meat and raw salmon. Although stearic acid (C18:0) was no in raw salmon meat, was seen in both oven-baked and combination cooked salmon meat groups.

The application of the oven temperature of 180°C has the potential to induce lipid oxidation and lipid hydrolysis in crude fats of salmon meat. The oven-baking group has the lowest values of both total monounsaturated fatty acids ( $\sum$ MUFA) at 47.12 and oleic acid (C18:1n9c) at 38.44%. Linoleic acid (C18:2n6c) has shown reductions for oven-baked and combination cooked salmon in comparison with the initial value because of probably high temperature and dry heating from the oven. The statistical analysis of eicosapentaenoic acid (EPA) (C20:5) and docosahexaenoic acid (DHA) (C22:6) levels in salmon meat indicates that there is a significant difference ( $P < 0.05$ ) between the steaming and combination cooking methods (oven baking and steaming) compared to the raw and oven baking methods. The combination cooking of salmon meat has been found to yield a statistically significant difference ( $P < 0.05$ ) in the  $\alpha$ -linolenic acid (ALA) (C18:3n3) content, with the lowest value seen compared to the other groups. The EPA and ALA values of all cooked salmon groups exhibited a decrease as a result of heat treatment. Nevertheless, the cooked groups, excluding oven baking, exhibited a decrease in DHA value.

**Table 2.** Fatty acid composition results of groups (g/100 g of total fatty acids)

Fatty acids	Raw salmon	Oven baking	Steaming	Combination cooking
C4:0	0.04±0.00 <sup>a</sup>	0.04±0.00 <sup>a</sup>	0.04±0.01 <sup>a</sup>	0.05±0.00 <sup>a</sup>
C8:0	0.01±0.00 <sup>a</sup>	0.0±0.0 <sup>a</sup>	0.02±0.00 <sup>b</sup>	0.02±0.00 <sup>b</sup>
C10:0	0.00±0.00 <sup>a</sup>	0.00±0.00 <sup>b</sup>	0.01±0.00 <sup>c</sup>	0.01±0.00 <sup>ac</sup>
C12:0	0.04±0.01 <sup>a</sup>	0.03±0.00 <sup>a</sup>	0.04±0.00 <sup>a</sup>	0.03±0.00 <sup>a</sup>
C13:0	0.01±0.00 <sup>a</sup>	0.01±0.00 <sup>a</sup>	0.01±0.00 <sup>a</sup>	0.01±0.00 <sup>a</sup>
C14:0	1.89±0.02 <sup>a</sup>	1.85±0.02 <sup>a</sup>	1.99±0.02 <sup>b</sup>	1.88±0.01 <sup>a</sup>
C15:0	0.16±0.00 <sup>a</sup>	0.16±0.00 <sup>a</sup>	0.18±0.00 <sup>b</sup>	0.16±0.00 <sup>a</sup>
C16:0	10.25±0.04 <sup>a</sup>	9.67±0.07 <sup>b</sup>	10.36±0.05 <sup>a</sup>	9.91±0.02 <sup>c</sup>
C17:0	0.17±0.00 <sup>a</sup>	0.16±0.00 <sup>b</sup>	0.18±0.00 <sup>c</sup>	0.17±0.00 <sup>a</sup>
C18:0	0.0±0.0 <sup>a</sup>	3.09±0.02 <sup>b</sup>	0.0±0.0 <sup>a</sup>	3.20±0.01 <sup>c</sup>
C20:0	0.55±0.01 <sup>a</sup>	0.55±0.05 <sup>a</sup>	0.59±0.03 <sup>a</sup>	0.55±0.00 <sup>a</sup>
C21:0	0.02±0.00 <sup>a</sup>	0.0±0.0 <sup>b</sup>	0.0±0.0 <sup>b</sup>	0.02±0.00 <sup>c</sup>
C22:0	0.24±0.00 <sup>a</sup>	0.24±0.03 <sup>a</sup>	0.25±0.03 <sup>a</sup>	0.24±0.00 <sup>a</sup>
C23:0	0.28±0.03 <sup>a</sup>	0.30±0.02 <sup>a</sup>	0.27±0.03 <sup>a</sup>	0.27±0.01 <sup>a</sup>
C24:0	0.14±0.01 <sup>a</sup>	0.11±0.01 <sup>b</sup>	0.0±0.0 <sup>a</sup>	0.11±0.00 <sup>c</sup>
∑SFA	13.80	16.21	13.94	16.63
C14:1	0.01±0.00 <sup>a</sup>	0.02±0.00 <sup>a</sup>	0.01±0.00 <sup>a</sup>	0.01±0.00 <sup>a</sup>
C16:1	2.27±0.02 <sup>a</sup>	2.09±0.02 <sup>b</sup>	2.14±0.01 <sup>c</sup>	2.12±0.01 <sup>bc</sup>
C18:1n9t	0.05±0.01 <sup>a</sup>	0.0±0.0 <sup>b</sup>	0.05±0.00 <sup>a</sup>	0.05±0.00 <sup>a</sup>
C18:1n9c	39.60±0.03 <sup>ac</sup>	38.44±0.41 <sup>b</sup>	40.13±0.14 <sup>a</sup>	39.08±0.04 <sup>c</sup>
C20:1	5.43±0.04 <sup>a</sup>	5.39±0.06 <sup>a</sup>	5.78±0.02 <sup>b</sup>	5.56±0.01 <sup>c</sup>
C22:1n9	0.85±0.03 <sup>a</sup>	0.82±0.04 <sup>a</sup>	0.87±0.01 <sup>a</sup>	0.84±0.01 <sup>a</sup>
C24:1	0.47±0.02 <sup>a</sup>	0.40±0.0 <sup>b</sup>	0.47±0.02 <sup>a</sup>	0.42±0.00 <sup>b</sup>
∑MUFA	48.68	47.12	49.45	48.08
C18:2n6c	16.70±0.03 <sup>a</sup>	16.14±0.14 <sup>b</sup>	16.84±0.07 <sup>a</sup>	16.14±0.01 <sup>b</sup>
C18:3n6	0.10±0.01 <sup>ac</sup>	0.13±0.01 <sup>b</sup>	0.10±0.00 <sup>a</sup>	0.11±0.00 <sup>c</sup>
C18:3n3	10.40±0.02 <sup>a</sup>	10.07±0.06 <sup>b</sup>	10.07±0.03 <sup>b</sup>	9.70±0.01 <sup>c</sup>
C20:2	1.72±0.01 <sup>a</sup>	1.63±0.10 <sup>a</sup>	1.72±0.03 <sup>a</sup>	1.64±0.01 <sup>a</sup>
C20:3n6	0.21±0.00 <sup>a</sup>	0.29±0.01 <sup>b</sup>	0.22±0.02 <sup>a</sup>	0.25±0.01 <sup>c</sup>
C20:3n3	1.01±0.00 <sup>a</sup>	1.03±0.02 <sup>a</sup>	1.06±0.10 <sup>a</sup>	1.00±0.01 <sup>a</sup>
C22:2	0.18±0.04 <sup>a</sup>	0.14±0.01 <sup>a</sup>	0.15±0.04 <sup>a</sup>	0.12±0.03 <sup>a</sup>
C20:5	2.82±0.04 <sup>a</sup>	2.68±0.03 <sup>b</sup>	2.47±0.05 <sup>c</sup>	2.42±0.01 <sup>c</sup>
C22:6	4.37±0.03 <sup>a</sup>	4.53±0.06 <sup>b</sup>	3.97±0.03 <sup>c</sup>	3.89±0.01 <sup>c</sup>
∑PUFA	37.51	36.64	36.60	35.27
PUFA/SFA	2.71	2.26	2.62	2.12
∑n6	17.02±0.03 <sup>a</sup>	16.55±0.15 <sup>b</sup>	17.17±0.07 <sup>a</sup>	16.50±0.01 <sup>b</sup>
∑n3	18.61±0.05 <sup>a</sup>	18.30±0.16 <sup>a</sup>	17.57±0.15 <sup>b</sup>	17.01±0.04 <sup>b</sup>
∑n3/∑n6	1.09	1.10	1.02	1.03
DHA/EPA	1.55	1.69	1.60	1.61

At the level of P<0.05 significances, the same letter of meaning on the same line do not differ in any appreciable ways

The samples were analysed using a combination cooking method to find the lowest values for several parameters, including total polyunsaturated fatty acids (∑PUFA), the ratio of polyunsaturated fatty acids to saturated fatty acids (PUFA/SFA), total omega 6 fatty acids (∑n6), and total omega 3 fatty acids (∑n3). The group that undergoes oven baking exhibits the highest value for the ratios of ∑n3/∑n6 and

DHA/EPA when compared to all other groups. Even though ∑n6 values for the steamed group were found to be higher than that of the uncooked samples, ∑n6 values fell after cooking the salmon meat groups using oven-baking and combination cooking methods, as seen in Table 2. However, these differences have no statistically meaning (P<0.05). DHA/EPA was seen to be lower in raw salmon compared to the three other groups, although PUFA/SFA ratio of raw salmon was the highest value.

Oven baking, out of all the thermo-processes examined, was shown to be the most efficient heat treatment for preserving all lipid attributes of the meat, such as the PUFA content and n-3/n-6 ratio (Table 2). The effects shown in previous studies exhibit variation contingent upon the cooking manner employed and the impact of heat (Garcia-Arias et al., 2003; Gladyshev et al., 2006; Sioen et al., 2006; Schneedorferova et al., 2015). The consumption of foods that are abundant in omega-3 polyunsaturated fatty acids (PUFAs) is associated with numerous advantages, primarily attributed to their good impact on human well-being. However, the thermal treatments had a significant impact on the most widely recognised EPA and ∑PUFA, observed across all groups, with the combination cooking group exhibiting the lowest levels of these substances. A same movement was likewise detected in ALA. The three main types of n-3 polyunsaturated fatty acids, namely ALA, DHA and EPA, are predominantly obtained from seafood and are effectively utilised by the human body (Ng, 2006). According to Grosso et al. (2014), the primary omega-3 FA, ALA, can be converted into long-chain PUFA as well as DHA and EPA. The aforementioned results provide further support for the argument that ALA remains a viable precursor for the synthesis of EPA and DHA, primarily due to its limited influence during the thermal processing. The effects of various cooking techniques on the fatty acid content of different fish species have been the subject of numerous research.

According to a study conducted by Koubaa et al. (2012), the effects of steaming and oven-baking on the fatty acid profiles of cooked fish species were found to have minimal affect. Similarly, Moradi et al. (2009), indicated that the oven-baking technique resulted in little alterations in both the fat content and fatty acid composition of the fillets of *Parastromateus niager*. Furthermore, the utilisation of the oven baking technique resulted in an enhancement in the quantity of EPA and DHA in grams within the meat of New Zealand king salmon (Larsen et al., 2010). The ratio of n3/n6 fatty acids in the oven-baked salmon was found to be higher in comparison to the steamed salmon (Şengör et al., 2013). On the other hand, a previous study conducted by Fomena Temgoua et al. (2022), has reported that the concentration of n-3/n-6 and EPA+DHA in steamed salmon is significantly higher (p < 0.05) compared to the oven-baking treatment. The preservation of EPA and DHA content in rainbow trout is maximised through the process of steaming (Cano-Estrada et al., 2018). The findings in the present study indicate that oven-baking had a higher positive impact on the content of n3/n6, EPA, DHA, and ∑PUFA in salmon meat compared to steaming. The observed

variations in outcomes among same cooking processes, as previously discussed, may be attributed to factors such as the application method, cooking duration, or temperature.

### Values of lipid quality indexes

Lipid quality indices' results can be seen in Table 3. Lower values of both AI and TI indicate superior nutritional quality of fatty acids. Consequently, diets characterised by low AI and TI values have the potential to mitigate the risk of developing coronary heart disease (CHD). Higher values of the h/H ratio are beneficial when considering the specific effects of fatty acids on cholesterol metabolism. h/H ratio possesses the capacity to offer a more accurate evaluation of the influence of fatty acid composition on cardiovascular disease (Karimian-Khosroshahi et al., 2016; Chen and Liu, 2020). FLQ index can be regarded as an adjunct to EPA + DHA, given that the absolute quantity of EPA and DHA holds greater significance (Senso et al., 2007; Chen and Liu, 2020). Oven-baked salmon flesh has lowest value of AI and highest value of FLQ and h/H. However, steamed salmon flesh has highest value of AI and, lowest value of FLQ, TI and h/H. For AI, determined raw salmon value has no statistically difference ( $P>0.05$ ) when compared with oven baking and combination cooking groups, separately. Highest value of TI is 0.17 was determined in combination cooking groups. h/H ratios of raw and combination cooking salmon showed no statistically significance ( $P>0.05$ ) but statistical differences were determined in oven baking and steaming groups.

**Table 3.** Results of lipid quality indexes (%)

Lipid Quality Indexes	Raw salmon	Oven baking	Steaming	Combination cooking
AI (%)	0.21±0.0 <sup>ac</sup>	0.20±0.0 <sup>a</sup>	0.22±0.0 <sup>b</sup>	0.21±0.0 <sup>c</sup>
TI (%)	0.14±0.0 <sup>a</sup>	0.15±0.02 <sup>ab</sup>	0.14±0.0 <sup>a</sup>	0.17±0.0 <sup>b</sup>
FLQ (%)	7.19±0.07 <sup>a</sup>	7.21±0.09 <sup>a</sup>	6.32±0.02 <sup>b</sup>	6.43±0.06 <sup>b</sup>
h/H (%)	5.75±0.02 <sup>a</sup>	5.88±0.04 <sup>b</sup>	5.65±0.03 <sup>c</sup>	5.74±0.02 <sup>a</sup>

At the level of  $P<0.05$  significances, the same letter of meaning on the same line do not differ in any appreciable ways. AI: Atherogenic Index. TI: Thrombogenic Index. FLQ: Flesh Lipid Quality Index. h/H: Hypocholesterolemic/ Hypercholesterolemic ratio

### Cooking loss results

Heat treatment effects on cooking loss values on salmon flesh can be seen at Table 4.

**Table 4.** Initial and cooked weights (g) and cooking loss percentages of salmon steaks

	Oven baking	Steaming	Combination cooking
Initial weight (g)	114.21±2.30 <sup>a</sup>	115.22±4.27 <sup>a</sup>	113.29±4.15 <sup>a</sup>
Cooked weight (g)	100.30±1.86 <sup>a</sup>	102.37±3.83 <sup>a</sup>	101.11±3.71 <sup>a</sup>
Cooking loss (%)	12.17±0.15 <sup>a</sup>	12.24±0.07 <sup>a</sup>	9.63±0.12 <sup>b</sup>

At the level of  $P<0.05$  significances, the same letter of meaning on the same line does not differ in any appreciable ways

Water and volatiles within salmon meat retires with increase of heat and temperature. This leads to a loss at total

weight. Cooking loss percentages for three cooking methods were given at Table 4. Steamed salmon steaks showed highest percentage of cooking loss. Salmon steaks by cooking combination methods had the lowest cooking loss value. Between the oven baking and steaming techniques no statistical difference was determined. However, significant differences were seen when compared with these two techniques with the combination cooking techniques. The combination method's water holding capacity was greater than that of the other procedures, as shown in Table 4. This may be the reason of heat treatment techniques and time. Combination method first treatment was steaming (9 min) this process may keep the moisture of the salmon meat later oven baking (9 min) treatment decrease the moisture of the salmon meat (evaporation). But the process time of the heat treatments were 50% lower than each techniques, this was the reason of determining higher water holding capacity (lower Cooking loss). Similar results were also determined in previous studies in Szlinder-Richert and Malesa-Ciecwierz, 2018. Although cooking loss value depends on cooking method and fish species (Szlinder-Richert and Malesa-Ciecwierz, 2018), the results of oven baked and steamed salmon steaks have nearly given the same values. However, 11.6% value of cooking loss of salmon fillet by steamed similarly above-mentioned method (Gluchowski et al., 2020) was not statistically differed the present steamed salmon steaks' value. Steaming, a relatively mild heating process, is expected reducing cooking losses (Wang et al., 2020).

### Colour measurements

Following the cooking process, the lightness parameters ( $L^*$ ) of the salmon steaks exhibited an increase (Table 5). Statistically significance ( $P<0.05$ ) between  $L^*$  results of cooked salmon meat groups and raw salmon meat was determined. Salmon meat cooked by combination method of oven baking and steaming has highest  $L^*$  value, but lowest  $a^*$  (redness) and  $b^*$  (yellowness) value.  $a^*$  value of oven baked salmon meat increased while the others decreased after cooking and differed statistically significance ( $P<0.05$ ) from other cooked salmon meat groups.

**Table 5.** Colour measurements

	Raw salmon	Oven baking	Steaming	Combination cooking
$L^*$	63.42±3.71 <sup>a</sup>	72.40±6.30 <sup>b</sup>	76.44±7.90 <sup>b</sup>	76.55±4.17 <sup>b</sup>
$a^*$	13.63±0.85 <sup>a</sup>	13.97±0.53 <sup>a</sup>	11.01±0.97 <sup>b</sup>	10.86±0.75 <sup>b</sup>
$b^*$	21.87±1.73 <sup>a</sup>	20.82±2.39 <sup>a</sup>	20.12±1.66 <sup>ab</sup>	18.35±1.59 <sup>b</sup>

At the level of  $P<0.05$  significances, the same letter of meaning on the same line do not differ in any appreciable ways

The observed increases in  $L^*$  values among the cooked salmon meat groups may be attributed to the denaturation of proteins and subsequent whitening of the meat that occurs during the heating process (Wan et al., 2019). Wang et al. (2020) reported the natural pink colour of the whitefish (*Coregonus peled*) muscle rapidly transitions to a pale whitish colour during the process of steam cooking. This change is accompanied by an increase in the  $L^*$  value, reaching a high

reading at a specific time point. The observed rise in  $L^*$  value during the initial phase of steaming can be attributed to the progressive denaturation of myosin and the oxidation of haemoglobin and myoglobin. As the myosin underwent incremental modifications, the pigmentation of the fish progressively transitioned to a white colour (Wan et al., 2019; Wang et al., 2020). In the context of combination cooking, the  $L^*$  value exhibited a modest increase compared to that of steamed salmon meat. This might perhaps be attributed to the occurrence of browning events on involving proteins, or amines, as well as protein-lipid reactions. The changes in the  $a^*$  values of steamed and combination cooked samples were

impacted by the oxidation of haemoglobin that takes place during the cooking process, which may lead to a reduction in the  $a^*$  values (Thanonkaew et al., 2006; Wan et al., 2019).

### Sensory evaluation

Sensorial panel results of the groups can be seen at Figure 1. Oven-baked salmon showed highest scores in appearance, odour and flavour. Steamed salmon has given lowest results for all criteria except odour. Odour scores of oven baked, steamed and combination-cooked salmon was respectively presented  $4.14 \pm 0.69$ ,  $3.42 \pm 0.78$  and  $3.28 \pm 0.75$ . No statistical differences were found in all criteria ( $P < 0.05$ ).

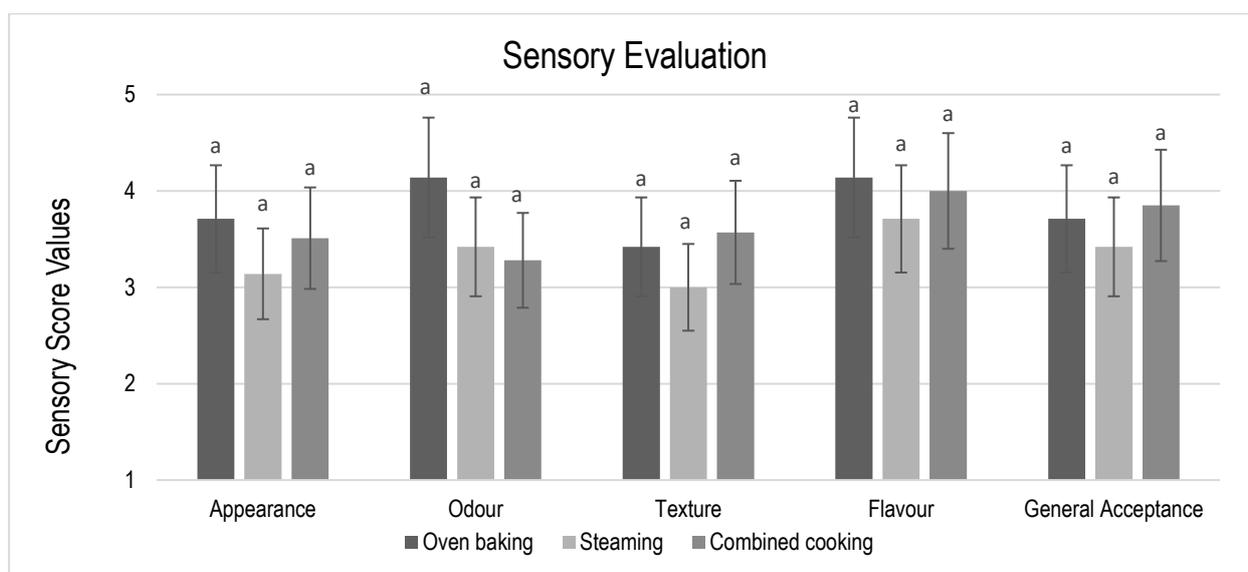


Figure 1. Sensory evaluation results of cooked salmons

Due to the results preferences in parameter of general acceptance are given as follows; Combination cooking> Oven baking>steaming. A comprehensive assessment of sensory criteria has been conducted by Larsen et al. (2011), revealing that the oven-baking procedure resulted in an enhanced preference for salmon meat. In the sensory evaluation of king salmon subjected to various heat treatments, it was observed that oven-baking was preferred above alternative methods such as steaming. In the sensory evaluation, oven-baked king salmon received the highest ratings in terms of colour, texture, and scent criteria, indicating its superior quality. Conversely, steamed king salmon was found to be less attractive in comparison (Larsen et al., 2011). The firm and chewy texture of oven-baked salmon meat is a result of the dehydration process that takes place during preparation, which reduces its moisture content. The high temperatures can also enhance the formation of corresponding smells, tastes, and flavours. In a study conducted by Alexi et al. (2019), it was shown that both steam-cooking and oven-cooking methods yielded comparable sensory profiles for meagre and gilthead seabream. The varying impact of culinary techniques on the lipid and sensory attributes of meagre and gilthead seabream suggests that a universal guideline cannot be used. Instead, the selection of a specific preparation method should be contingent upon the fish species and their corresponding fat composition.

### CONCLUSION

The primary objective of this study was to investigate the effects of combining oven baking and steaming techniques on the nutritional characteristics, fatty acid content, and lipid indices of Atlantic salmon. While heat treatments of salmon meat decreased  $\Sigma n3$  values, oven baking salmon meat was affected at least. The Atlantic Salmon exhibited an elevation in  $\Sigma n6$  fatty acid content during the steaming procedure. The study findings indicate that the combination cooking method yields the most favourable value in terms of PUFA/SFA ratio. Based on the analysis of  $\Sigma n3/\Sigma n6$  and DHA/EPA values, it can be concluded that oven-baking is marginally more efficient compared to other heat treatments.

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### AUTHOR CONTRIBUTIONS

Ömer Alper Erdem: Performed heat treatment processes, proximate analyses, cook loss, colour measurements, sensory evaluation, statistical analyses, writing- original draft. Mehmet Tolga Dinçer: Performed supplies frozen Atlantic salmon

steaks, heat treatment processes, cook loss, sensory evaluation, fatty acids composition, statistical analyses, writing-original draft.

### CONFLICTS OF INTEREST

The authors declare that there are no conflicts of interest or competing interests.

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### ETHICS APPROVAL

No specific ethical approval was necessary for the study.

### DATA AVAILABILITY

For any questions, the corresponding author should be contacted.

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# Effects of feeding different densities of *Artemia* nauplii on the growth and survival of larvae of the hairy river prawn, *Macrobrachium rude* (Heller, 1862)

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**Abstract:** The effects of feeding at different densities of *Artemia* nauplii on the growth and survival of *Macrobrachium rude* larvae were explored in this study. Two experiments were carried out. In the first trial, larvae were fed three different feeding densities: 1, 3, and 5 nauplii/mL. In the second experiment, feeding densities of 5, 10, and 15 nauplii/mL were used to determine the maximal feeding density of *Artemia* nauplii for *M. rude* larvae. There were no significant differences statistically in growth rate or survival between larvae fed 1, 3, or 5 nauplii/mL ( $P>0.05$ ). Increased feeding density from 5 to 10 nauplii/mL resulted in growth but drastically decreased survival. Feeding above 10 nauplii/mL decreased both growth rate and survival. According to the results of the study, the optimal feeding density of *M. rude* with *Artemia* nauplii should be between 5 and 10 nauplii/mL. The study suggests further research into determining ideal feeding density at various phases of larval development in order to better understand the individual feeding requirements at each stage.

**Keywords:** Survival rate, total length, gain in length, water quality, broodstock

## INTRODUCTION

Freshwater prawn of the genus *Macrobrachium* are decapods, palemonids and are found on all continents except Europe. *Macrobrachium* is a diverse group of about 240 species, showing great similarity (Makombu et al., 2015). *Macrobrachium* prawn has a very diverse habitat, distributed in rivers, lakes, ponds, irrigation ditches, and aqueducts in subtropical and tropical climates (Valencia and Campos, 2007). Although they spend most of their time in freshwater, the majority of prawn species migrate to brackish water, mainly during the reproductive and larval stages of development, to complete their life cycle (Lima et al., 1997; Barbieri et al., 2016). In general, *Macrobrachium* prawn reach an adult size large enough to be eaten by humans. Prawns are mainly the target of artisanal fishermen and an important source of income in many developing countries, especially in Africa (Nwosu and Wolfi, 2006). About 10 species of *Macrobrachium* prawns have been described from Africa (Makombu et al., 2015). Among the species of interest is the hairy prawn (*M. rude*), which is associated with the economy of small-scale fishermen in Thailand, India, Kenya and Tanzania (Schoonbee et al., 1989). *M. rude* is the most abundant freshwater prawn species in Kenya, accounting for about 11% of all prawns caught by

small-scale fishermen (Kimani et al., 2018). It is distributed in two major freshwater rivers in Kenya, namely the Tana and Athi rivers where prawns are harvested by small-scale fishermen from these rivers and sold to local people as an important source of food, employment and livelihood for people in Tana River and Kilifi counties, Kenya (Kimani et al., 2018; Kochev, 2018). *M. rude* presence in both rivers has been reported in most months of the year except March, June, October and November, with a peak in January, April, September and May (Kochev, 2018). Due to overfishing and seasonality of river species, catch rates have plummeted, affecting the incomes of small-scale fishermen and fish-dependent traders (Kimani et al., 2018). It is also reported that female prawns with eggs are more preferred by consumers and are sold by the majority of fishermen (Kochev, 2018). Due to the high local demand, the sustainability of the prawn fishery is threatened and it justifies a sustainable production technique to ensure sufficient supply for the local people. Prawn farming can be a sustainable alternative to prawn fishing in Kenya. Several commercially important species of *Macrobrachium* have been bred in captivity with great success, and in some cases, others are being grown commercially. These include but are not limited to

*M. rosenbergii*, De Man, 1879 and *M. nipponensis*, De Haan 1849 (Weimin and Xianping, 2002), *M. australe*, Guérin-Méneville, 1838, *M. lar*, Holthuis 1980 (Williams, 2018), *M. vollenhovenii*, Herklots 1857 (Ndao et al., 2019), *M. olfersii*, Wiegmann 1836 (Barbieri et al., 2016), *M. amazonicum*, Heller 1861 (Soeiro et al., 2016) and *M. malcolmsonii*, Milne-Edwards 1844 (Soeiro et al., 2016 and Nair and Salin, 2012). For *M. rude*, some grow out trials in ponds at different stocking densities have been undertaken in Bangladesh (Awal et al., 2021). However, no breeding initiative for *M. rude* has been done even though it has contributed to the economy of some fishing communities, particularly in Kenya, where it accounts for a large share of the prawn population hence the need for this study. A major challenge in freshwater prawn breeding is feeding the larvae for the first time. The feeding of *Macrobrachium* prawn larvae is generally fraught with serious problems, especially poor survival and growth during the first months of independent life (González et al., 2009, 2011). *Artemia* nauplii remain the most essential food for marine crustacean larvae and fish due to their nutritional quality, digestibility, ability to combine the benefits of live and dry diets, and convenience of dry cysts that can hatch within 24 h (Bardócz et al., 1999; Nkambo et al., 2019; Van Stappen et al., 2020). Although *Artemia* nauplii have been widely used in other freshwater prawn larval culture (Kovalenko et al., 2002; Barros and Valenti, 2003; De Aviz et al., 2018), their use in larval rearing of *M. rude* larvae has not been documented. In addition, optimal feeding density of *Artemia* nauplii is essential for the survival of *M. rude* and avoid overfeeding, which can lead to poor water quality, high costs of tank cleaning and maintenance, and stress on larvae (De Aviz et al., 2018). This study was conducted to determine the optimal feeding density of *Artemia* nauplii for *M. rude* larvae.

## MATERIALS AND METHODS

### Study Area

The study was conducted at the Kenya Marine and Fisheries Research Institute (KMFRI), Mombasa Center (Figure 1). The station, which is located between 4° 03' 19.29" and 39° 40' 54.53", is served by a well and seawater.



**Figure 1.** A map of Kenya showing the location of KMFRI's Mombasa station where the study was conducted

### Broodstock collection

*Macrobrachium rude* broodstock was obtained from local fisherman fishing with prawn seine nets and traps in the Sabaki River near Sabaki Bridge (3° 8' 55" S, 40° 7' 31" E), Kilifi County. Captured broodstock were kept in the river using pre-established hapa nets and were selected based on egg development stage, health status and appearance. Only healthy broodstock with all appendages intact and bearing eggs were chosen for females. As for the males, only those with blue claws were selected. Selected broodstock was delivered to the KMFRI Mombasa Center for spawning in polyethylene fish packaging bags filled with pure oxygen. The broodstock were acclimated before being placed in aerated circular tanks filled with freshwater. The broodstock were fed commercial feed (Skretting ME-0.5 GR starter 315-630 µm) that contained 40% crude protein. Natural photoperiod (12 h light/12 h dark) and a temperature range of 26-28°C were maintained (Valenti et al., 2010). To induce hatching, gravid females bearing grayish-black eggs were put into individual plastic hatching basins with 5 ppt salty water and kept under continuous aeration until the eggs hatched. When the eggs hatched, the female was removed, and the larvae were gathered with a 100 µm net and put into 12 ppt saline water.

### Experimental design

One day after hatching, batches of 100 larvae were collected and put in a 10 L glass aquarium with 5 L of 12 ppt saline water at a stocking density of 20 larvae/L. Two experiments were carried out. The larvae were treated to three feeding densities of *Artemia* nauplii/mL in triplicate for 42 days in the first experiment. *Artemia* nauplii were obtained by decapsulating and hatching *Artemia franciscana* cysts grown in Kenyan artisanal salt ponds at Kadzuhoni (20 58'54" S, 400 08' 37" E) under ideal hatching circumstances according to Lavens and Sorgeloos (1996). After 18 hours of incubation, instar 1 *Artemia* nauplii were gathered using a 100 µm net and washed, then concentrated in a 1 L glass beaker with autoclaved saltwater. After thorough mixing, six samples of 250 L were collected from the beaker and counted under a dissecting microscope (Carl Zeiss Microscopy GmbH, Germany) to determine concentration. The beaker containing *Artemia* was kept in a refrigerator at 4 °C. For 42 days, the larvae were fed once a day. In addition, 10 days after larvae stocking, 1 g of commercial feed was added to each tank once a day as a supplement. Every morning, dead larvae and other wastes were drained from the bottom of the aquaria, and 50% of the water was replaced. Based on the results of experiment I, a second experiment was conducted using the same procedure as in experiment I. The feeding densities, however, were reviewed to 5, 10, and 15 nauplii/mL. The second experiment's culture time was 14 days because 100% larval mortality occurred after day 14.

### Data collection

A YSI professional plus multi-parameter water probe (Model No. 6050000, YSI Industries, Yellow Springs, OH, USA)

was used to measure water temperature, dissolved oxygen (DO), and pH on a regular basis. Every day, the salinity was measured with a portable refractometer (Extech Instruments RF20, USA). Fortnightly growth sampling was performed by selecting five larvae from each tank, fixing them with 1% Lugol's solution, and measuring the total length (TL) of each larva using a STEMI 305 dissecting microscope equipped with an Axiocam (RS5S) camera (Carl Zeiss Microscopy GmbH, Germany). Active swimming larvae were physically counted for survival using a Petri plate and a micropipette. The following formulas were used to compute the growth parameters below:

- i. Specific growth rate (SGR, %) =  $100 \times [(\text{Ln final length (g)} - \text{Ln initial length (g)}) / \text{days of the experiment}]$
- ii. Percentage Survival (%) =  $100 \times (\text{final number of prawns}) / (\text{initial number of prawns})$
- iii. Length gain (LG) = final length - initial length of larvae at stocking.

#### Data analysis

Shapiro-Wilk test was used to check the normality of the collected data. Descriptive statistics such as mean growth, survival rate and standard error were calculated on Microsoft Excel spreadsheet (Version 2016) using formulas (i), (ii) and (iii) below. Leven's test and one-way analysis of variance (ANOVA) were used to evaluate the equality of variance and the respective means significant difference between treatments. The Tukey HSD test was used to compare each pair

of treatments. All statistical tests were performed using R statistical software (version 4.1.0 for Windows) and considered significant at the 95% confidence interval. The results were presented using tables.

## RESULTS

### Experiment 1

#### Water quality

Water quality parameters were monitored during the feeding trial (Table 1). The average temperature ranged from 24.32 to 24.34°C while the salinity ranged from 13.78 to 14.00 g/L. The mean dissolved oxygen (DO) ranged from 4.87 to 5.23 mg/L and the pH ranged from 7.82 to 7.90, respectively. The combined results showed that the water quality parameters amongst the feeding densities had small differences but were not statistically significant at the 95% confidence level ( $P > 0.05$ ).

#### Growth parameters

Table 2 shows the growth parameters during the feeding trial. For all feed administrations, the mean total length rose gradually over the culture period. The final total length was greatest in larvae fed 5 nauplii/mL, followed by 3 nauplii/mL, and lowest in larvae fed 1 nauplii/mL. Overall mean length increase, SGR, and SR were all higher in the 5 nauplii/mL treatment than in the 3 nauplii/mL treatment, with the lowest in the 1 nauplii/mL treatment. A one-way analysis of variance in all parameters examined, however, revealed no significant difference amongst the feed treatments ( $P > 0.05$ ).

**Table 1.** Water quality parameters during larval rearing of *M. rube* fed different feeding densities of *Artemia* nauplii

Parameter	Feeding density			P value
	1 np/mL	3 np/mL	5 np/mL	
Temperature (°C)	24.34±0.23 <sup>a</sup>	24.32±0.22 <sup>a</sup>	24.33±0.22 <sup>a</sup>	$P > 0.05$
Salinity (ppt)	13.78±0.15 <sup>a</sup>	14.00±0.00 <sup>a</sup>	14.00±0.00 <sup>a</sup>	$P > 0.05$
pH	7.82±0.27 <sup>a</sup>	7.86±0.25 <sup>a</sup>	7.90±0.26 <sup>a</sup>	$P > 0.05$
Dissolved oxygen (mg/l)	5.23±0.12 <sup>a</sup>	5.05±0.10 <sup>a</sup>	4.87±0.11 <sup>a</sup>	$P > 0.05$

Values are presented as mean ± standard error. All statistical tests were considered significant at  $P < 0.05$ . Superscript letters compare mean values between groups. Different letters in a row represent significant differences between groups.

**Table 2.** Growth parameters of *M. rube* larvae fed different densities of *Artemia* nauplii

Parameter	Feeding density			P value
	1 np/mL	3 np/mL	5 np/mL	
Initial TL (mm)	1.92±0.28 <sup>a</sup>	1.92±0.28 <sup>a</sup>	1.92±0.28 <sup>a</sup>	$P > 0.05$
Final TL (mm)	3.95±0.06 <sup>a</sup>	4.05±0.14 <sup>a</sup>	4.24±0.21 <sup>a</sup>	$P > 0.05$
Mean TLG (mm)	1.71±0.06 <sup>a</sup>	1.81±0.14 <sup>a</sup>	2.00±0.21 <sup>a</sup>	$P > 0.05$
SGR (TL) (%)	1.35±0.04 <sup>a</sup>	1.41±0.08 <sup>a</sup>	1.51±0.12 <sup>a</sup>	$P > 0.05$
Survival rate (%)	11.67±0.09 <sup>a</sup>	11.67±0.09 <sup>a</sup>	18.00±3.51 <sup>b</sup>	$P > 0.05$

TL=Total length, TLG=Total length gain, SGR=Specific growth rate, SR=Survival rate and np/mL=nauplii of *Artemia* per millilitre. Values are presented as means ± standard error. Superscript letters compare mean values between groups. Different letters in a row show significant differences between groups.

## Experiment 2

### Water quality

The water quality parameters for experiment 2 are presented in Table 3. The results showed that the water quality parameters did not differ between the feeding densities.

The average temperature ranged from 24.53 to 24.59°C, the salinity ranged from 13.97 to 14.29 g/l. The average dissolved oxygen (DO) content ranged from 4.80 to 4.88 mg/l and the corresponding pH ranged from 7.94 to 8.01.

### Growth parameters

Total final length also varied significantly between dietary treatments ( $P<0.05$ ). The highest total final length was observed in the 10 nauplii/mL treatment, followed by the 5 nauplii/mL treatment and the lowest in the 15 nauplii/mL treatment. A similar observation of total final length was also observed for SGR and total length gain (Table 4). Survival varied significantly between different dietary treatments ( $P<0.05$ ). The highest mean survival was observed in the 5 nauplii/mL treatment, while the lowest survival was observed in the 10 and 15 nauplii/mL treatments.

**Table 3.** Water quality parameters during larval rearing of *M. rude* fed different feeding densities of *Artemia* nauplii

Parameter	Feeding density			P value
	5 np/mL	10 np/mL	15 np/mL	
Temperature (°C)	24.59±0.08 <sup>a</sup>	24.58±0.07 <sup>a</sup>	24.53±0.08 <sup>a</sup>	$P>0.05$
Salinity (ppt)	13.97±0.10 <sup>a</sup>	14.29±0.07 <sup>a</sup>	14.18±0.32 <sup>a</sup>	$P>0.05$
pH	8.01±0.20 <sup>a</sup>	7.94±0.18 <sup>a</sup>	7.99±0.19 <sup>a</sup>	$P>0.05$
Dissolved oxygen (mg/l)	4.88±0.18 <sup>a</sup>	4.84±0.12 <sup>a</sup>	4.80±0.07 <sup>a</sup>	$P>0.05$

Values are presented as mean± standard error. All statistical tests were considered significant at  $P<0.05$ . Superscript letter compares mean values between groups. Different letters in a row show significant differences between groups.

**Table 4.** Growth parameters of *M. rude* larvae fed different densities of *Artemia* nauplii

Parameter	Feeding density			P value
	5 np/mL	10 np/mL	15 np/mL	
Initial TL (mm)	1.03±0.01 <sup>a</sup>	1.03±0.01 <sup>a</sup>	1.03±0.01 <sup>a</sup>	$P>0.05$
Final TL (mm)	1.93±0.03 <sup>a</sup>	2.36±0.18 <sup>b</sup>	1.82±0.05 <sup>a</sup>	$P<0.05$
TLG (mm)	0.90±0.03 <sup>a</sup>	1.33±0.18 <sup>b</sup>	0.80±0.05 <sup>a</sup>	$P<0.05$
SGR (% day <sup>-1</sup> )	4.48±0.09 <sup>a</sup>	5.86±0.56 <sup>b</sup>	4.08±0.21 <sup>a</sup>	$P<0.05$
SR (%)	20.00±1.40 <sup>a</sup>	5.71±0.80 <sup>b</sup>	5.71±0.80 <sup>b</sup>	$P<0.05$

Values are presented as means ± standard error. TL=Total length, TLG=Total length gain, SGR=Specific growth rate, SR=Survival rate and np/mL=nauplii of *Artemia* per millilitre. Superscript letters compare mean values between groups. Different letters in a row show significant differences between groups.

## DISCUSSION

Freshwater prawns like many crustaceans undergo a complex life cycle characterized by a planktonic larval phase and a benthic adult phase. The transition from one life style to another is accompanied by morphological changes in internal organs, tissue systems, and most importantly, the gastrointestinal tract (Anger, 2006; Korzelecka-Orkisz et al., 2012). Due to the rapid changes, the larval stage differs from the adult stage in several respects, including behaviour, nutrition, and physiology. Newly hatched larvae are lecithotrophic and are completely dependent on yolk mass to meet nutritional requirements lasting a few days. When external feeding is initiated, the larvae must accumulate enough food reserves to survive through the different metamorphosis stages into juvenile and adult stages (Le Vay and Gamboa-Delgado, 2011).

Therefore, determining the optimal feeding density of *Artemia* nauplii for *M. rude* larvae are essential to maximize growth, development and survival rates. In experiment 1 of the

study, three feeding densities of *Artemia* nauplii were compared, namely 1, 3 and 5 nauplii/mL. The results showed that the growth parameters of *M. rude* larvae were not significantly different between the 3 feed densities. The observation depicted a similar intake pattern of *M. rude* larvae treated with feed densities of 1, 3 and 5 nauplii/mL (Table 2). According to Kurmaly (1990), a small percentage of decapod larvae search for food, while the majority depend on chance encounters to capture food. Therefore, increasing *Artemia* densities from 1 to 5 nauplii/mL did not provide a better opportunity to encounter and capture the food by *M. rude* larvae. A similar result has also been reported in other studies. For example, Barros and Valenti (2003) observed similar growth parameters in *M. rosenbergii* larvae fed 2 and 4 *Artemia* nauplii/mL. In experiment 2, *M. rude* larvae survived better at the feeding density of 5 nauplii/mL compared with the feed densities of 10 and 15 nauplii/mL. Overall, a downward trend in survival was observed from 5 nauplii/mL to the highest

feeding density, 15 nauplii/mL. The poor survival at the highest feeding density could be associated with evolution of ammonia from the excess *Artemia* nauplii supplied that remained uneaten in the culture tanks. According to De Aviz et al. (2018), increasing *Artemia* feeding densities is wasteful and results in increased waste in the culturing tanks in this case nitrogenous waste since *Artemia* is highly proteinous. Another pattern was observed for growth, where the highest mean total length was observed at a feeding density of 10 nauplii/mL, followed by 5 nauplii/mL with lowest observed in larvae fed 15 nauplii/mL. Increasing the feeding density from 5 to 10 nauplii/mL increased feed intake, as demonstrated by mean total length, total length gain and SGR, but significantly decreased survival. Growth was affected at 15 nauplii/mL, which could be a result of excess feed intake. According to El-Sayed (2002), increased feed density in water may increase feed intake, but high intake of particles may cause feed to flow rapidly through the intestine, resulting in poor digestion and poor assimilation of nutrients hence the poor growth performance observed in the prawn larvae fed at high *Artemia* nauplii densities. These results are consistent with the study of De Aviz et al. (2018), who noted that the survival rate of *M. rosenbergii* decreased when *Artemia* nauplii density increased from 5 to 10 and 20 nauplii/mL. In another study, Maciel et al. (2012) observed an increase in feed intake as feed density increased, but this did not lead to an increase in yield.

The results of the present study are in contrast to those reported by Daniel et al. (2019) on the increase in larval growth parameters of Amazon aquarium fish when the *Artemia nauplii* feeding density was increased from 50 to 150 nauplii/mL. The survival rate of *M. rude* larvae in the present study ranged from 6 to 20% in both experiments. This is consistent with the study of Makombu et al. (2014), who observed survival rates of 3 to 9% when rearing *Macrobrachium vollenhovenii* larvae. The survival rates observed in the present study were much lower than those associated with other *Macrobrachium* species. For example, research by Gomes et al. (2014) reported survival rates of 56 to 78% with *Macrobrachium equidens*. In another study, Habib et al. (2014) reported a 64% survival rate with *Macrobrachium rosenbergii* larvae. The survival observed in the present study was also lower when compared to other crustaceans. The study of Rodríguez-Serna et al. (2010) on Mexican crayfish (*Procambarus llamasii*) fed different farm animal feed reported 100% survival whereas Kaldre et al. (2015) observed 89% and 78% survival with marbled crayfish (*P. virginalis*) fed with carp and discus feeds. Amanyazov and Karadal (2023), on the other hand stated 58-75% survival with red swamp crayfish (*P. clarkii*) fed with three different commercial aquarium feeds. The survival of prawn larvae is related to several factors. Brown (2005) associated poor survival with sub-optimal nutritional factors that render larvae incapable of transitioning from one developmental stage to another.

In contrast, Armstrong et al. (1976) and Aquacop (1983) linked prawn larval survival to the maintenance of good water

quality, the quality and quantity of feed as well as the ability of the larvae to obtain food from the water. In the present study, the water quality parameters monitored (Table 1 and 3) were within the optimal range for prawn larval development. In addition, feed density treatments were also within the recommended range, consistent with previous studies. Therefore, the overall lower survival rates observed in the present study as compared to other studies could be due to handling and other zootechnical challenges (Brown, 2005).

## CONCLUSION

In summary, the results of this study have important implications in determining the density of *Artemia* nauplii fed to *M. rude* larvae to optimize larval growth and survival. From the study, it was clear that feeding *Artemia* nauplii at lower densities (1-5 nauplii/mL) gave similar results in terms of growth rate and survival.

The study also demonstrated that increasing the density of *Artemia* nauplii fed to *M. rude* larvae would increase growth parameters, but there was an optimal range of 5 to 10 nauplii/mL. According to the study, increasing the feeding densities beyond 10 nauplii/mL not only leads to wasted feed but also reduces the growth and survival rates of the prawn larvae. The study recommends repeating the same work but with *Artemia* nauplii enriched with highly unsaturated fatty acids (HUFA) to determine if survival could be improved.

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## AUTHORSHIP CONTRIBUTIONS

Sheban Mdzomba Hinzano: Conceptualization, data curation, formal analysis, investigation, methodology, software, supervision, validation, visualization, writing original draft, writing review and editing. Morine Mukami Ngarari: Conceptualization, funding acquisition, investigation, methodology, project administration, resources, supervision, visualization, writing original draft, writing review and editing. Mary Opiyo: Conceptualization, funding acquisition, methodology, project administration, resources, supervision, review and editing. Francis Okalo: Conceptualization, funding acquisition, resources, writing review and editing. Betty Nyonje Mindraa: Conceptualization, project administration, supervision, writing review and editing. David Midumbi: Data curation, investigation, methodology, writing review and editing. Derrick Gitari: Data curation, investigation, methodology, writing review and editing.

## CONFLICTS OF INTEREST

The authors state that there is no conflict of interest to declare.

## ETHICS APPROVAL

The experiment was carried out in accordance with the Kenya Marine and Fisheries Research Institute (KMFRI) guidelines for animal handling, as registered with the National

Commission for Science, Technology, and Innovation (NACOSTI) registration number NACOSTI/2016/05/001, and in accordance with the Prevention of Cruelty to Animals Act 1962, CAP 360 (Revised 2012) of Kenyan laws, and the EU regulation (EC Directive 86/609/EEC).

## DATA AVAILABILITY

All relevant data is in the article.

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# Bioinformatics studies and comparison of mRNA transcription of glutathione S-transferase gene in some tissues of common carp (*Cyprinus carpio*) and brown trout (*Salmo trutta*)

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**Abstract:** Bioinformatics has revolutionized the way we study gene expression and regulation, enabling researchers to analyze large-scale genomic data with unprecedented speed and precision. In this study, we use bioinformatics tools and methods to compare mRNA transcription of glutathione S-transferase (*gstr*) gene in two different fish species: common carp and brown trout. In this study, liver, intestine, muscle, brain, heart, eye, spleen, gill, kidney, stomach, ovary and testis samples were taken from male and female brown trout and common carp, and total RNA was isolated from each tissue to synthesize cDNA from these tissues. Then, the transcript amounts of the *gstr* gene were determined by qPCR from all tissue samples. Gene structures, conserved gene synteny design, phylogenetic tree analyzes and similarity-identity ratios with other vertebrates were determined. When the transcriptional differences between male and female tissues for the brown trout *gstr* gene were examined, it was seen that the intestine, gill, kidney, stomach, muscle and gonads were significantly higher in male fish ( $p < 0.05$ ), but the differences between other tissues were not statistically significant. It has been determined that the highest gene expression was liver ( $p < 0.05$ ) and brain, eye, spleen, kidney, heart and spleen tissues have significantly lower *gstr* gene expression than other tissues in both male and female in common carp. In addition, the in-silico analysis determined that the brown trout *gstr* gene shared the highest similarity and identity ratio with rainbow trout, and the common carp *gstr* gene shared the highest similarity and identity ratio with goldfish.

**Keywords:** Brown trout, common carp, in silico analysis, *gstr*, gene expression

## INTRODUCTION

Aquaculture is an important industry that helps meet the growing demand for seafood while reducing pressure on wild fish populations (Chen et al., 2021). Brown trout and common carp are two popular species that are extensively farmed for their economic and nutritional benefits (Adamek et al., 2023; Franěk et al., 2021). Common carp farming has been shown to improve glucose metabolism disorder in fish. Carp farming, however, can also contribute to increases in turbidity and internal nutrient load by resuspending sediments, which may eventually reduce the water quality (Arlinghaus and Mehner, 2003). Brown trout is another important aquaculture species that faces challenges due to global warming and a changing climate (Keiz et al., 2023). Inland fisheries, including aquaculture, contribute significantly to food security and economic security by providing primary sources of animal protein, essential for human health and well-being (Lynch et al., 2016).

Glutathione S-transferase (GST) is an enzyme that plays a crucial role in the detoxification of xenobiotics and endogenous compounds by catalyzing the conjugation of glutathione to electrophilic substrates. GSTs are encoded by a large gene family, and their expression is induced by various environmental stressors, including microcystin-LR, cadmium, and weathered polyethylene microplastics. GSTs have been studied in various fish species, including common carp (Chen et al., 2017), Nile tilapia (Liang et al., 2007), and

zebrafish (Glisic et al., 2015; Tierbach et al., 2018). The expression of GST genes varies among different tissues and fish species. For example, alpha-class GST gene expression was higher than that of rho-class GST gene in both exposed and control fish of silver carp and grass carp, whereas rho-class GST gene expression was higher than that of alpha-class GST gene in both exposed and control fish of Nile tilapia (Liang et al., 2007). The induction of GST enzyme activity corresponds to *gstr* gene expression at the latter stages of exposure to weathered polyethylene microplastics (Pandi et al., 2022). In cadmium-exposed river pufferfish, seven genes of the GST family were cloned and expressed, and GST1.18 was found to play a critical role in detoxification pathways (Kim et al., 2010). GSTs also play an important role in phase II detoxification of lipid peroxides and demonstrate the functions such as glutathione peroxidase activity towards (Rudneva et al., 2010). Overall, GSTs have an important role in the detoxification of xenobiotics and endogenous compounds in fish (Glisic et al., 2015).

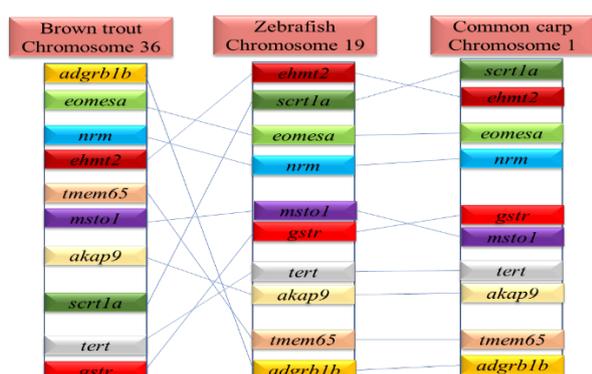
Bioinformatics studies of mRNA transcription in fish have become increasingly popular as they provide insights into the biological mechanisms involved in various physiological processes (Qian et al., 2014). In genetics research, bioinformatics plays a crucial role in studying genetic information, such as DNA and RNA sequences, and their interactions with various biological processes (Bayat, 2002).

In this study, bioinformatics tools and techniques were used to compare the mRNA transcription of the *gstr* gene in the tissues of common carp and brown trout. By employing bioinformatics tools and techniques, we aim to gain a deeper understanding of the expression patterns of the *gstr* gene in different tissues of these two species, and explore potential differences in expression levels between them. Our findings may have significant implications for understanding the role of *gstr* gene expression in aquatic organisms and its potential effects on their health and survival in varying environmental conditions.

## MATERIALS AND METHODS

### In silico analysis

In-silico analysis for the identification of the *gstr* gene in brown trout and common carp were performed using bioinformatics tools such as Ensembl, NCBI, and UniProt databases. The cDNA sequences of brown trout and common carp *gstr* were obtained from the Ensembl database and their accuracy was confirmed by performing a BLAST search on the NCBI database. It was observed that both brown trout and common carp have one isoform of the *gstr* gene, which was identified through Ensembl database searches. In the study, to determine the mRNA expression of the *gstr* gene in both brown trout and common carp, as well as the reference genes for common carp, actin beta 1 (*actb*) and glyceraldehyde-3-phosphate dehydrogenase (*gapdh*), primers were designed according to the exon-exon junction model (Table 1). The primer sequences used for beta-actin and elongation factor 1a (*eef1a*) genes, which were reference genes for brown trout, were obtained from Özdemir and Bayır (2023) (Table 2). Additionally, genomic primers were designed (Table 3) to

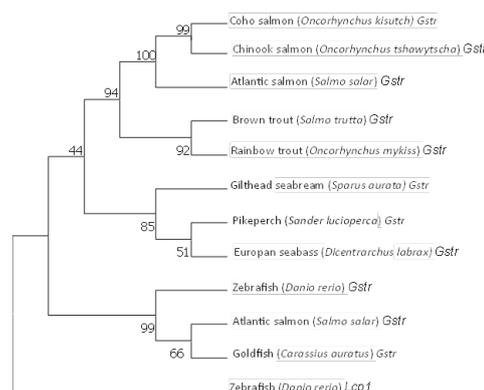


**Figure 1.** Conserved gene synteny among brown trout, common carp, and zebrafish *gstr* gene

The protein sequence accession numbers used in the phylogenetic tree, created using the maximum likelihood method (Felsenstein, 1989), are as follows: Atlantic salmon (*Salmo salar*) ENSSSAG00000056150, common carp (*Cyprinus carpio*) ENSCCRG00000013532, brown trout (*Salmo trutta*) ENSSTUG00000037965, rainbow trout (*Oncorhynchus mykiss*) ENSOMYG00000034408, Chinook salmon (*Oncorhynchus tshawytscha*) ENSOTSG00005006610,

amplify the desired regions and obtain the sequence of PCR products from the beginning and end parts of the open reading frame by designing the primers from the closest regions possible to the start and end of the open reading frame. The PCR products obtained from the designed primers for gDNA were placed in three nuclease-free Eppendorf tubes containing 30  $\mu$ L of PCR product each and sent to a specialized sequencing company for Sanger sequencing.

The design of the conserved gene synteny manually using the Ensembl database (Figure 1). The chromosomes and regions where the *gstr* gene are found in brown trout and common carp are recorded. The other genes found outside the *gstr* gene in the identified chromosomes and regions, as well as the chromosomal regions of these genes in another organism, rainbow trout, are also identified. A conserved gene synteny is created based on the common genes and their chromosomal locations in the genomes of these three organisms. The CLUSTALW BioEdit program (<http://www.mbio.ncsu.edu/bioedit/page2.html>) was used to determine the phylogenetic relationship of brown trout and common carp using the *gstr* gene, and to construct a phylogenetic tree (Figure 2). The nucleotide sequences of the *gstr* genes in brown trout and common carp were determined using the Ensembl database. Separate nucleotide sequences were designed for both species, indicating the exons, introns, amino acids synthesized by the exons, 5' and 3' ends, TATA box, poly-A signal, and stop codon of the *gstr* gene (Figure 3, 4). The similarity-identity ratios between the *gstr* genes of common carp and goldfish, zebrafish, rainbow trout, Atlantic salmon, brown trout, and gilthead seabream were calculated using the BioEdit program based on the protein sequences synthesized by these genes (Figure 5, 6).



**Figure 2.** The phylogenetic relationship of brown trout and common carp *gstr* genes with those of other fish species

coho salmon (*Oncorhynchus kisutch*) ENSOKIG00005022094, goldfish (*Carassius auratus*) ENSCARG00000006155, zebrafish (*Danio rerio*) ENSDARG00000042620, gilthead seabream (*Sparus aurata*) ENSAUG00010003870, European seabass (*Dicentrarchus labrax*) ENSSLUG00000008281, Nile tilapia (*Oreochromis niloticus*) ENSONIG000000034559, European seabass (*Dicentrarchus labrax*) ENSDLAG00005030493.

**Table 1.** Primer sequences *gstr*, *actb1*, and *gapdh* genes of common carp

Common carp	Forward primer (5'→3')	Reverse primer (5'→3')	Tm (°C)
<i>gstr</i>	CCAGAGCTCAGGTCCAAC	GGTCTCAAACATTCGCTGGT	62
<i>actb1</i>	CCCAGGCATCAGGGAGTGA	TCCATATCATCCAGTTGGTCA	62.5
<i>gapdh</i>	CAACATGGGGATTGGCCGT	AGACGGTGATAGCGTGACCA	60

**Table 2.** Primer sequences for *gstr*, *actb*, and *ef1a* genes of brown trout

Brown trout	Forward primer (5'→3')	Reverse primer (5'→3')	Tm (°C)
<i>gstr</i>	GGACAGCTCCCTGCTTTCAA	CGGGGACACGGTAGTTGTAG	62
<i>b-actin</i>	ATGGAAGTGAAATCGCC	TGCCAGATCTTCCATG	52.1
<i>ef1a</i>	GTCMMTGGAACGCACTCG	CTACTGATTGGCTGCTCCG	59.45

**Table 3.** Genomic primers for brown trout and common carp *gstr* genes.

<i>gstr</i>	Forward primer (5'→3')	Reverse primer (5'→3')	Tm (°C)
Brown trout	CCAGAGCTCAGGTCCAAC	GGTCTCAAACATTCGCTGGT	61
Common carp	TAACACAAGCGCACCTG	AGACTGTTAATGTGCGCTGC	59

5' tatacaggttaactagctgagattaggagcacactcttaaggaggatgctcctaactctc  
 agctcgttacctgtataaaagacacctgggagccagaaatctttctgattgagagggggg  
 caaatacttatttcctcattaaaatgcaaatcaatttataacatttttgacatgctgtt  
 ttctggatttttagttgttattctgtctctcagtggttcaaatcaacctaccattaaaat  
**TATA**gactgatcatttctttgtcagtgaggcaaacgtacaaaatcagcaggggatcaata  
**+1**  
 CTTTTTCCCCTCACTGTATATTTGGTTCTTAACTTCCCCTGAAAGTTGCATATTGCCGGGGC  
 TATTCGATTCTAATGCGTACTATTTCCATTTTTCTATTTTTCTGTTTCTTACTTTTTTAA  
 CTGTGCATTGTTTGGAAAGAGCTCGTACTGTAACCTAAGCGTTTCACGGTAAAGTCTACAC  
 CTGTTGTATTTCGGCGCAGGTGACAAACACAATTTGATATGACTTCTTTTATGCTGTAGCC  
 AAC**ATGACTACGCGGAATTCATGTGTTGATAGAAGACCAGTAGAACTGGACTGTCTATGAC**  
**-M--T--R--N--S--C--V--D--R--R--P--V--E--L--D--C--H--D--**  
**TCGTACATTAAG**gtgac' N361' agcag**ATTTCGACCATCATGGCCAAGGACATGACACT**  
**-S--Y--I--K--** **-I--S--T--I--M--A--K--D--M--T--L**  
**GCTGTGGGGCTCCGGCTCTCCTCCGTGCTGGCGTGCATGATCGCTCTGGAGGAGAAGAA**  
**-L--W--G--S--G--S--P--P--C--W--R--V--M--I--A--L--E--E--K--K**  
**ACTGCAGGGTACAATCACAACCTCTCTCCTTCGAGAAAGCAGAGCACAAGTCAAAGA**  
**--L--Q--G--Y--N--H--K--L--L--S--F--E--K--A--E--H--K--S--K--E**  
**AGTCCTGGATATCAATCCAGAGGACAG**gttagt' N448' ccag**CTCCCTGCTTTCAAAC**  
**-V--L--D--I--N--P--R--G--Q--** **-L--P--A--F--K--**  
**ACGGAGACAACATACTCAACGAGTCAATGCAGCATGCATGTACCTGGAG**gtaag' N2045'  
**H--G--D--N--I--L--N--E--S--Y--A--A--C--M--Y--L--E--**  
 tacag**AGCCGGTTCAGGTCCAGGGACCCAGTTGATTCCTGAGGGCCAAGTAGAGCAGG**  
**-S--R--F--R--S--Q--G--P--Q--L--I--P--E--G--Q--L--E--Q--**  
**CCCTGATGTACCAGCGCATGTTTGTGATCCTCAACCTCAGTGACAACTCA**gtaag' N415'  
**A--L--M--Y--Q--R--M--F--E--I--L--N--L--S--D--K--L--**  
 ccag**GTAACGTCATCTACTACAACCTACCGTGTCCCGAGGGAGAGACATGACTCTGC**  
**S--N--V--I--Y--Y--N--Y--R--V--P--E--G--E--R--H--D--S--A**  
**TATCAAGAGGAACAAGGAGAACCTGGCCACGGAAATCAAACCTGTGGGAGGGATACTTTCA**  
**--I--K--R--N--K--E--N--L--A--T--E--I--K--L--W--E--G--Y--F--Q**  
**GAAG**gtgca' N756' tccag**ATGGAGGTGGGTTCTTACCTGGCAGGAAAAGCCTTCTCAT**  
**--K--** **-M--E--V--G--S--Y--L--A--G--K--A--F--S--**  
**TGGCTGACGTTATTGCTTCCCTGTGATTGCCTACGCCCTCCGCTTGG**gtaag' N67' t  
**L--A--D--V--I--V--F--P--V--I--A--Y--A--F--R--F--G**  
 ccag**GCTGTCTACGGAGCGTTACCCCAAACCTGGGAGCATACTACGATATGATGAAGGAAA**  
**--L--S--T--E--R--Y--P--K--L--G--A--Y--Y--D--M--M--K--E--**  
**GACCCAGCGTTAAAGCTACCTGGCCCCACACTGGCTGGAGAACCCTCAGGGAGGGGACG**  
**R--P--S--V--K--A--T--W--P--P--H--W--L--E--N--P--Q--G--G--D--**  
**CTCTCAAGGAGTTCTGA**gacacacaggaacaacacagcacattatcttaaggatgtaata  
**A--L--K--E--F--\***  
 cgtcacttctctgtatatactggtgtaaccacgggaaacgcaagttgcttttaaatgtacg  
 tttcctcagatgagatcagtcagtagtcttccactaagtgacacaatttttttgcat  
 tgcccttctgggggtttttgtaacaaatgcttttttttttacttctatatatacacttt  
 aactgaaacataaacacaaagtgtgtttttacgaacatgactttataataacagtcacat  
 cctccatataatttctgtgtttgtgtacagaccacatacaactgggtgtgg**AATTAA**taaa  
 aaaaatcataccaag 3'

**Figure 3.** Exon-intron organization of the brown trout glutathione S-transferase (*gstr*) gene

5' attggatctgtgcatttccggcatccctagagagtaataaataatactgatcatgtttg  
atcatatttagttaatagatacactaaacaggcccttgaatacataacatttttaagcgt  
ttttatttttgtaactcttgcaaatctttttacatgtaaatatttttcagcttttttcat  
gtatttttaaccttttttttagtttttttaatttttttttaattagtagtatttggtaaatta  
ctttttattcat **TATTA**ttctgtgatttttttaattatcatttttaaatcattattatt  
+1  
ATTTCTTCTATTGAGATAAATTAACACCAGAGCACCCTGTATATCCATTATTTTCAGTAT  
TTTCTAATTCAAACCAGAGCCGAGTCCATCTCCGGCCGGCAGACGGCAGGCCCGC  
CCCTCAGTGAAGGCGCTTATAAGCGTGTGTCAAATTCAGCGTGACGAGTAAATCTGT  
GGTCCGTTCTGCCGAGTATTAATCATTTTCTCAATTAACGCGATATTAGCGGTC **ATGG**  
-M--  
CGCAGAGTATGATGTTGACTGGTCTCGTCTCCCTCCGTCGTCGGAGATCATGATCG  
A--Q--S--M--M--L--Y--W--C--S--G--S--P--P--C--W--R--V--M--I--  
CGCTGGAGGAGAAGCTGCTGCAGGGATACAAACACAAACATTTGGCGTTCGACAAGAACG  
A--L--E--E--K--L--L--Q--G--Y--K--H--K--H--L--A--F--D--K--N--  
AACACAAGTGTGAAGAAGTGAAGCTCTCAATCCCAGAGCTCAGgtgcg' N75185' tgc  
E--H--K--C--E--E--V--K--A--L--N--P--R--A--Q--  
agGTTCCAACTTTCAAGCACGGAGACATCGTCTGTAACGAGTCTGGCAGCGTCTGT  
-V--P--T--F--K--H--G--D--I--V--V--N--E--S--L--A--A--C--L--  
ATCTGGAGgtaaa' N4858' tgtagAGCGCGTTAAGTCTCACGGCACCCGTTTGATCCC  
Y--L--E--  
-S--A--F--K--S--H--G--T--R--L--I--P  
AGACGACCCGACTGAACAAGCGCTCTACCAGCGAATGTTTGAGACCAACAACCTGCA  
--D--D--P--T--E--Q--A--L--V--Y--Q--R--M--F--E--T--N--N--L--Q  
GCAGAAAATGTgtaag' N550' ttcagATGACGTGGCTTTCTATGAGTATTATGTTCTCTG  
--Q--K--M--  
Y--D--V--A--F--Y--E--Y--V--P--  
AAGGAGAAAGACTTGAATCGGCTCTGAAGAGGAATAAAGAGAGTTTAGTCACCAGACTCA  
E--G--E--R--L--E--S--A--L--K--R--N--K--E--S--L--V--T--E--L--  
AAGTGTGGGATGGATCTGGAGAAGgtbcag' N6371' agaagCTGCTGCAGGGATACAA  
K--L--W--D--G--Y--L--E--K--  
-L--L--Q--G--Y--K  
ACACAAATTTCTGTCGTTTGATAAGAACAACCAAGTGTGAAGAAGTGAAGCTCTCAA  
--H--K--F--L--S--F--D--K--N--E--H--K--C--E--E--V--K--A--L--N  
TCCAGAGCTCAGgtgcg' N122' tgtagCTTCCAACTTTCAAGCACGGAGACATCGTCG  
--P--R--A--Q--  
-L--P--T--F--K--H--G--D--I--V--  
TGAACGAGTCTGACGCCCTGTCTGTATCTGGAGgtaaa' N3697' tctagAGCGCGTT  
V--N--E--S--Y--A--A--C--L--Y--L--E--  
-S--A--F  
TAAGTCTCAAGGCACCCGCTGTGATCCCAGACGACCCGGCTGAACAAGCGCTCGTCTACCA  
--K--S--Q--G--T--R--L--I--P--D--D--P--A--E--Q--A--L--V--Y--Q  
GCGAATGTTTGAGACCAACAACCTGCAGCAGAAAATGTgtaag' N955' ttcagATGAGG  
--R--M--F--E--T--N--N--L--Q--Q--K--M--  
Y--E--  
TGGCTTTCTATGAGCATTATGTTCTCTGAAGGAGAAAGACTTGAATCGGCTCTGAAGAGGA  
V--A--F--Y--E--H--Y--V--P--E--G--E--R--L--E--S--A--L--K--R--  
ATAAAGAGAGTTTAGTCGCCGAGCTCAAACCTGTGGGATGGATACTTGGAGAAGgtcgg' N342'  
N--K--E--S--L--V--A--E--L--K--L--W--D--G--Y--L--E--K--  
atcagATGGGAAAAGGCTCGTACCTCGCTGGAAGAGCTTCACTATGGCCGATGTGGTGT  
-M--G--K--G--S--Y--L--A--G--K--S--F--T--M--A--D--V--V--  
GTTTCCCACATCATCGCATTTTTTCCGGACTTCAgtgag' N694' tccagCTGTCTCGA  
C--F--P--I--I--A--F--F--P--R--L--H  
--C--P--R--  
GAGCGTTGTCACAGCTGATGGAGTACTACGAGATGCTGAAGGACCGTCCAGTATTA  
E--R--C--P--R--L--M--E--Y--Y--E--M--L--K--D--R--P--S--I--K--  
GCCAGCTGGCCTCCTCACTGGCTGGAGAAACCTGAGGGTCCAGACACGCTCAAGAACCTG  
-A--S--W--P--P--H--W--L--E--K--P--E--G--P--D--T--L--K--N--L--  
TGAagaacatcctgaacacaccagcaacttaaacatcagtgtaattcagatttacctt  
-\*--  
agcttactgtattaaatcacaaccgtgtggtcagctctcatataccgttttcaatcattta  
tgttttaaccctgctggattcattattttttctgtaaatgattcattttttatttgc  
ttctgtggtt **AATAAA**gtgttatcctgttcggtccaaataaaaaaacatatttacc 3'

Figure 4. Exon-intron organization of the common carp glutathione S-transferase (*gst*) gene

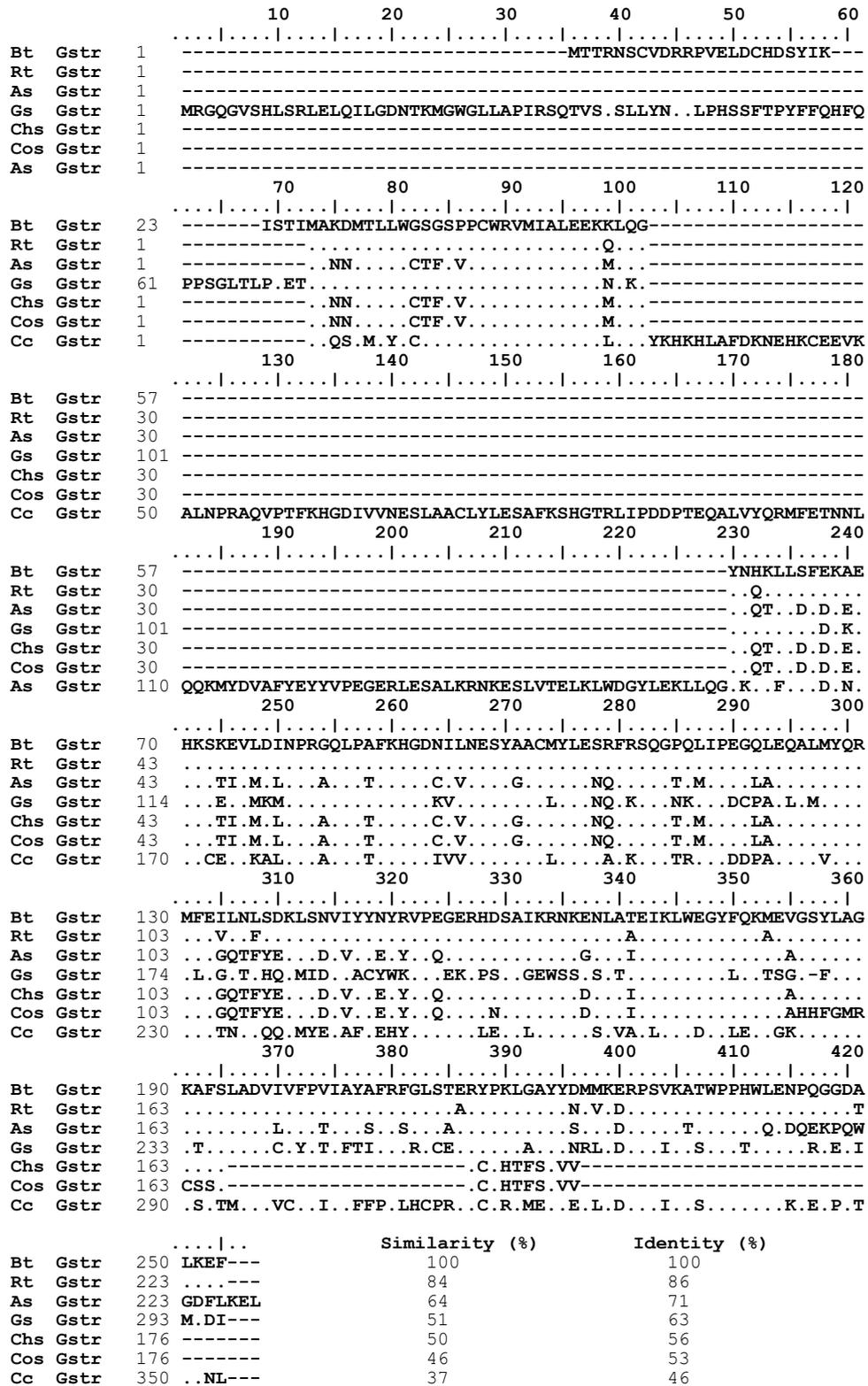


Figure 5. Similarity-Identity rates among *gstr* genes of brown trout (Bt) and rainbow trout (Rt), Atlantic salmon (Ats), gilthead seabream (Gs), chinook salmon (Chs), coho salmon (Cos), and common carp (As)

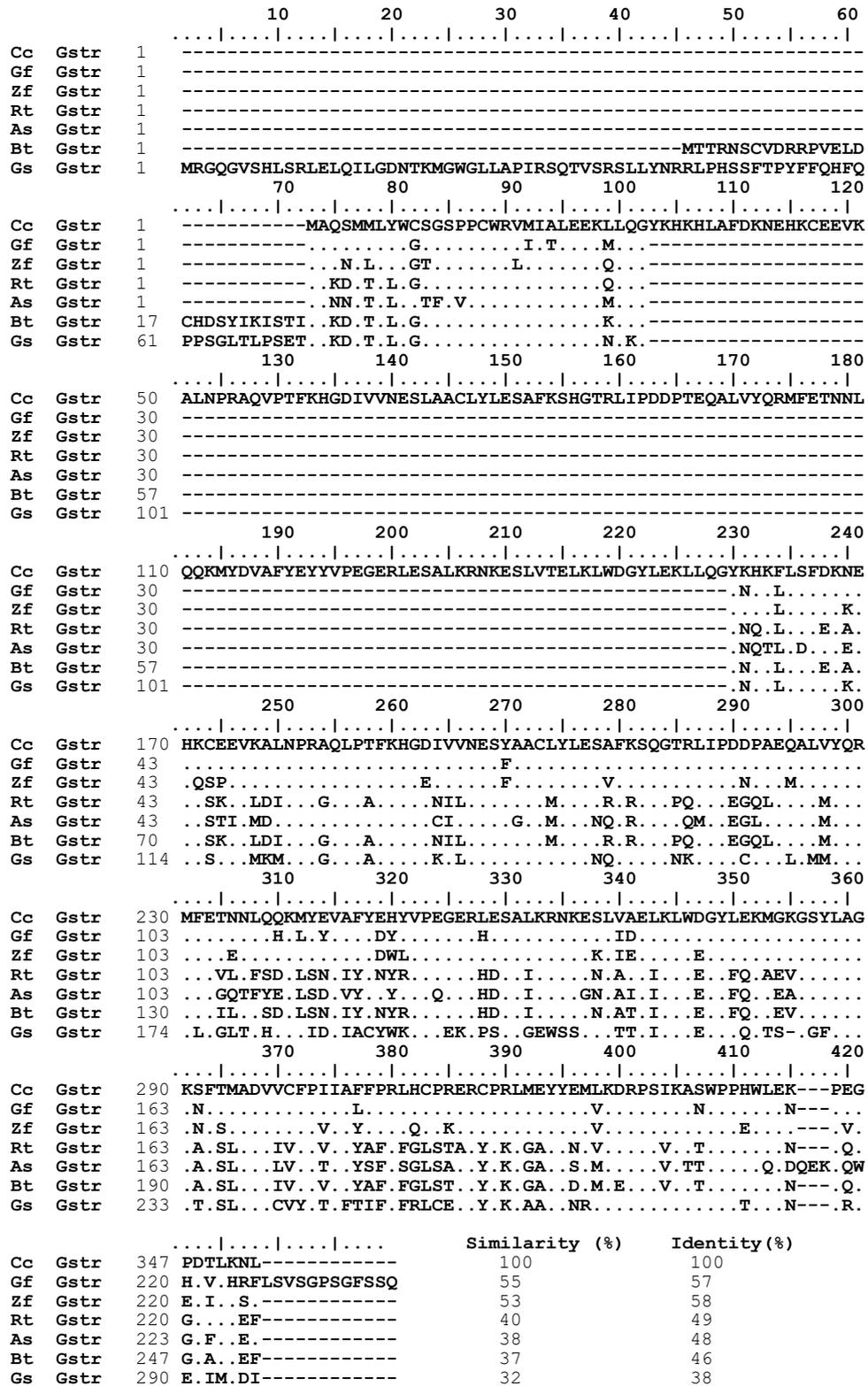


Figure 6. Similarity-identity rates between the brown trout (Bt) and the rainbow trout (Rt), Atlantic salmon (As), Gilthead seabream (Gs), zebrafish (Zf), and common carp (Cc), goldfish (Gf) gstr genes.

### Husbandry and dissection of fish

The study obtained three adult female and three adult male brown trout, in addition to three female and three male common carp from the Faculty of Fisheries at Atatürk University. These fish were housed in a 100-liter aquarium at temperatures maintained at  $29 \pm 1^\circ\text{C}$  for common carp and  $9 \pm 1^\circ\text{C}$  for Brown trout. They were fed a commercial diet twice daily until they were fully satiated. The stocking density was set at 100 fish per cubic meter, and the pH level was maintained at 7.5 for common carp and 7 for Brown trout. A diurnal light: dark cycle of 12:12 hours was provided by fluorescent lighting. Molecular analyses were conducted at the Agricultural Biotechnology Laboratory. In the study, liver, intestinal muscle, brain, heart, eye, spleen, gill, kidney, stomach, and gonad samples were taken from all fish. The samples were placed in 2 ml Eppendorf tubes containing 1 ml of RNA later and stored at  $+4^\circ\text{C}$  for 24 hours and then at  $-80^\circ\text{C}$  until the day of analysis. Prior to sample collection, the fish were anesthetized using clove oil. Before the dissection process, the dissecting instruments and the work area were sterilized and cleaned using RNase ZAP (Invitrogen™). The entire study was conducted in accordance with the rules of the Local Ethics Committee for Animal Experiments at Atatürk University (29.04.2021/E-75366018-000-2100117626).

### RNA isolation and reverse transcriptase (RT) and real-time PCR (qPCR) analysis

To extract total RNA, liver and gill tissue samples were taken out of RNAlater and homogenized using trizol reagent (Life Technologies). The concentration of RNA was measured using a Nanodrop 8000 spectrophotometer, and the quality of the total RNA was assessed through agarose gel-electrophoresis. For cDNA synthesis, 2 µg of RNA from each tissue was utilized. The RNA underwent DNase treatment (DNase I, Amplification Grade, Life Technologies) and was then converted into cDNA using the High-Capacity cDNA Reverse Transcription Kit (Life Technologies). After RNA isolation, the isolated RNA samples were quantitatively analyzed using nanodrop measurements. RNA samples with quantities ranging from 800 to 1000 ng/µl and OD260/OD280 ratio between 1.8-2 were used. In cases where the RNA concentrations were high, dilutions were performed.

The quantity of brown trout and common carp *gstr* transcript (copy number/µL) was determined using the SYBR Green PCR Kit method on a qPCR instrument. Each qPCR tube contained 10 µL SYBR Green, 5 µL DNase/RNase-free water, 2 µL forward primer, 2 µL reverse primer, and 1 µL cDNA. For each sample, two replicates were performed, and a negative control was included in each analysis. The qPCR procedure consisted of an initial denaturation at  $95^\circ\text{C}$  for 15 minutes, followed by 40 cycles of denaturation at  $95^\circ\text{C}$  for 20 seconds, annealing at the optimum temperature determined for each gene for 30 seconds, and elongation at  $72^\circ\text{C}$  for 30 seconds.

### Statistical analysis

The statistical analyses were conducted using GraphPad Prism 9 software in the United States. The data underwent one-way ANOVA, and significance was determined using Duncan's multiple range post hoc test. These statistical tests were used to compare the levels of *gstr* gene expression in different tissues of both brown trout and common carp. All data are presented as mean  $\pm$  SEM. Values were considered statistically significant when  $p < 0.05$ .

## RESULTS

### Bioinformatics studies of *gstr* gene in brown trout and common carp

The *gstr* gene and other genes such as *adgrb1b*, *eomesa*, *nrm*, *tmem65*, *msto1*, *akap9*, *srt1a*, and *tert* which are conserved among these organisms, were found on chromosome 36 in brown trout, chromosome 1 in common carp, and chromosome 19 in zebrafish.

The in-silico analysis of the *gstr* gene in brown trout and common carp aimed to provide basic data for the development of modern strategies to protect against the harmful effects of oxidative stress in both cultured fish and other vertebrates. The analysis revealed that the brown trout *gstr* gene has 7 exons and 6 introns, while common carp *gstr* gene has 6 exons and 5 introns, both with a highly conserved exon-intron organization. Alignment analysis of the brown trout and common carp Gstr/GSTR sequences using CLUSTAL W revealed that the polypeptide identity and similarity rates between brown trout and other species, such as rainbow trout, Atlantic salmon, sea bream, Chinook salmon, Coho salmon, and common carp, were quite high. Similarly, the polypeptide identity and similarity rates between common carp and goldfish, zebrafish, rainbow trout, Atlantic salmon, brown trout, and sea bream were also quite high. The analysis also revealed that the brown trout *gstr* gene shared the highest similarity and identity rates with rainbow trout, while common carp *gstr* gene had the highest similarity and identity rates with goldfish.

### Tissue-specific transcription of *gstr* gene in brown trout and common carp

In this study, the tissue-specific distribution of the *gstr* gene was determined in female and male brown trout and common carp using qPCR (Figure 7). For female brown trout, the tissue-specific distribution of the *gstr* gene was determined as follows: liver  $25.66 \pm 1.49$ , intestine  $13.68 \pm 0.61$ , muscle  $0.42 \pm 0.02$ , brain  $1.73 \pm 0.39$ , heart  $2.89 \pm 0.43$ , eye  $2.35 \pm 0.18$ , spleen  $0.96 \pm 0.21$ , gill  $14.27 \pm 0.82$ , kidney  $0.98 \pm 0.17$ , stomach  $1.25 \pm 0.15$ , and ovary  $7.39 \pm 0.32$ . For male brown trout, the tissue-specific distribution was determined as follows: liver  $32.60 \pm 1.70$ , intestine  $22.08 \pm 0.59$ , muscle  $4.01 \pm 0.25$ , brain  $1.38 \pm 0.15$ , heart  $4.79 \pm 0.25$ , eye  $1.84 \pm 0.13$ , spleen  $1.33 \pm 0.08$ , gill  $24.70 \pm 1.14$ , kidney  $1.83 \pm 0.08$ , stomach  $2.74 \pm 0.13$ , and testis  $15.86 \pm 0.83$ . The results showed that the liver had higher gene expression than all other tissues, and the intestine and gill

had significantly higher gene expression than the liver in both female and male brown trout.

The ovary and testis tissues had the third-highest *gstr* gene expression. When the transcriptional differences between male and female tissues were examined, it was observed that the intestine, gill, kidney, stomach, muscle, and gonads had significantly higher expression in male brown trout, while other tissues did not show significant differences between

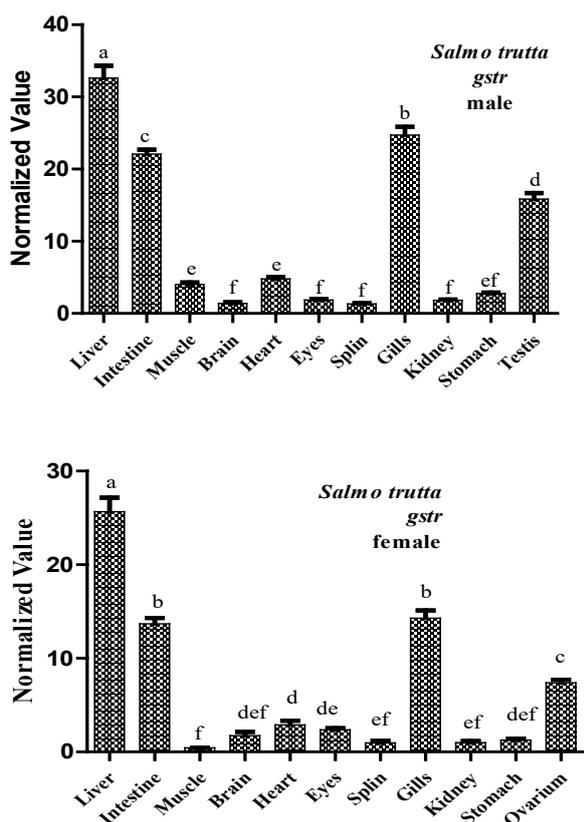


Figure 7. The tissue-specific distribution of brown trout *gstr* gene

In male common carp, the tissue-specific distribution showed the following expression levels: liver  $77.81 \pm 5.95$ , intestine  $46.25 \pm 0.91$ , muscle  $45.95 \pm 3.42$ , brain  $2.56 \pm 0.23$ , heart  $2.20 \pm 0.25$ , eye  $0.92 \pm 0.081$ , spleen  $1.32 \pm 0.18$ , gill  $7.27 \pm 0.37$ , kidney  $1.99 \pm 0.27$ , stomach  $2.46 \pm 0.33$ , and testis  $16.29 \pm 1.16$ . The highest gene expression was observed in the liver for both female and male common carp, while the second-highest gene expression in females was in the intestine, and in males, it was in both the intestine and muscle. The brain, eye, spleen, kidney, heart, and gill tissues showed significantly lower *gstr* gene expression in both female and male common carp. In brown trout, the *gstr* gene exhibits the highest gene expression in the liver tissue in both females and males ( $p < 0.05$ ), while the intestine and gills are identified as tissues with the second-highest gene expression.

The differences between these two tissues are statistically insignificant in both female and male fish. The results indicate that the liver has the highest gene expression among all

male and female brown trout.

The tissue-specific distribution of the *gstr* gene in common carp (Figure 8) was also determined, and the *gstr* gene in female common carp showed the following expression levels: liver  $39.06 \pm 3.63$ , intestine  $29.48 \pm 2.98$ , muscle  $19.32 \pm 1.32$ , brain  $4.07 \pm 0.50$ , heart  $5.96 \pm 0.39$ , eye  $2.11 \pm 0.08$ , spleen  $1.09 \pm 0.093$ , gill  $8.43 \pm 0.33$ , kidney  $1.79 \pm 0.21$ , stomach  $3.00 \pm 0.43$ , and ovary  $12.11 \pm 0.62$ .

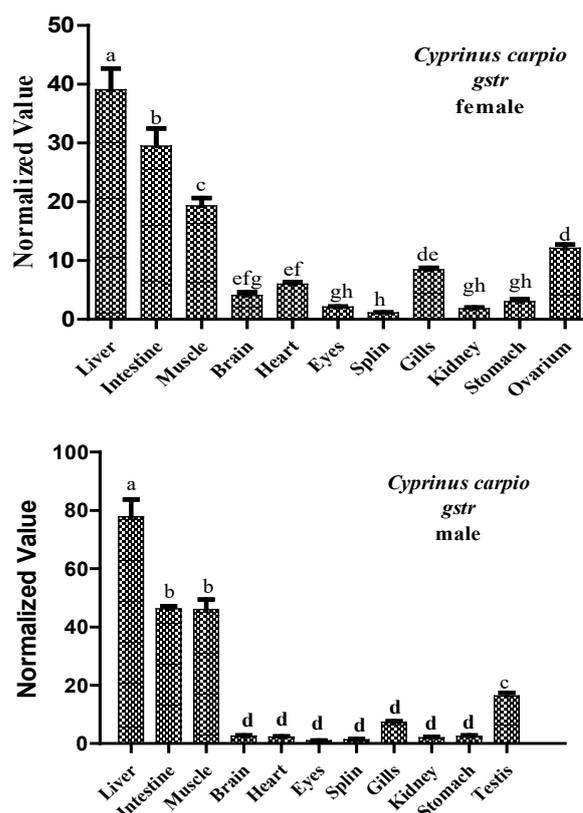


Figure 8. The tissue-specific distribution of common carp *gstr* gene

tissues, the intestine and gills have significantly lower *gstr* gene expression compared to the liver, and ovaries and testes have the third-highest *gstr* gene expression. When examining transcriptional differences between genders, the intestine, gills, kidney, stomach, muscle, and gonads show significantly higher gene expression in males ( $p < 0.05$ ), while the differences among other tissues are statistically not significant.

In common carp, the *gstr* gene shows the highest gene expression in the liver tissue in both females and males ( $p < 0.05$ ). In females, the intestine has the second-highest gene expression, while in males, both the intestine and muscle tissues exhibit the highest gene expression.

## DISCUSSION

Gene expression analysis to determine the effects of various sources of stress on cells compared to healthy cells is commonly used in the diagnosis and treatment of disease

(Aubrecht and Caba, 2005). This approach can also be used to develop compounds that bind to expressed proteins and to identify transcriptional regulators that cause changes in expression levels. The common carp (*Cyprinus carpio*) and brown trout (*Salmo trutta*) will be used in this study to identify and characterize *gstr* gene which is antioxidant enzyme (AE) gene and to determine the biological significance of a signaling pathway. The tissue-specific distribution of the glutathione s transferase (*gstr*) gene in common carp and brown trout will be studied, and the results will be used as essential and fundamental precursor data for other studies. Antioxidant enzymes play a vital role in the antioxidant defense system in biological systems. Therefore, this study will be important for developing gene therapy for stress-induced diseases in the future.

#### Bioinformatics Studies of of *gstr* gene in brown trout and common carp

The designed conserved gene syteny indicates that the *gstr* gene in brown trout and common carp resulted from teleost whole-genome duplication (TTGD). Based on the syteny, it can be said that the conservation rate of the *gstr* gene is quite high (Figure 1). After the teleost-specific genome duplication in teleost fish, many genes have duplicate copies (Braasch and Postlethwait, 2012). However, it was determined that both brown trout and common carp have only one copy of the *gstr* gene. Therefore, it is suggested that this gene underwent duplication first and then one of the copies was lost.

In brown trout and common carp, in-silico analyses were conducted to characterize and identify the *gstr* gene. Especially, valuable data for developing molecular strategies to protect against the effects of reactive oxygen species in cultured fish were obtained and presented to the scientific community. In this study, the *gstr* gene in the brown trout and common carp genomes was found to have 7-6 and 6-5 exon-intron counts, respectively, based on Ensembl database searches. Alignment analyses of the *gstr* gene of brown trout and common carp with their orthologs in rainbow trout, Atlantic salmon, sea bream, sea bass, Coho salmon, and common carp, and Japanese medaka, zebrafish, rainbow trout, Atlantic salmon, brown trout, and sea bream, respectively, using CLUSTAL W (Thompson et al., 1994) revealed that brown trout has high identity and similarity rates with rainbow trout (Figure 5). On the other hand, common carp was found to have the highest identity and similarity rates with Japanese medaka (Figure 6).

#### Tissue-specific transcription of *gstr* gene in brown trout and common carp

Genetic expression changes are primary responses in fish, making genomic analyses a valuable advantage for research, and measurements of gene expression could facilitate the early detection and assessment of adverse effects on fish caused by various stressors (Larsen et al., 2010; Rojas-Hernandez et al., 2019). Approaches to gene expression have the potential to identify sensitive,

mechanism-based biomarkers that can also reveal long-term harmful effects (Voelker et al., 2007). When examining the applications of genomic analysis in aquaculture, it has been observed that responses to stress factors might involve not only small changes in gene expression but also a series of gene interactions (Guo et al., 2023). Core genes generally regulate metabolic pathways, and alterations in these core genes can lead to various outcomes observable through genomic responses (Papin et al., 2003).

#### CONCLUSION

In conclusion, genomic analysis and measurements of gene expression are valuable tools for assessing the effects of stressors on fish and identifying sensitive, mechanism-based biomarkers that can reveal long-term harmful effects. The *gstr* gene exhibits the highest gene expression in the liver tissue of both brown trout and common carp, with statistically significant differences observed between tissues. Additionally, transcriptional differences between genders were observed in several tissues. The importance of examining gene interactions and alterations in core genes that regulate metabolic pathways when examining responses to stress factors in fish. Overall, the use of genomic analysis and gene expression measurements can provide valuable insights into the health of aquatic ecosystems and the effects of environmental contaminants on fish populations.

#### ACKNOWLEDGMENTS AND FUNDING

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#### AUTHOR CONTRIBUTIONS

The manuscript, produced from Badrul Islam Elsevar's master thesis, involves collaborative contributions from the authors. Badrul Islam Elsevar has taken on responsibilities such as literature review, drafting, writing, laboratory experiments, and data analysis and management. Meanwhile, the role of another author, referred to as Mehtap Bayir, includes conceptualization, drafting, writing, review, editing, and supervision. It is important to note that all authors have collectively reviewed and endorsed the final version of the manuscript.

#### CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

#### ETHICAL APPROVAL

The research adhered to all relevant international, national, and institutional guidelines for the ethical care and use of animals. Approval was granted by the Local Ethics Committee for Animal Experiments of Atatürk University (27.05.2021/No:127)

#### DATA AVAILABILITY STATEMENTS

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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# The gonadal health status of Cyprinidae fish species collected from the river impacted by anthropogenic activities

## Antropojenik aktivitelerden etkilenen nehirden toplanan Cyprinidae familyasına ait balık türlerinin gonad sağlığı durumları

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**Abstract:** Many freshwater ecosystems are contaminated with heavy metals released by municipal wastewater, cultivation and factory wastewater. The aim of the study was to evaluate the negative impact of metal pollution on the fish reproductive system. It was performed using the gonadal histopathology, hepatosomatic index (HSI), and gonadosomatic index (GSI) of three fish species, *Capoeta damascina*, *Squalius semae* and *Alburnus sellal* inhabiting in Karasu River (Erzurum, Turkey) contaminated by various anthropogenic activities. The highest GSI values were determined for each sex according to the seasons, and lower GSI values were observed in polluted stations in all three species. It was observed that HSI values in fish varied significantly from station to station. In addition, an increase in ovarian and testicular lesions (degeneration in oocyte and spermatocytes, atresia, congestion, infiltration, edema, vascular hypertrophy, fibrosis) was detected in the polluted areas. The results clearly showed that the metal pollution in the river adversely affected the reproductive system of the fish species living in the river.

**Keywords:** Freshwater fish, Karasu River, gonad histology, GSI, HSI, water pollution, histopathology

**Öz:** Birçok tatlı su ekosistemi, belediye atık suları, tarım ve fabrika atık sularında bulunan ağır metallerle kirlenmektedir. Bu çalışmanın amacı, metal kirliliğinin balıkların üreme sistemi üzerindeki olumsuz etkilerini değerlendirmektir. Bunun için çeşitli antropojenik faaliyetlerle kirlenen Karasu Nehri'nde (Erzurum) yaşayan üç balık türünde (*Capoeta damascina*, *Squalius semae* ve *Alburnus sellal*) gonadal histopatoloji, hepatosomatik indeks (HSI) ve gonadosomatik indeks (GSI) analizleri yapıldı. Mevsimlere göre en yüksek GSI değerleri her cinsiyet için belirlenmiş ve her üç türde de kirliliği istasyonlarda düşük GSI değerleri gözlemlenmiştir. HSI değerleri ise istasyonlar arası önemli oranda değişkenlik göstermiştir. Ayrıca özellikle kirliliği bölge balıklarının yumurtalık ve testislerinde tespit edilen patolojik lezyonlarda (oosit ve spermatozoidlerde dejenerasyon, atrezi, konjesyon, infiltrasyon, ödem, vasküler hipertrofi, fibrosis gibi) belirgin artışların olduğu saptanmıştır. Sonuçlar nehirdaki metal kirliliğinin nehirden yaşayan balık türlerinin üreme sistemini olumsuz etkilediğini açıkça göstermiştir.

**Anahtar kelimeler:** Tatlısu balığı, Karasu Nehri, gonad histolojisi, GSI, HSI, su kirliliği, histopatoloji

## INTRODUCTION

Pollutants merged in both terrestrial and aquatic environments due to anthropogenic activities have a negative impact on both human and other organisms. It is known that anthropogenic chemical production has increased in recent years. This production reaches up to 400 million tons annually (Gavrilescu et al., 2015). This increase causes a rise in the amounts of substances merging in aquatic system. There is not enough information on the potential environmental risks of these substances as of now (Naidu et al., 2016). Mixing of unwanted substances in aquatic systems results in an unbalance regarding physical, chemical, and biological properties of water ecologically (Yadav et al., 2018). Among these substances, industrial wastes cause water pollution, thereby posing a threat to both aquatic plants and animals (Gupta et al., 2015). This pollution leads to a constant decrease in water flora and fauna, especially in fish population. All aquatic species, including fish, either absorb pollutants directly from water or take them through food chain (Łuczynska et al.,

2018). Fish, being the most important species used in the estimation of pollutant levels in water, provide some advantages in terms of identifying natural properties of aquatic systems and evaluating habitat changes (Martinez-Haro et al., 2015). In addition, due to being in most of the aquatic systems exposed to pollutants, their effects on the structure of food chain, and their ecological suitability, fish are considered as a main bioindicator in evaluating the quality of aquatic ecosystems (Corredor-Santamaria et al., 2019).

Exposure to pollutants may cause an exposure to acute or chronic toxicity in fish organs, especially gonads. This leads to a deficiency in reproduction. The health of the fish reproductive process is an important indicator that the organism is self-sustainable (Zulfahmi et al., 2018). Pesticides, heavy metals, polycyclic aromatic hydrocarbons, polychlorinated biphenyls, alkylphenolic compounds, phthalates, and endocrine disrupting chemicals may damage the reproductive physiology of fish populations (Agbohessi et al., 2015). In some studies, it

was reported that gonadal abnormalities, decreased gonadosomatic index values, varied hormone levels, delay in plasma vitellogenin levels and gametogenesis occurred in fish which were found in areas with wastewater containing agricultural and industrial chemicals (Gilroy et al., 2012; Kaptaner, 2015). However, there is not enough information on the ecological risks caused by reproductive disruption following exposure to toxic substances in freshwater fish species in Turkey and the subject needs further research.

*Capoeta damascina* (Güldenstädt, 1773), *Squalius semae* (Linnaeus, 1758) and *Alburnus sellal* (Heckel, 1843) species used in this study belong to Cyprinidae family. These species are widespread in Euphrates and Tigris River systems in the Eastern and Southeastern Anatolia regions in Turkey (Geldiay and Balık, 2009). Wastewater in Erzurum province, agricultural activities in Karasu Basin and industrial wastes pollute the surface water of the Karasu River (Sönmez et al., 2012; Anonymous, 2016; Aydoğan et al., 2017; Dane and Şişman, 2017). In fact, previous reports have shown that the surface water and sediment of the river are particularly contaminated with metals (Dane and Şişman 2020a, 2020b). In this study, it was aimed to evaluate histopathologically how the fish species found in the natural fauna of selected locations are affected in terms of gonadal health due to metal pollution.

## MATERIALS AND METHODS

Karasu River is unfortunately polluted by discharge of domestic and industrial (cement, paint, and plaster factories) wastes. Wastewater caused by industrial facilities located in the organized industrial zone in Erzurum is connected to municipality's sewage, and the sewage waste is discharged into Karasu River (Anonymous, 2016). In the study, four different stations were selected on the river. The stations were chosen by paying attention to the pollution load of the river and the regions where the fish species were observed. The first station was Dumlu (1st station 40° 05' 36.1" N 41° 22' 49.0" E). Other stations were as follows: Ilıca (2nd station 39° 57' 10.6" N 41° 04' 15.2" E), Aşkale 1 (3rd station 39° 54' 52.7" N 40° 40' 29.4" E) and Aşkale 2 (4th station 39° 56' 15.1" N 40° 37' 25.9" E) (Figure 1).

Dumlu station was taken as the reference region. Livestock and pasture farming are carried out around it and there is a settlement with a population of 1413. There are two factories around the Ilıca (2nd) and agricultural activities are carried out. In addition, the sewage water of the city is given to the river from here. Aşkale stations (3rd and 4th) are the last areas where the river leaves the Erzurum plain and where all the wastes of the city mix, and there are paint and cement factories nearby. Average heavy metal levels and physico-chemical parameters of the surface waters of the sampling stations are shown in Table 1 (Dane and Şişman, 2020a).

Species belonging to the natural fauna of the river, *Capoeta damascina*, *Squalius semae* and *Alburnus sellal* were caught from the stations using nets in May, June, July, August, and September (2015-2016). A total of 158 mature fish were

caught from the river, including 54 *C. damascina* (28 ♀♀ 26 ♂♂), 52 *A. sellal* (29 ♀♀ 23 ♂♂) and 52 *S. semae* (24 ♀♀ 28 ♂♂). Permissions required for the study were taken from the relevant authorities before the study was initiated. The fish were brought to the laboratory alive and taken to intensely air-conditioned aquariums. No morphological abnormalities were observed in the fish. The mean total lengths and weights of the fish were  $20.79 \pm 3.42$  cm and  $89.08 \pm 21.32$  g (*C. damascina*),  $17.83 \pm 3.96$  cm and  $44.22 \pm 5.37$  g (*A. sellal*),  $16.07 \pm 2.03$  cm and  $48.09 \pm 9.26$  g (*S. semae*).

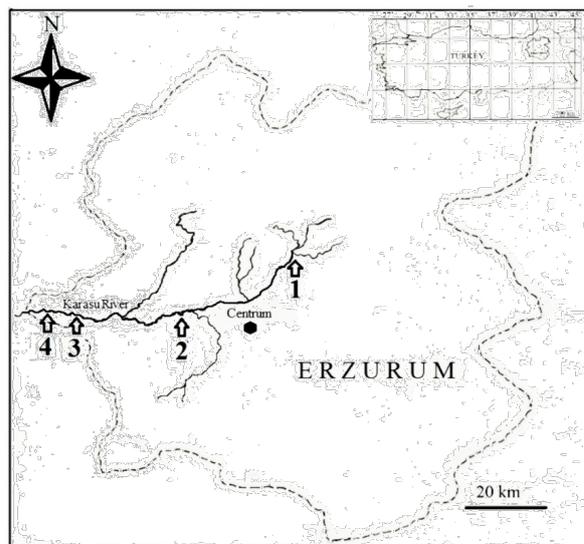


Figure 1. General view of the sampling stations

The hepatosomatic index (HSI) is expressed as the ratio of liver weight to body weight, and provides information about the health status of the fish and the quality of water. The fish were decapitated and the liver were removed. Hence the total organ weight of liver was taken for HSI. HSI was calculated according to the following formula:  $HSI = (\text{Liver weight (g)} / \text{Fish weight (g)}) \times 100$  (Sadekarpawar and Parikh, 2013).

The gonadosomatic index (GSI) represents the ratio of fish gonad weight to body weight and used in identifying gonadal development in fish. For GSI calculation, fish were euthanized using MS 222 (75 mg/L). After measuring fish weight, the abdomen was cut from the front of the anus to the bottom of the gill, and organs were taken out the body. After measuring gonadal weight, the following formula was used in GSI calculation.  $GSI = (\text{Gonadal weight}) / (\text{Total body weight}) \times 100$  (Sadekarpawar and Parikh, 2013).

Fifteen fish from each station were used in histological analysis. Gonad samples were fixed in 10% neutral buffered formalin for up to 48 hours and subjected to a standard histological procedure. Paraffin embedded samples were cut with microtome with 5µm thickness. Slides were stained with hematoxylin and eosin (H&E) (Gautier, 2011) and microscopically analyzed with Leica DM750 light microscope and LASEZ software programme. The 10 sections of the gonads of each fish were analyzed. Twenty fields per section of tissue were observed.

**Table 1.** Current data of the mean metal levels and physico-chemical parameters of surface water samples of the stations (mg/L), and the water quality classes of the river water according to Turkish Water Pollution Control Regulation, and maximum acceptable limits of metal for river waters according to United Nations Economic Commission for Europe (UNECE, 1994), (Dane and Şişman, 2020a)

Metals	1. Station	2. Station	3. Station	4. Station	TS IV	UNECE 1994
Cr	8.55 ± 1.5 <sup>ab</sup>	6.7 ± 1.2 <sup>ab</sup>	12.1 ± 2.1 <sup>ab,*</sup>	13.1 ± 1.8 <sup>ab,*</sup>	>0.2	0.016
Mn	5.5 ± 1.1 <sup>a</sup>	5.7 ± 1.3 <sup>a</sup>	9.3 ± 1.5 <sup>a,*</sup>	7.7 ± 1.4 <sup>a,*</sup>	>3.0	
Fe	4.1 ± 0.9	5.5 ± 1.1 <sup>a,*</sup>	8.4 ± 1.3 <sup>a,*</sup>	7.8 ± 1.6 <sup>a,*</sup>	>5.0	
Co	0.7 ± 0.1 <sup>a</sup>	0.8 ± 0.1	1.26 ± 0.2 <sup>a,*</sup>	1.2 ± 0.1 <sup>a,*</sup>	>0.2	
Ni	0.8 ± 0.1 <sup>a</sup>	0.74 ± 0.1 <sup>a</sup>	1.17 ± 0.1 <sup>a</sup>	1.01 ± 0.1 <sup>a</sup>	>0.2	1.400
Cu	0.51 ± 0.1 <sup>ab</sup>	0.57 ± 0.1 <sup>ab</sup>	0.88 ± 0.1 <sup>ab,*</sup>	0.82 ± 0.1 <sup>ab,*</sup>	>0.2	0.018
Zn	0.42 ± 0.1 <sup>b</sup>	0.46 ± 0.1 <sup>b</sup>	0.66 ± 0.1 <sup>b</sup>	0.61 ± 0.1 <sup>b</sup>	>2	0.120
As	1.14 ± 0.1 <sup>ab</sup>	1.27 ± 0.1 <sup>ab</sup>	1.55 ± 0.2 <sup>ab,*</sup>	1.46 ± 0.2 <sup>ab,*</sup>	>0.1	0.360
Se	0.11 ± 0.01 <sup>a</sup>	0.20 ± 0.01 <sup>a,*</sup>	0.24 ± 0.01 <sup>a,*</sup>	0.35 ± 0.05 <sup>a,*</sup>	>0.02	
Pb	0.29 ± 0.01 <sup>ab</sup>	0.69 ± 0.1 <sup>ab,*</sup>	2.55 ± 0.5 <sup>ab,*</sup>	2.96 ± 0.6 <sup>ab,*</sup>	>0.05	0.082
Physico-chemical parameters						
Temperature (°C)	21±4.1	23±4.8 <sup>*</sup>	25±5.7 <sup>*</sup>	25±5.5 <sup>*</sup>	>30	-
pH	7.81±1.5	7.74±1.6	8.03±1.2	8.06±1.4	9.0	-
Dissolved oxygen (mg/L)	7.62±1.0	6.32±1.5	5.60±1.1 <sup>*</sup>	4.31±0.8 <sup>*</sup>	<3	-

Values are expressed as mean ± standard errors. Asterisk shows statistical difference compared to reference station (1st Station). TS IV; Turkish Standard IV means the surface water are polluted. The letter "a" indicates that metal concentration exceeds the TS IV value, and the letter "b" indicates that metal concentration exceeds the UNECE limit.

Histological damage detected in gonads was assessed via the Degree of Tissue Change (DTC). Damages detected in tissues are grouped as the following according to DTC parameter: 0 (no abnormality), 1 (low abnormality frequency), 2 (medium abnormality frequency), and 3 (high abnormality frequency) (Abdel-Moneim et al., 2012). Abnormalities in gonads were classified according to the damage phase in DTC calculation. These phases are as follows: 1st Phase: Tissue has a normal function. 2nd Phase: Normal function of the tissue is disrupted at medium severity. 3rd Phase: An irreversible damage has occurred in the tissue (Bernet et al., 1999). DTC values were found using the formula:  $DTC = (1 \times \Sigma I) + (10 \times \Sigma II) + (100 \times \Sigma III)$ . In the formula,  $\Sigma I$ ,  $\Sigma II$  and  $\Sigma III$  indicate the total number of abnormalities observed in the phases respectively. After finding the DTC value for each fish, the mean index was calculated for each station. This index was analyzed according to following criteria. DTC: between 0-10: organ functions are normal; between 11-20: mild organ damage; between 21-50: medium-level organ damage; between 51-100: severe organ damage; above 100: irreversible organ damage (Poleksic and Mitrovic-Tutundzic, 1994).

The general evaluation of GSI and HSI were performed by ANOVA. Duncan test was used for multiple comparisons in variance analysis. The data were interpreted by considering  $p < 0.05$  significance level.

## RESULTS

Mean HSI values of the species caught according to stations are given in Table 2. The highest HSI values for *C. damascina* and *S. semae* were recorded in the 3rd station, The highest value for *A. sellal* was obtained in the 4th station. When a comparison was made between the stations in terms of HSI values, it was determined that the HSI values were significantly higher in the other three stations compared to the 1st station ( $p < 0.05$ ).

**Table 2.** HSI values of the species according to stations

Stations	<i>Capoeta damascina</i>	<i>Alburnus sellal</i>	<i>Squalius semae</i>
1. Station	0.34 ± 0.06 <sup>c</sup>	0.40 ± 0.07 <sup>c</sup>	0.46 ± 0.06 <sup>d</sup>
2. Station	0.63 ± 0.07 <sup>b</sup>	0.95 ± 0.08 <sup>b</sup>	0.90 ± 0.07 <sup>c</sup>
3. Station	1.34 ± 0.03 <sup>a</sup>	1.29 ± 0.04 <sup>a</sup>	1.70 ± 0.10 <sup>a</sup>
4. Station	1.11 ± 0.06 <sup>a</sup>	1.43 ± 0.08 <sup>a</sup>	1.38 ± 0.08 <sup>b</sup>

Data are presented as mean ± SD. Differences between the averages indicated by the different letters in the same column are statistically significant ( $p < 0.05$ )

The spawning time of the fish caught in the Karasu River was determined by analyzing the gonadosomatic index (GSI) of the male and female individuals. In Table 3, the mean GSI values of female and male individuals are presented for three species. The highest GSI values were recorded in June, whereas the lowest values were recorded in August for *C. damascina*. On the other hand, the highest GSI value was found in *A. sellal* females in June, males in May, and the lowest in both sexes in August. The mean highest value for both female and male individuals of *S. semae* was recorded in May, whereas the lowest value was recorded in July. When the GSI values of fish were compared, the highest average index among the species was observed in *A. sellal*. When the values of the female and male individuals were compared, it was found that the GSI values of the female individuals were higher than the males in all three species. According to the data, the reproductive period for the species was found to be May and June.

The change in mean GSI values in these species by station is given in Table 4. When GSI values of species were analyzed by station, the lowest value for *C. damascina* was recorded in the 3rd station, and the highest value was recorded in the 1st station. The highest mean GSI value for *A. sellal* was obtained in the 1st station, and the lowest GSI value was recorded in the 4th station. The lowest mean value for *S. semae* was recorded in the 3rd station, and the highest mean value was recorded in the 1st station.

**Table 3.** GSI values of the species by months

Period	<i>Capoeta damascina</i>		<i>Alburnus sellal</i>		<i>Squalius semae</i>	
	♀♀	♂♂	♀♀	♂♂	♀♀	♂♂
May	3.86 ± 1.08 <sup>b</sup>	2.52 ± 0.33 <sup>b</sup>	5.04 ± 0.25 <sup>b</sup>	4.75 ± 0.58 <sup>a</sup>	4.72 ± 0.65 <sup>a</sup>	3.24 ± 0.16 <sup>a</sup>
June	5.87 ± 1.01 <sup>a</sup>	3.85 ± 1.05 <sup>a</sup>	7.65 ± 1.99 <sup>a</sup>	3.81 ± 0.35 <sup>b</sup>	3.65 ± 0.11 <sup>b</sup>	2.59 ± 0.12 <sup>b</sup>
July	1.24 ± 0.03 <sup>d</sup>	0.98 ± 0.03 <sup>d</sup>	2.56 ± 0.35 <sup>c</sup>	2.02 ± 0.22 <sup>c</sup>	0.82 ± 0.05 <sup>e</sup>	0.25 ± 0.08 <sup>e</sup>
August	1.04 ± 0.05 <sup>e</sup>	0.39 ± 0.02 <sup>e</sup>	0.92 ± 0.07 <sup>e</sup>	0.87 ± 0.01 <sup>e</sup>	1.06 ± 0.03 <sup>d</sup>	0.96 ± 0.07 <sup>c</sup>
September	1.36 ± 0.02 <sup>c</sup>	1.14 ± 0.02 <sup>c</sup>	1.26 ± 0.03 <sup>d</sup>	1.12 ± 0.02 <sup>d</sup>	1.20 ± 0.02 <sup>c</sup>	0.81 ± 0.04 <sup>d</sup>

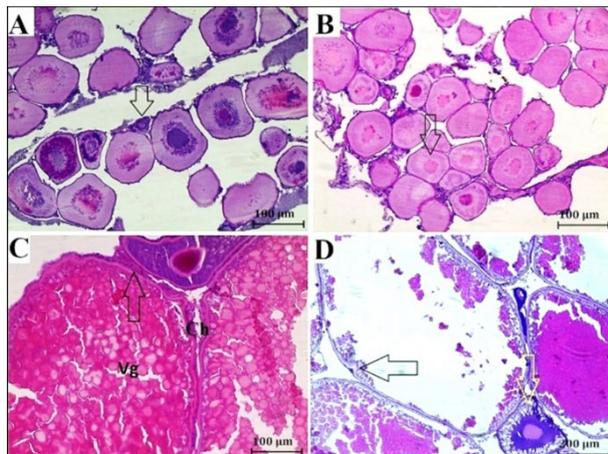
Data are presented as mean ± SD. Differences between the averages indicated by the different letters in the same column are statistically significant ( $p < 0.05$ )

**Table 4.** GSI values of the species according to stations

Stations	<i>Capoeta damascina</i>	<i>Alburnus sellal</i>	<i>Squalius semae</i>
1. Station	5.90 ± 0.20 <sup>a</sup>	6.13 ± 0.94 <sup>a</sup>	5.58 ± 1.04 <sup>a</sup>
2. Station	5.56 ± 0.10 <sup>a</sup>	4.28 ± 0.51 <sup>b</sup>	4.03 ± 0.23 <sup>b</sup>
3. Station	3.34 ± 0.15 <sup>b</sup>	3.41 ± 0.18 <sup>c</sup>	3.01 ± 0.05 <sup>c</sup>
4. Station	4.12 ± 0.13 <sup>b</sup>	3.06 ± 0.12 <sup>d</sup>	3.27 ± 0.12 <sup>c</sup>

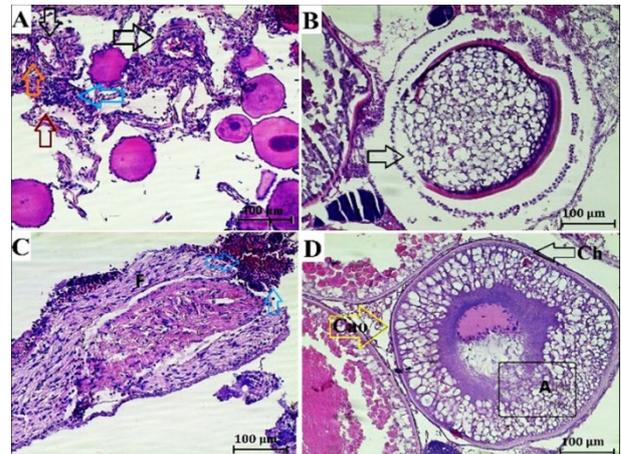
Data are presented as mean ± SD. Differences between the averages indicated by the different letters in the same column are statistically significant ( $p < 0.05$ )

According to these data, it was concluded that mean GSI values were remarkably low, especially in the 3rd and 4th stations, for all three species ( $p < 0.05$ ). When the current state of the surface waters of the stations where the fish samples were taken, the physico-chemical parameters were within the allowable limit values, while the metal levels (Cr, Mn, Fe, Co, Ni, Cu, Zn, As, Se, Br and Pb) were higher at the third and fourth stations compared to the other stations (Table 1). On the histological slides of fish caught from Station 1, follicles containing multiple oocysts at different developmental stages (chromatin nucleolar, perinucleolar, cortical alveolar, vitellogenic phase, and maturation stage) were observed (Figure 2).



**Figure 2.** Normal ovarian histology of fish from the Karasu River. A) Chromatin nucleolar oocyte (arrow), (*C. damascina*). B) Perinucleolar oocyte (arrow). C) Vitellogenic oocyte (arrow), Vg: vitellus granule, Ch: chorion (*C. damascina*). D) Cortical alveolar oocyte (yellow arrow), and mature oocyte (black arrow: animal invagination) (*A. sellal*). H&E

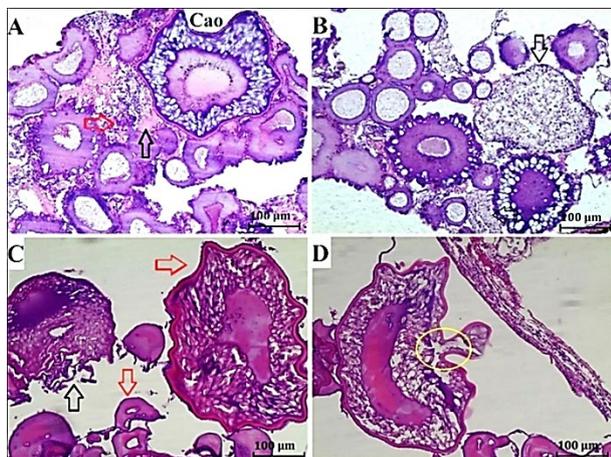
When the ovaries were evaluated according to the stations, histopathological damage was observed at varying rates in all three species, especially from the last two stations. In the section in which oocysts were placed belonging the chromatin nucleolar phase in the fish analyzed, congestion in blood vessels, melanomacrophage, mononuclear cell infiltration, and edema were observed (Figure 3A). In addition to the frequently observed enlargement of the follicular epithelium of the cortical alveolar oocyte (Cao) (Figure 3B), mononuclear cell infiltration damage (Figures 3C and 4A), and a severe case of fibrosis (Figure 3C) were detected. Cao shows the cell membrane of the oocyte. The abnormality showed that the vacuoles borders in the cell and the cytoplasm were mixed together in some places. Disorder of cytoplasm and vacuole in the Cao (Figure 3D), proteinaceous fluid and edema in the interstitial space (Figure 4A), as well as atresia (Figure 4B) were identified. Other pathologies were degeneration and malformation in oocytes (Figure 4C) and degeneration in the cytoplasm of the transformed cortical alveolar oocyte (Figure 4D).



**Figure 3.** The ovarian pathologies detected in fish species of Karasu River. A) Congestion (black arrows), melanomacrophage (orange arrow), infiltration (blue arrow), edema (red arrow), (*C. damascina*). B) Enlargement of the follicular epithelium (arrow), (*A. sellal*). C) Infiltration (blue arrows) and fibrosis (F), (*C. damascina*). D) Cytoplasm and vacuoles disorder (square), Cao; cortical alveolar oocyte, Ch; chorion, A; alveol (*A. sellal*). H & E

In Table 5, the histological damages detected in the ovary tissues of fish species according to the stations were given with

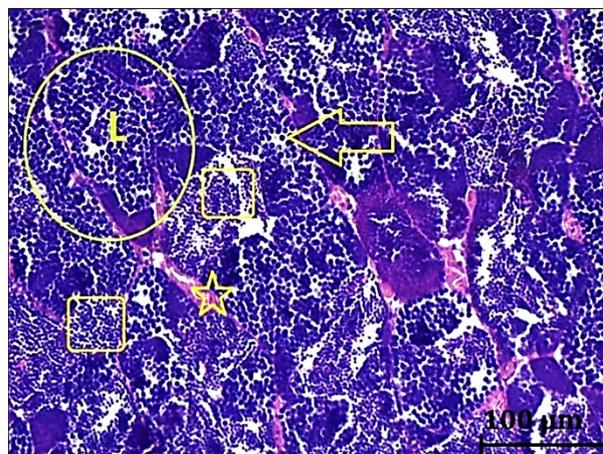
DTC frequencies. Accordingly, it was concluded that there was no difference between the species in terms of the type of histopathological abnormality, and the frequency of histopathological damage from the 1st station to the others increased even more for all three species.



**Figure 4.** The ovarian pathologies detected in fish species of Karasu River. A) Edema and interstitial proteinaceous fluid (black arrow), infiltration (red arrow), Cao; cortical alveolar oocyte, (*A. sellal*). B) Atresia (arrow), (*A. sellal*). C) Degeneration in the oocyte (black arrow) and oocyte deformity (red arrows), (*S. semae*). D) Degeneration in the oocyte cytoplasm of the deformed cortical alveolar oocyte (yellow circle), (*S. semae*). H & E

When the testicular tissue of the fish caught from Station 1 was examined, a normal structure consisting of numerous seminiferous tubules and interstitial spaces between the tubules, curved, oval or round shaped and of different sizes, containing germ cells at different developmental stages was observed. Secondary spermatocytes that were dark stained in mature testis were observed as clusters in an area close to the tubule lumen. Being the smallest cells, spermatids that were coloured darker was on the lumen. In many sections, it was found that sperms filled the inside of tubules completely (Figure 5).

On the other hand, histological damages were detected at varying frequencies in the testicles of fish caught from other stations. In fish testes analyzed, especially vascular hypertrophy (Figure 6A) and severe congestion (Figures 6A and 6B) were remarkable. In addition, degenerations in the efferent duct and seminiferous tubules (Figure 7A), proteinaceous fluid and inflammatory infiltrate (Figure 7A), edema (Figure 7A and 7B), hypertrophy and degeneration in spermatocytes (Figure 8A), separation in the interstitial area (Figure 6B, 7A, and 8B), and fibrous formations (Figure 6B, 7A, and 8B) were observed. While the lumen of the efferent duct should be smooth, a part of the lumen surface was fragmented in polluted area fish testis (Figure 7A).



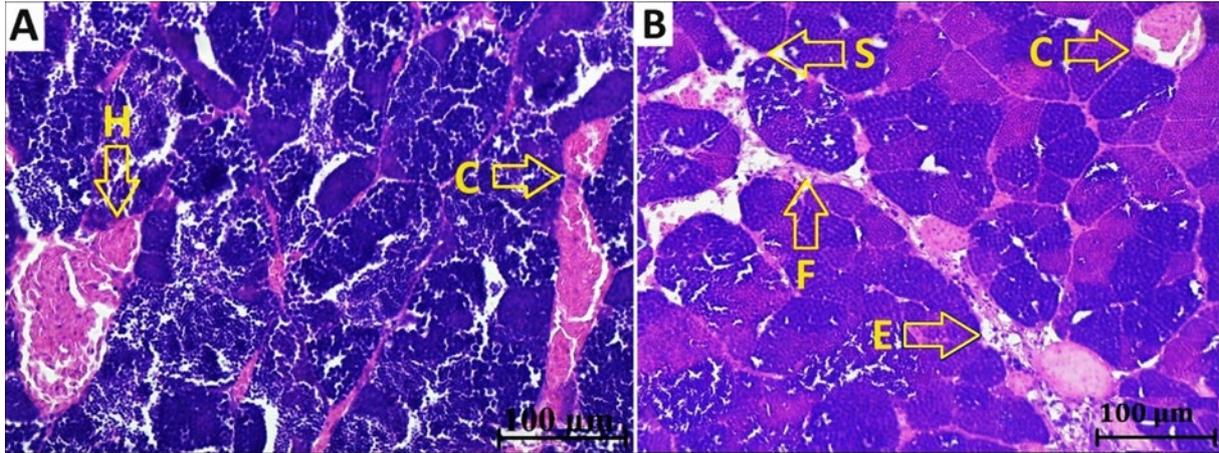
**Figure 5.** Normal testis histology of fish from the Karasu River (*C. damascina*). Blood vessel (star), spermatids (squares), secondary spermatocyte (arrow), lumen (L), and seminiferous tubule (circle). H & E

In many testes sections, the borders of epithelium surrounding tubules could not be seen clearly, and tissue integrity was disrupted (Figure 8A). Major degeneration was also noted in the seminiferous tubule epithel (Figure 8B). Congestion in tissues with abnormalities has been observed as a common pathology (Figures 8A and 8B).

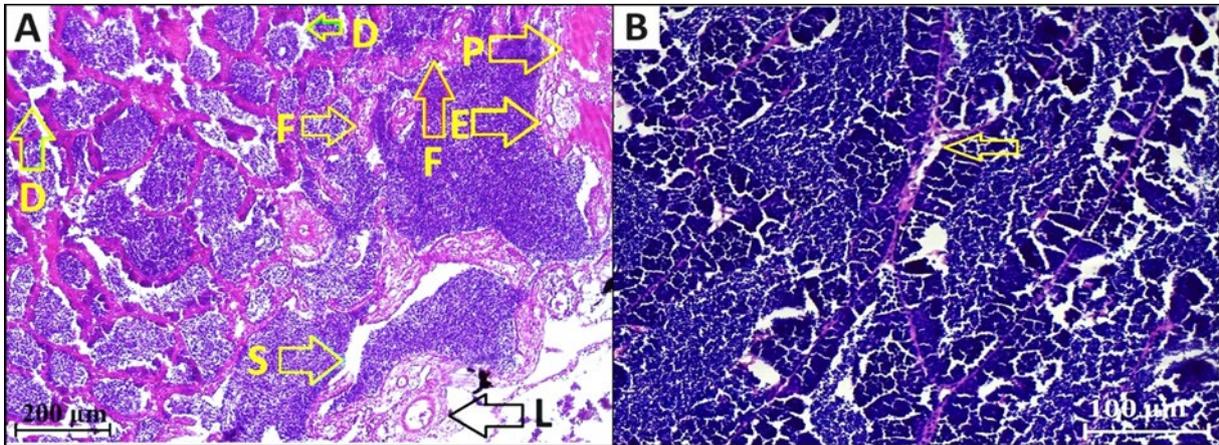
**Table 5.** Histological abnormalities and DTC frequencies detected in the ovaries of the species according to the stations

Stations Fish species	DTC level	1. St			2. St			3. St			4. St			
		C	A	S	C	A	S	C	A	S	C	A	S	
Ovarium pathologies	DTC level													
Atresia	I	1	1	1	1	1	1	1	2	2	1	2	1	
Infiltration	I	0	0	0	1	0	1	2	2	2	1	2	2	
Proteinaceous fluid	I	0	0	0	0	0	1	1	2	2	1	2	2	
Congestion	I	0	0	0	0	0	0	2	1	2	2	2	2	
Melanomacrophage center	I	1	1	1	1	1	1	2	1	3	1	3	3	
Oocyte deformity	I	0	0	0	0	0	0	1	0	1	0	1	1	
Edema	I	0	0	0	0	0	1	1	1	2	1	1	1	
Enlargement of the follicular epithelium	II	0	0	0	0	0	0	1	2	2	0	1	1	
Degeneration in the oocyte cytoplasm	II	0	0	0	0	1	0	0	1	2	1	1	1	
Degeneration of oocytes	II	0	0	0	0	0	1	1	1	2	1	1	1	
Fibrosis	III	0	0	0	0	0	0	1	0	1	0	1	0	

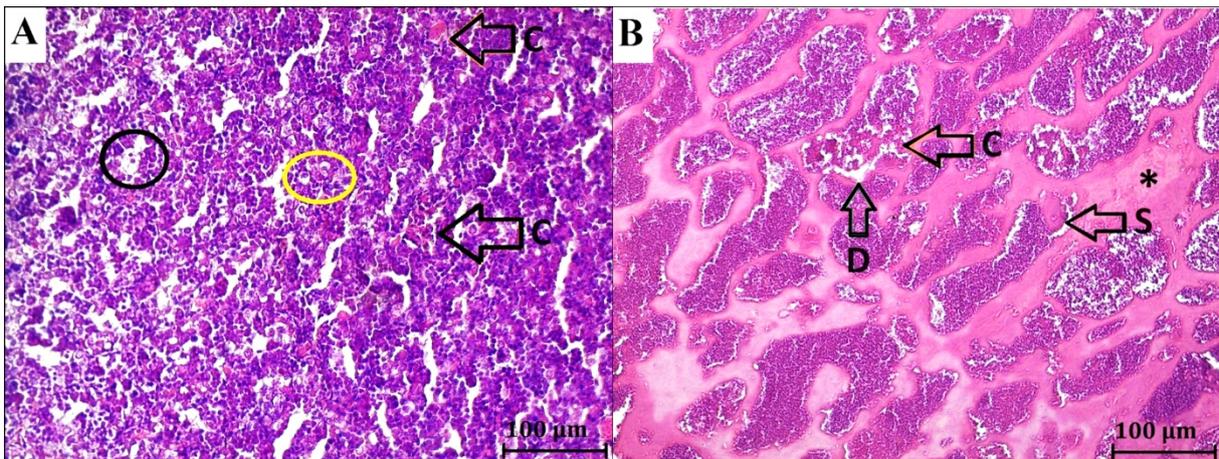
0: no alteration, 1: mild and focal, 2: moderate and multi-focal, 3: severe and diffuse alterations. St; Station, C; *Capoeta damascina*, A; *Alburnus sellal*, S; *Squalius semae*.



**Figure 6.** The testis pathologies detected in fish species of Karasu River. A) Vascular hypertrophy (H) and congestion (C), (*C. damascina*). B) Congestion (C), fibrosis (F), separation in the interstitial area (S) and edema (E). H & E



**Figure 7.** The testis pathologies detected in fish species of Karasu River. A) Proteinaceous fluid and inflammatory infiltrate (P), degeneration of seminiferous tubule (D), fibrosis (F), edema (E), separation in the interstitial area (S), lumen degeneration in the efferent duct (L), (*A. sellal*). B) Edema (yellow arrow) (*A. sellal*). H & E



**Figure 8.** The testis pathologies detected in *S. semae*. A) Degeneration in primary spermatocyte (black circle), hypertrophy in primary spermatocyte (yellow circle), congestion (C), and undetermined seminiferous tubule boundaries (general view). B) Degeneration of the seminiferous tubule epithelium (D), congestion (C), separation in the interstitial area (S), and severe fibrosis (asterisk). H & E

The histological damages detected in the testes of fish species according to stations were given with DTC frequencies in Table 6. Accordingly, it was concluded that there was no difference among fish species in terms of the type of histopathological damage.

Similarly, in all three species, a significant increase was observed in the frequency of the damages at stations 3 and 4. Mean DTC values of fish gonads are given in Table 7. The DTC values demonstrated that gonads had a normal function in the 1st station in all three species, whereas gonads had mild or medium-level damage in other stations. DTC values for *C. damascina* revealed that gonads had mild damage in the 4th station, medium-level

damage in the 3rd station, and had normal structure in the 2nd station. DTC values for *A. mossulensis* revealed that the organ had medium-level damage in the 3rd and 4th stations, and mild damage in the 2nd station. DTC values for *S. semae* revealed that gonads had medium-level damage in the 3rd and 4th stations, and mild damage in the 2nd station.

When DTC values for these species were compared, it was seen that the highest values belonged to *S. semae*. While the highest DTC values for *C. damascina* and *S. semae* were recorded in the 3rd station, the highest value for *A. sellal* was recorded in the 4th station. It was found that the differences in DTC values were statistically significant ( $p < 0.05$ ).

**Table 6.** Histological abnormalities and DTC frequencies detected in the testes of the species according to the stations

Station	1. St			2. St			3. St			4. St			
	C	A	S	C	A	S	C	A	S	C	A	S	
<b>Testis pathologies</b>	<b>DTC level</b>												
Proteinaceous fluid and inflammatory infiltrate	I	0	0	0	0	1	1	2	1	3	1	2	2
Separation in the interstitial area	I	0	0	0	0	0	1	2	1	2	1	1	1
Congestion	I	1	1	1	1	1	1	2	2	3	2	2	2
Edema	I	0	0	0	0	0	0	1	1	2	1	2	1
Hypertrophy in spermatocyte	I	0	0	0	0	0	0	1	1	2	1	1	1
Deformity of the seminiferous tubule	I	0	0	0	0	0	1	1	2	2	1	1	1
Undetermined seminiferous tubule boundaries	I	0	0	0	1	1	1	2	2	3	2	2	3
Vascular hypertrophy	I	0	0	0	1	1	1	1	2	2	1	1	2
Lumen degeneration of efferent duct	II	0	0	0	0	0	0	1	1	1	1	1	1
Degeneration in spermatocyte	II	0	0	0	0	0	0	1	1	1	1	1	1
Degeneration of seminiferous tubule	II	1	1	1	1	1	1	3	2	3	2	3	3
Fibrosis	III	0	0	0	0	0	0	1	0	1	0	1	1

0: no alteration, 1: mild and focal, 2: moderate and multi-focal, 3: severe and diffuse alterations. St; Station, C; *Capoeta damascina*, A; *Alburnus sellal*, S; *Squalius semae*.

**Table 7.** Average DTC values for three fish species from the stations

Stations	<i>Capoeta damascina</i>	<i>Alburnus sellal</i>	<i>Squalius semae</i>
1. Station	5.85 ± 0.22 <sup>d</sup>	8.03 ± 0.31 <sup>d</sup>	8.07 ± 0.35 <sup>d</sup>
2. Station	8.61 ± 0.32 <sup>c</sup>	16.02 ± 0.25 <sup>c</sup>	18.20 ± 0.14 <sup>c</sup>
3. Station	28.60 ± 0.34 <sup>a</sup>	23.16 ± 0.27 <sup>b</sup>	47.63 ± 0.25 <sup>a</sup>
4. Station	18.54 ± 0.19 <sup>b</sup>	40.10 ± 0.24 <sup>a</sup>	39.50 ± 0.36 <sup>b</sup>

Data are presented as mean ± standard deviation. Differences between the averages indicated by the different letters in the same column are statistically significant ( $p < 0.05$ ).

## DISCUSSION

Heavy metal pollution is considered to be a serious problem especially in aquatic systems (Joshi, 2011). The reason for the pollution is the increasing industrial, agricultural and mining activities. These activities are increasing day by day (Ashraf et al., 2012). The Karasu River takes all the pollutants of the Karasu Basin and the pollution in the river unfortunately continues. In previous studies, it was reported that the metals analyzed in the water and sediment of the river were above the reported standard values (Sönmez et al., 2012; Aydoğan et al., 2017; Dane and Şişman, 2017), and that the surface waters were extremely polluted water of 4th class quality. In addition, in 2015-2016, concentrations of 6 elements each (V, Mn, Fe, Co, Ni, Sr) in 3rd station and (Ti, Cr, Cu, Zn, As, Pb) in 4th station in water samples were found to be higher compared to the others, and the abiotic parameters (temperature, pH, and dissolved oxygen) did not exceed the standard (Dane and Şişman, 2020a, 2020b). Therefore, it is highly probable that the low GSI values and high gonad

histopathologies detected in the fish caught from the 3rd and 4th stations in the current study are the effects of heavy metals in the water.

The GSI value was analyzed on a monthly basis in order to identify gonad development in the fish. In Karasu River, the highest mean GSI value was recorded in June and the lowest value in August for *C. damascina* female and male population. Similarly, Sen et al. (2008) reported that the spawning period for *C. damascina* was between the first week of June and second week of July, while the highest GSI value was recorded in late May for females, and in early June for males, and the lowest values were recorded in July. For *A. sellal*, the highest GSI value was recorded in June for females, and in May for males, while the lowest value was recorded in August. In many studies, it was reported that the highest GSI values of the species were in June, as it was the case in our study (Uçkun and Gökçe, 2015). In Karasu River, the highest mean GSI

value was recorded in May and the lowest value in July for *S. semae*. The spawning period for *S. semae* was also reported to be in May and July in Karakaya Dam Lake and Muş Karasu Stream (Kalkan et al., 2005; Sen and Saygin, 2008). GSI is also an indicator of reproductive success being sensitive to various chemical pollutants. Monitoring pollutants which have negative effects on germ cells development and spawning of fish is necessary for preserving their genetic distribution in their region and ecological processes (Corsi et al., 2003). The comparison of GSI values between the stations in the study revealed that the mean GSI values were significantly lower in the 3rd and 4th stations compared to the 1st station for all three species. At the same time, this finding showed that these stations are the most polluted locations of the river. Similarly, low GSI values were reported at stations with the highest pollution density in different fish species (Ribeiro et al., 2013; Kaptaner, 2015). Sadekarpawar and Parikh (2013) reported that pollution in freshwater resources negatively affects the gonads of *Oreochromis mossambicus* based on GSI values and histopathological analysis results.

Aquatic pollution causes an increase in HSI value. HSI is accepted as a good indicator for chemical pollution and provides information on the fish health (Pyle et al., 2005). In the current study, significant differences between HSI values and stations were determined. There are some studies that support this situation. Authman (2011) reported that HSI value in fish exposed to high-dose AI was higher than control group. Monsefrad et al. (2012) reported that some heavy metals were determined in the liver and muscle of fish caught in the Caspian Sea, and the metals increased the fish liver weight and there was a positive correlation between Cd levels and HSI values.

Histopathological abnormalities detected in gonads of the species analyzed in the study has revealed that metal pollution causes serious damages for all three species. In the study, the increase in the frequency of ovarian histopathology in polluted stations was remarkable. The atresia process observed in the study may occur as a normal physiological mechanism in the fish ovary. On the other hand, it is known that atresia is an important response to water pollution. Atresia observed especially in previtellogenic oocyte is an important indicator of a pathological case (Kaptaner, 2015). Hyperplasia and hypertrophy in granulosa cells taking part in the atresia process is a typical sign of atresia (İşisağ Üçüncü and Çakıcı, 2009). The increase in melanomacrophage centers storing xenobiotic substances and containing pigment in ovary in terms of number and size reflects the stress conditions surrounding fish such as chemical pollution. Blazer (2002) reported that severe fibrosis detected in ovaries could be a chronic tissue response to damages caused by pollutants. Studies investigating the effects of heavy metal pollution on the ovaries have reported deformation in oocytes and a decrease in the number of oocytes (Ambani, 2015; Khillare et al., 2017). On histopathological changes in oocysts, which is one of the damages detected in this study, Berois et al. (2011) noted that

oocyte sheaths, and particularly zona radiata, are useful bioindicators to identify changes in the aquatic environment. Later, membrane damage detected in primary oocysts at later stages was accepted as an epithelial response to pollution.

Testes, an important part of male reproductive system, is one of the most affected tissues by inner and outer environment changes. Hormones, defects in growth factors or chemical substances may pose serious problems to testis. It was reported that mercury, a xenobiotic metal, caused proliferation in the interstitial tissue of mature individuals' testes in *Rasbora dandia* as well as a decrease in GSI and spermatozoa, thereby decreasing reproductive success (Rajan and Kuzhivelil, 2015). Bashir et al. (2022) reported that there were histopathological abnormalities such as testes degeneration, generalized tissue degeneration produced by fragmentation and detachment of basement membrane, necrosis, and fibrosis in the testis of the fish collected from a metal-polluted river. Another study also demonstrated that environmental pollutants affect estradiol and testosterone levels in fish (Hayati et al. 2022). Panti et al. (2017) demonstrated that pollutants also affect the cell and tissue structure of fish testes resulting in changes in the size of the seminiferous tubules. Many other studies have shown that there are serious changes (various inflammations, degenerative lesions, increase in melanomacrophage centers, disintegration in the seminiferous borders, accumulation of proteinaceous water in the interstitial area of the ovaries, follicular atresia) in fish gonads exposed to various chemicals in their habitats (Feist et al., 2015; Torres-Martinez et al., 2017). In light of all these studies on gonads and our findings, it could be easily said that irreversible histopathological damages in fish may alter the reproductive success and population balances of the species in the future.

## CONCLUSION

The findings of the present study clearly showed that the reproductive system of the natural fish species of Karasu River was affected by the pollution. Although species are histologically affected, they can still survive despite the pollution on the river. However, if pollution continues in this way, it is obvious that reproductive health of the fish species will be disrupted. Since the reproductive success will decrease due to pollution, there is a possibility that a distinct decrease will be seen in these populations in the near future. Therefore, further studies both on the field and in the laboratory are needed in order to identify pollutants and mixtures in the river and to analyze how specific changes in fish are related to reproductive health and population effects.

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## AUTHORSHIP CONTRIBUTIONS

Hatice Dane performed experimental parts. Turgay Şişman purposed the research idea, analyzed histological slides, designed the study protocol, wrote the manuscript draft and prepared the final version of the paper, and supervised the whole research. All authors approved the submission and publication of this manuscript.

## CONFLICTS OF INTEREST

The author declares that there is no conflict of interest on

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this manuscript.

## ETHICS APPROVAL

The legal permissions was obtained from Atatürk University Animal Experiments Local Ethics Committee (ATA36643897/25.09.2013).

## DATA AVAILABILITY

The data supporting the conclusions of this paper are available in the main paper.

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# Investigation of toxic effects of BPA and BPA analogues (BPS and BPAF) on *Spirulina* sp., *Desmodesmus subspicatus* and *Chlorella vulgaris*

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**Abstract:** Bisphenols (BPs) are produced for many applications for used in industry. BPs have been found all part of aquatic environments such as sediment and surface water that is poses a risk to the aquatic ecosystem. Restricting the use of BPA, environmental concentrations of bisphenol S, and bisphenol AF begin to increase. The present study aims to indicate that toxicity BPA and BPA analogues (BPS and BPAF) by algal growth inhibition test for the green algae *Chlorella vulgaris*, *Spirulina* sp., *Desmodesmus subspicatus*. In this way, result of this study present the nominal effective concentrations of BPA analogues and the suitability of the species for use as a biomarker in ecotoxicology tests. LC<sub>50</sub> values (growth rate inhibition by 50%, respectively) for three toxicants were determined separately. Results of this study showed the effects of these chemicals on photosynthesis (primer production). The result of algal growth inhibition test showed that BPAF (72h EC<sub>50</sub> 3.80 mg/L) was found to be more toxic than BPS (3d EC<sub>50</sub> 6.31 mg/L) for *Spirulina* sp. BPS (3d EC<sub>50</sub> 2.43 mg/L) showed the most toxic effect on the growth of *C. vulgaris*, followed by BPAF with 3d EC<sub>50</sub> 3.32 mg/L. BPS (3d EC<sub>50</sub> 0.88 mg/L) and BPAF (3d EC<sub>50</sub> 6.48 mg/L) were found to be toxic for *D. subspicatus*, respectively, from highest to lowest toxicity. These results indicate that bisphenol analogues are hazardous to primer production. Therefore, it is necessary to study their combined effects as well as to study how they act individually.

**Keywords:** Bisphenols, toxicity, freshwater algae, aquatic environment, aquatic ecology

## INTRODUCTION

Plastic pollution threat to marine ecosystems due to its widespread use in all areas. So that, it has several impacts on aquatic organisms, many of which have not been investigated (Uibel, 2016). The use of a wide variety of plastic products has increased considerably in recent years due to their social benefits such as ease of use, practicality, etc. Being durable and light, plastic has become the preferred base material for many applications, especially industrial applications. On the other hand, the multifaceted use of plastic has led to an increase in environmental pollution and a threat to natural life. Certain additives/chemical compounds are used in order to have the desired properties (durability, etc.) and to facilitate the production of plastics during the production phase. The most widely used of these compounds, bisphenol A (BPA), is used in the production of polycarbonate and epoxy resins (Huang et al., 2012). BPA is one of the important chemicals with the highest production volume in industrial areas worldwide (Abraham and Chakraborty, 2019).

BPA is commonly used as a stabilizer, an antioxidant in polycarbonate plastic (Grignard et al., 2012). BPA has a wide range of uses, such as food packaging, bottles, straws, thermal receipt paper, toys, CDs and medical devices (European Commission, 2018). The burning and photo degradation of plastics cause a BPA contamination in aquatic environment (Kang et al., 2007). Because of the decomposition of BPA occurs rapidly in UV light, heat, acidic or basic environments, it causes pollution in the environment and human exposure to natural life (Frenzilli et al., 2021). The toxic effects of bisphenol A, has received great attention that it acts as a xenoestrogen

and causes endocrine disruption. Today, due to the ban on the use of BPA in many countries (Liu et al., 2021). There are many studies concerning that BPA has toxicity to fish and invertebrates (LC<sub>50</sub> 1.1 to 10 mg/L) (Colborn et al., 1996).

Because of the lack of data especially its toxicities at low dose exposure Today, believed that the BPA alternatives are "safer". BPS and BPAF are the second and third most abundant analogues in the environment, detected at even higher levels than BPA in surface waters (Liu et al., 2021). A few studies have documented that BPS may be equally or more harmful than BPA (Rochester and Bolden, 2015). So, new researchers advised that necessary to investigate the current alternatives used instead of BPA. Chen et al. (2016) have identified the potentially toxic effects of BPA alternatives on non-target organisms. Furthermore, these BPA analogues have also been determined as endocrine-disrupting chemicals (Moreman et al., 2017). A large number of studies showed that BPS, BPF, and BPAF are found lower concentrations in water, sediment (Liao et al., 2012; Chunyang and Kurunthachalam, 2013; Chen et al., 2016) and bio accumulate in the body of several animal species (Wang et al., 2021). Restricting the use of BPA leads to greater use of BPA alternatives and increases their production. Therefore, concentrations of BPA alternatives are expected to increase in all areas of the environment. The predicted no-effect concentration (PNEC) reported as 1500 ng/L by European Union (Morales et al., 2020).

Effects of pollutants on natural ecosystems can be defined by Ecotoxicology. The toxicity of chemicals was ranged according

to species (Hammer et al., 2006). Algae and aquatic plants are the most important primary producer's waters and provide oxygen and shelter for many aquatic organisms. Because of this, they are the most important parts of the aquatic food chain. Algae have been reported as more sensitive than animals (Ferreira and Graça, 2002) and have been widely used in toxicity tests.

Recent studies have shown that BP analogues are detected in different environmental media, such as water, air, soil, biomass and sediment (Song et al., 2012; Liu et al., 2016). The use of BPS and BPAF in the production of BPA-free products leads to their detection in the aquatic environment at concentrations ranging from ng/L to µg/L (Chen et al., 2016; Zhao et al., 2019).

Their presence in the aquatic environment, BPS and BPAF have caused some risks for primary producers (Barboza et al., 2020; Czarny et al., 2021). As primary producers, microalgae at the base of the aquatic food chain are of essential for important in aquatic ecology (Fromme et al., 2002). Their sensitivity to toxic substances is the main reason for microalgae to be preferred as good testing organisms. Their readily available, small individual size, and rapid reproduction allow to for rapid assessment of chemical concentrations and generational effects of multiple populations (Abdel-Hamid, 1996). According to previous study report, BPA inhibited the growth and accumulation of chlorophyll in the test organisms. *C. mexicana* had a higher effective concentration value than *C. vulgaris*. Biodegradation and bioaccumulation of BPA were observed in both microalgae. *C. vulgaris* was exposed to concentrations of 1, 10, and 100 mg L<sup>-1</sup> BPS, and the inhibition rate of *C. vulgaris* was 41.6%, 103.7%, and 238.4%, respectively (Ding et al., 2020).

New studies have indicated that bisphenols affect ecosystem health (Ji et al., 2013), but studies on the comparative toxicity of bisphenol analogues are limited. Little data reported the toxic effects of BPS and BPAF on growth of phytoplankton. Especially no data available about the effects of BPS and BPAF on *Spirulina* sp., *Desmodesmus subspicatus* and *Chlorella vulgaris*.

The aim of this study is to obtain more data on the acute effects of BPA and BPA analogues on freshwater algae, and the acute toxic effects of BPA and its analogues (BPS and BPAF) on *Spirulina* sp., *Desmodesmus subspicatus* and *Chlorella vulgaris* were examined. This study is a part of the doctoral thesis.

## MATERIALS AND METHODS

### Chemicals

The chemicals used for the phytotoxicity tests were bisphenol A (BPA) CAS No. 80-05-7, bisphenol S (BPS) CAS No. 80-09-1, bisphenol AF (BPAF) CAS No. 1478-61-1 from Sigma-Aldrich (St. Louis, MO, USA). BPA, BPS and BPAF were prepared according to the conditions recommended by the manufacturer. Dilutions of 1/10 of the stock solution

prepared from each chemical were used to prepare intermediate stock solutions.

### Test species and culture conditions

Test organisms *Spirulina* sp., *D. subspicatus* and *C. vulgaris* were obtained from Ege University Fisheries Faculty Aquaculture Department and the cultures were grown in the Algae Culture unit of Ege University Ecotoxicology Laboratory.

To reproduce the pure cultures of the phytoplankton to be used in the study, the necessary medium and appropriate environmental conditions were provided for each of them. *Spirulina* sp. the standard Zarrouk broth medium was prepared according to the method Madkour et al. (2012) for the propagation of the pure culture of phytoplankton. The enrichment and environmental conditions suitable for *D. subspicatus* were prepared according to the protocol (OECD, 2011). This algae culture was grown at 21±2 °C in 4000 lux lighting and 24 h of light. BBM (bold basal medium) was prepared for the enrichment of *Chlorella vulgaris*. The pH value of BBM was adjusted to 6.8. *Chlorella vulgaris* culture was grown at 23±2 °C in 4000 lux lighting and 24 h of light. A shaker was used to prevent the samples from sticking to the surfaces of the erlenmeyer. For the growth of phytoplankton, firstly, 10 ml of the main algae stock was taken and added to the erlenmeyer containing 20 ml of enrichment. The cultures, which were left to grow under suitable conditions, were transferred to erlenmeyer with volumes of 150 and 200 ml, respectively, as their volumes increased. This process was repeated for all three phytoplankton.

### Toxicity test

Algal growth inhibition tests were performed as described in (OECD, 2011). Experiments were started when the cell numbers for *C. vulgaris* and *D. subspicatus* phytoplankton reached 10<sup>5</sup> - 10<sup>6</sup> per ml. *Spirulina* sp.'s long filamentous structure is not suitable for visual microscope counting. For this reason, the cell density of *Spirulina* sp. was measured by fluorimetry (µg/L chlorophyll-a) (Turner Designs the Aquafuor Handheld Fluorometer 54555). Experiments were set up in 20 ml volume. The total duration of the experiments is three days. The experiments were performed in triplicate and cell counts were made at 0.h and 72. h. The determined growth curves were compared with the control group (under the same conditions without adding bisphenol analogues) and the percent inhibition was calculated. 7 different chemical concentrations (0.5, 1, 1.5, 3, 5, 10, 15 mg/L) for *Spirulina* sp., 10 different chemical concentrations (0.5, 0.8, 1, 1.5, 2, 3, 5, 7, 9, 15 mg/L) for *D. subspicatus* and *C. vulgaris* were tested. Algae growth rate and percent inhibition were calculated for each organism.

Cultures exposed to BPA, BPS and BPAF were grown at 23±2 °C in 4000 lux lighting and 24 h of light. The measurements of the experiments were calculated with the help of algae growth rate and inhibition (%) exponential function.

Algae growth rate ( $\mu$ ),  $\mu = (\ln x_j - \ln x_0) / (t_j - t_0)$  (day<sup>-1</sup>)

$X_0$ : number of cells counted at time  $t_0$  (cells/ml) (for *D. subspicatus* and *C. vulgaris*)

$X_j$ : number of cells counted at time  $t_j$  (cells/ml) (for *D. subspicatus* and *C. vulgaris*)

$t_j$ : days until the last measurement of the experiment

% Inhibition =  $[(\mu_c - \mu_r) / \mu_c] \times 100$

$\mu_c$  = control group growth rate

$\mu_r$  = concentration group growth rate

The toxicity of the chemicals used in the study on the test phytoplankton was classified according to the (The European Commission, 2013). According to this report, classifies substances according to their effective concentrations values as follows:

Effective concentration 50 ( $EC_{50}$ ) values in different classes:

- 1–10 mg L<sup>-1</sup> (toxic)
- < 1 mg/L (very toxic)
- 10–100 mg/L (harmful) for aquatic organisms

Substances with an  $EC_{50}$  above 100 mg/L are not classified.

### Statistical calculations

$IC_{50}$  values were calculated from the inhibition - concentration curve as 50% growth inhibition of test population compared to control treatment, based on growth rate. Data analysis. The 72 h  $IC_{50}$  values were calculated according to the "area under the curve" method prescribed by the OECD.  $IC_{50}$ -value was determined by nonlinear regression analysis. All results are presented as mean  $\pm$  SD. Differences were considered significant at  $P < 0.05$ . The SPSS Statistics 25 computer programmer was used in the data analysis (Hocking, 1996). The data of growth rates were compared with controls by Dunnet test.

## RESULTS

The aim of this study is to identify the acute toxic effects of BPA, BPS and BPAF on *Spirulina* sp., *C. vulgaris* and *D. subspicatus*. According to the results of the studies, *Spirulina* sp. gave different answers. As the toxic effects of three chemicals on the growth of the test organism were compared, BPA accelerated growth, while BPS and BPAF showed a limiting effect on growth. The toxic effect of BPAF has the most toxic effect on growth compared to the other two chemicals. The  $EC_{50}$  value for bisphenol A exposure could not be calculated for *Spirulina* sp. because BPA exposure caused the organism to grow.

BPS has a more toxic effect than BPA and BPAF for *D. subspicatus*. It has a more toxic effect on *D. subspicatus* than

bisphenol A and bisphenol AF.  $EC_{50}$  value could not be calculated for BPA due to overgrowth.

BPS is more toxic to *C. vulgaris* than BPAF. The acute toxicity of BPS is greater than BPA and BPAF for *C. vulgaris*. According to the research results, bisphenol A increased the growth of *Spirulina* sp. instead of stopping it. *Spirulina* sp. and *C. vulgaris* were recorded as the most resistant species to BPA.

As a result, it was observed that BPS and BPAF showed more toxic effects for all three species compared to BPA. Compared to the other two species, *D. subspicatus* is more sensitive to BPS and BPAF.

The  $EC_{50}$  values found for the three selected species are given in Table 1.

**Table 1.**  $EC_{50}$  values for phytoplankton species

Test Species	$EC_{50}$ (mg/L)		
	BPA	BPS	BPAF
<i>C. vulgaris</i>	26.5	2.43	3.32
<i>Spirulina</i> sp.	-	6.31	3.80
<i>D. subspicatus</i>	-	0.88	6.48

$EC_{50}$ : effective concentration; the dosage at which the desired response is present for 50 percent of the population

In the first experiments, an increase in the growth of *Spirulina* sp. was observed after three days of BPA exposure. BPA stimulated the growth of the organism. While the growth rate is less at low concentrations (0.5, 1, 1.5, 3 mg L<sup>-1</sup>), the growth rate is quite high at high concentrations (5, 10, 15 mg/L). The increase in negative inhibition is greater at higher concentrations (5, 10 and 15 mg/L). A decrease in the growth rate and the inhibition % of *Spirulina* sp. were increased after three days of exposure to BPS. In addition, after 3 days of exposure, while the growth rate was 0.58 in the control, parallel to increasing concentrations the growth rates were increased. The growth rate decreased at increasing BPS concentrations. Determination that the inhibition as a function of growth rate. While the growth rate for BPAF was 0.78 in the control group, in highest chemical concentrations (3, 5, 10 and 15 mg/L) it was observed as; -0.17, 0.21, -0.22, -0.19. These results showed that inhibition increasing with parallel to increasing BPS concentrations. BPAF exposure of *Spirulina* sp. resulted in increased inhibition percentage and decreased exposure to growth rate. The growth rate and inhibition graphs of *Spirulina* sp. as a result of BPA, BPS and BPAF exposures are as shown in (Figure 1). According to the results obtained, it is more toxic BPAF (3d  $EC_{50}$  = 3.80 mg/L) than BPS (72 h  $EC_{50}$  = 6.31 mg/L).

The effects of the chemicals were examined in all three phytoplankton species separately. BPA stimulated the growth of *D. subspicatus*. As compared to the growth rate of the control group (0.60), more growth was observed than the control at all concentrations of BPA exposure. BPS limited growth at all concentrations. It caused inhibition of BPAF in *D. subspicatus*. The highest concentration (15 mg/L) of BPAF showed a high inhibitory effect for *D. subspicatus* (Figure 2).

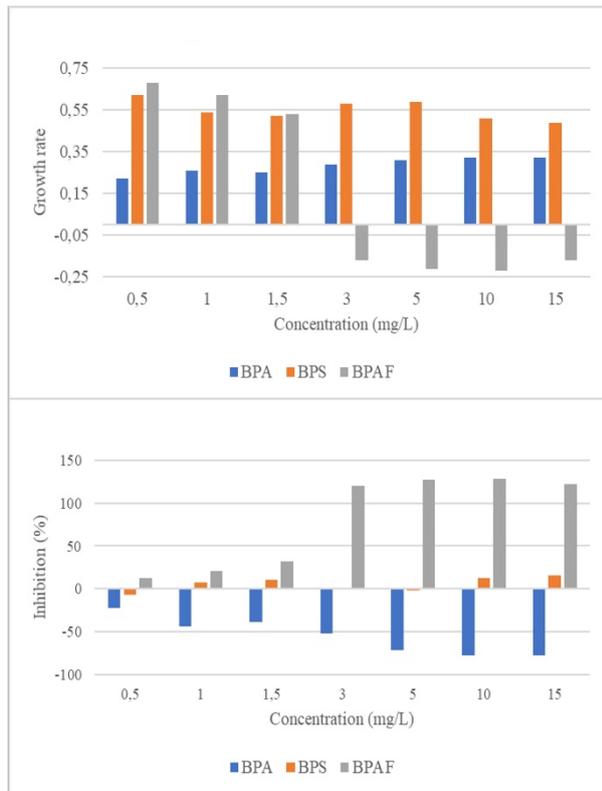


Figure 1. Effects of BPA, BPS and BPAF on growth rate and inhibition of *Spirulina* sp.

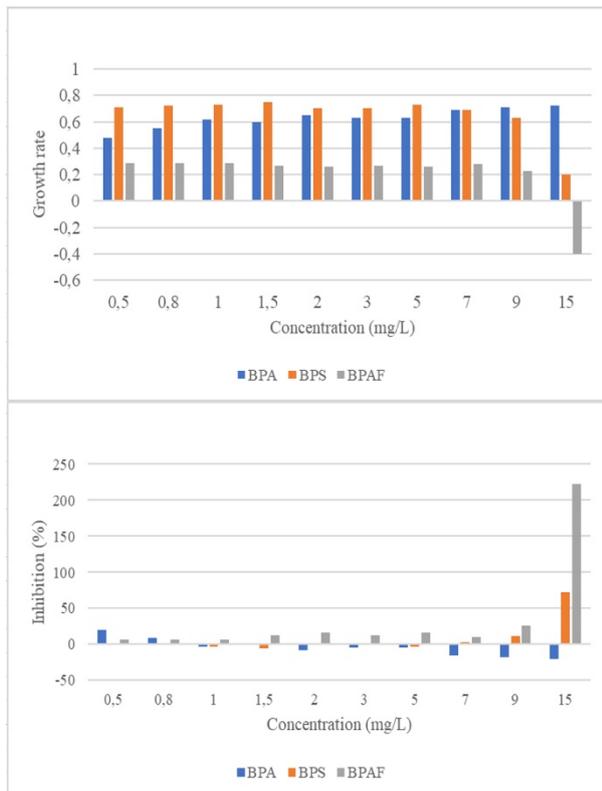


Figure 2. Effects of BPA and BPS, BPAF on growth rate and inhibition for *D. subspicatus*

The EC<sub>50</sub> value for BPS was calculated as 0.88 mg L<sup>-1</sup>, the EC<sub>50</sub> value for BPAF was 6.48 mg/L. EC<sub>50</sub> value could not be calculated for BPA due to overgrowth. It has been noted that BPS and BPAF inhibit *D. subspicatus*. According to the results obtained, BPS showed a more toxic effect than BPA and BPAF.

According to the results of the experiments conducted with *C. vulgaris*, BPS showed more toxic effects than BPAF and BPA. The EC<sub>50</sub> value for BPA was calculated as 26,5 mg L<sup>-1</sup>, the EC<sub>50</sub> value for BPS was 2,43 mg/L and the EC<sub>50</sub> value for BPAF 3,32 mg/L. According to these calculations, the acute toxicity of BPS is greater than BPA and BPAF. As a result of exposure to the chemical bisphenol A, the organism continued to grow at low concentrations (0.5, 1, 1.5, 2, 3 mg/L). At higher concentrations (5, 7, 9, 15 mg/L), growth was reduced compared to the control (0.92). A growth arresting effect was observed at all chemical concentrations applied for bisphenol S. BPAF had a growth-limiting effect on *C. vulgaris* from the lowest concentration at which exposure began (Figure 3). Results of this study, BPA and BPAF was found to be less toxic than BPS for *C. vulgaris*.

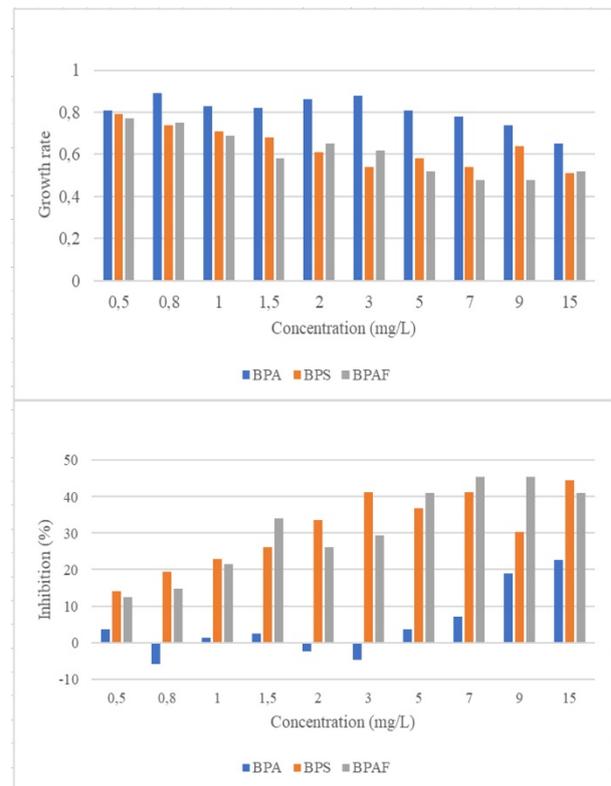


Figure 3. Effects of BPS and BPAF on growth rate and inhibition for *C. vulgaris*

## DISCUSSION

Bisphenols are widely available as alternatives to BPA in various environmental and biological samples. There are only few available data about toxic effects of analogues of BPA to microalgae. For example; Libralato et al. (2011) reported that

the ecotoxicological characterization of Lignin and tannin on testing species the marine alga *Phaeodactylum tricorutum* (Bohlin). This research showed that the Lignin and tannin effected the algae an EC<sub>50</sub> of 113.84 (100.90–128.45) mg/L and 26.04 (20.10–33.95) mg/L, respectively. They are also reported the NOEC and LOEC values as <0.1 mg/L and 0.1 mg/L for lignin and tannin. Seoane et al. (2021) noted that the toxicity of the emerging pollutant bisphenol A with three marine microalgae (*Tetraselmis suecica*, *Phaeodactylum tricorutum* and *Nannochloropsis gaditana*). Results of their studies showed that *P. tricorutum* was the most affected species. Researcher reported that After 96 h of exposure to three BPA concentrations, treated cultures of *P. tricorutum* and significant reduction ( $p < 0.05$ ) was observed. These results indicate that *P. tricorutum* growth was the most affected by BPA and also 96 h-EC<sub>50</sub> values of BPA were reported as 0.6 mg L<sup>-1</sup>.

The investigation of Czarny-Krzywińska et al. (2022), showed that because of the water solubility of Bisphenol analogues (log<sub>K<sub>ow</sub></sub> values of BPs were 3.64–6.56= log<sub>K<sub>ow</sub></sub> > 3) its easily cross the cell wall of microalgae and bioaccumulate. Furthermore researcher reported the toxicity of bisphenol A, its six analogues, on the the green algae *Chlorella vulgaris* (bisphenol AF for *C. vulgaris* 14 days, EC<sub>50</sub>: 22.39 mg L<sup>-1</sup>) and *Desmodesmus armatus* (EC<sub>50</sub>: 42.29 mg L<sup>-1</sup> for Bisphenol A, and bisphenol AF EC<sub>50</sub>: 27.16 mg L<sup>-1</sup>) (Czarny-Krzywińska et al., 2022). Tisler et al. (2016) reported that IC<sub>50</sub> values (3 days) were 3.00 mg-BPAF/L for *Desmodesmus subspicatus* and also showed that the BPAF was more harmful to *Desmodesmus subspicatus* than BPA. Ding et al. (2020) found that bisphenol S showed high toxicity to *C. vulgaris* than bisphenol A, and the obtained EC<sub>50</sub> values (2 d) were 3.16 and 41.43 mg L<sup>-1</sup>, respectively. Ding et al. (2020) emphasized that the acute toxicity of BPS in the aquatic ecosystem should be more attention than BPA. In our study, BPS was found toxic for *C. vulgaris*. Czarny-Krzywińska et al. (2022) carried out the first study explaining the effects of toxicity of bisphenol A and its derivatives on microalgae. According to this study with *D. armatus* and *C. vulgaris*, BPAF was found to be more toxic than BPA. The toxicity of BPF, BPA and BPAF on *D. magna*, *D. rerio* and *D. subspicatus* was investigated and BPAF concentrations in the surface waters were observed to pose a risk for aquatic organisms (Tišler et al., 2016).

In our study, the effect of BPA, BPS and BPAF on the growth of freshwater microalgae *Chlorella vulgaris*, *Spirulina* sp., *D. subspicatus* was investigated. The toxicities of BPA, BPS and BPAF chemicals on this three phytoplankton are different. bisphenol A increased the growth of *Spirulina* sp. *C. vulgaris* and *Spirulina* sp. were recorded as the most resistant species to BPA among the test organisms. At concentrations of 5 mg/L and above, BPAF dramatically reduced the growth

rate of *Spirulina* sp. BPS at high concentrations (7 mg/L and above) caused inhibition by slowing the growth rate of both *Desmodesmus subspicatus* and *C. vulgaris*. Comparison of calculated EC<sub>50</sub> values of chemicals tested for their toxicity on three phytoplankton was made according to The European Commission (2013). EC<sub>50</sub> values obtained from the study are shown in Table 1. As a result of comparing the EC<sub>50</sub> values obtained from the study with the report, it was determined that BPS and BPAF had toxic effects on all three species. *D. subspicatus* is more sensitive to BPS than BPAF. The most resistant phytoplankton to BPAF exposure is *D. subspicatus* and the most sensitive is *C. vulgaris*.

When the toxic effects of individual and mixed bisphenol analogues on cyanobacteria were examined, it was observed that the mixture of bisphenol analogues had a stronger toxic effect than BPA (Czarny et al., 2021).

In addition to these studies, the effects of BPS and BPAF on more phytoplankton are still unknown. These effects should be identified by acute and chronic toxicity tests and the presence of these chemicals in the aquatic system should be reduced. Investigation of the effect of BPA and analogues on phytoplankton in the first step of the aquatic system should be expanded.

These types of studies are important in predicting the toxic effects of chemicals on living organisms. Light of previous and our studies, BPS and BPAF concentrations in the environment may not be hazardous at present time. But BPA analogues such as; BPS and BPAF concentrations in aquatic environment must be monitoring for the ecosystem health. Furthermore, this study will enable us to obtain more information about BPA and its analogues by examining the toxic effects of widely used BPA derivatives, BPS and BPAF, on the primary producers, phytoplankton.

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#### AUTHOR CONTRIBUTIONS

Material preparation and research were carried out by Duygu Turan. The article was written and edited by Duygu Turan and all authors have read and approved the article.

#### CONFLICT OF INTEREST STATEMENT

The author declares no conflict of interest.

#### ETHICAL APPROVAL

Ethical approval is not required for this study.

#### DATA AVAILABILITY

All relevant data is inside the article.

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# The effect of feeds containing different protein levels on growth and survival rates of European sea bass (*Dicentrarchus labrax* L., 1758) juveniles grown in freshwater

## Farklı protein seviyesi içeren yemlerin tatlısuda yetiştirilen Avrupa levreği (*Dicentrarchus labrax* L., 1758) yavrularının büyüme ve yaşama oranları üzerine etkisi

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**Abstract:** In this study, the effect of the use of feeds containing different protein ratios on the growth performance of juvenile sea bass (*Dicentrarchus labrax* L., 1758) reared in freshwater was investigated. Sea bass fry with an average body weight of  $1.0 \pm 0.03$  g were stocked in 120 liter tanks in triplicate after their adaptation to freshwater. The feeds used in the study had different protein/similar fat content. Accordingly, the experimental groups were named as 45CP (45% CP / 18% CF), 50CP (50% CP / 18% CF) and 55CP (55% CP / 18% CF). At the end of the experiment, the highest body weight gain was  $5.84 \pm 0.03$  g in the 55CP group, while the other groups were  $5.73 \pm 0.09$  g (45CP) and  $5.8 \pm 0.08$  g (50CP). SGR rates were similar for all three groups and there was no statistical difference between the groups ( $P>0.05$ ). SGR values of the groups were calculated as  $1.94 \pm 0.04$  (45CP),  $1.89 \pm 0.01$  (50CP),  $1.91 \pm 0.02$  (55CP), respectively. There was no statistical difference between the 45CP and 55CP groups, while the 50CP group showed a statistically lower FCR rate than the other groups ( $P<0.05$ ). FCR values were calculated as  $1.36 \pm 0.05$ ,  $1.29 \pm 0.03$ ,  $1.37 \pm 0.04$ , respectively. There was no difference between the survival rates of the groups. According to the results of the study, it was concluded that sea bass fish can be raised in freshwater, especially in the fry stage, and that it is more effective than the commercial feeds currently used.

**Keywords:** Sea bass, *Dicentrarchus labrax*, freshwater, protein, growth performance, survival rate

**Öz:** Bu çalışmada tatlı suda yetiştirilen yavru levrek (*Dicentrarchus labrax* L., 1758) balıklarının beslenmesinde farklı protein oranları içeren yemlerin kullanımının büyüme performanslarına üzerine etkisi araştırılmıştır. Ortalama canlı ağırlıkları  $1,0 \pm 0,03$  gram olan levrek yavruları, tatlı suya adaptasyonlarından sonra 120 litre hacimdeki tanklarda üçer tekrarlı olacak şekilde stoklanmıştır. Çalışmada kullanılan yemler farklı protein / benzer yağ içeriğindedir. Buna göre deneme grupları 45CP (%45 HP / %18 HY), 50CP (%50 HP / %18 HY) ve 55CP (%55 HP / %18 HY) olarak isimlendirilmiştir. Deneme sonunda en yüksek canlı ağırlık artışı  $5,84 \pm 0,03$  g ile 55CP grubunda iken diğer gruplarda  $5,73 \pm 0,09$  g (45CP),  $5,8 \pm 0,08$  g (50CP) olarak tespit edilmiştir. SGR oranları her üç grup için benzer oranlarda olup gruplar arasında istatistiksel bir farklılık bulunmamaktadır ( $P>0,05$ ). Grupların SGR değerleri sırası ile  $1,94 \pm 0,04$  (45CP),  $1,89 \pm 0,01$  (50CP),  $1,91 \pm 0,02$  (55CP) olarak hesaplanmıştır. FCR değerlerine bakıldığında 45CP ve 55CP grupları arasında istatistiksel bir farklılık tespit edilmemişken, 50CP grubu istatistiksel olarak diğer gruplardan daha düşük bir FCR oranı göstermiştir ( $P<0,05$ ). FCR değerleri sırası ile  $1,36 \pm 0,05$ ,  $1,29 \pm 0,03$ ,  $1,37 \pm 0,04$  olarak hesaplanmıştır. Grupların yaşama oranları arasında bir farklılığa rastlanmamıştır. Çalışma sonucuna göre özellikle yavru dönemlerinde levrek balıklarının tatlı suda yetiştirilebileceği, halen kullanılmakta olan ticari yemlere göre daha düşük oranlarda protein içeren yemlerle de balıkların beslenebileceği gözlenmiştir.

**Anahtar kelimeler:** Levrek, *Dicentrarchus labrax*, tatlı su, protein, büyüme performansı, yaşama oranı

## INTRODUCTION

Aquaculture production is increasing rapidly all over the world. World aquaculture production in 2020 was 87.5 million tons in total, including 33.1 million tons of marine production and 54.4 million tons of production in inland waters (FAO, 2022). Türkiye's aquaculture production in 2022 was 514,815 tons, of which 368,742 tons were produced at sea and 146,63 tons were produced in inland waters (Turkish Statistical Institute, 2022). While most of the production in the sea in Türkiye is European sea bass and sea bream species, almost

all of the production in inland waters is trout production. The limited production areas in the seas will limit the increase in production capacity in the next years. Therefore, increasing recirculated aquaculture systems in terrestrial areas is an important issue for aquaculture. Water supply is the most important issue in recirculated or open production systems built on land. Even in closed aquaculture systems, 3-10% of the total water volume needs to be replaced with new water daily. This causes additional costs and problems for facilities that are

far from the sea or have difficult access to salty or brackish water from underground.

The adaptation period of European sea bass to freshwater has been investigated in many studies and it has been reported that direct adaptation of European sea bass to freshwater is possible, but long-term adaptation can reduce stress effects in fish (Nebel et al., 2005; Kokou et al., 2019).

The quantity and quality of protein in feed are very important for somatic growth in fish. Protein sources play a crucial role in providing adequate levels of amino acids needed to synthesize new tissue protein (Jana et al., 2021). Aquaculture with feeds with balanced essential amino acid composition and optimum protein levels will ensure better growth of fish as well as economically viable and environmentally friendly production.

In their natural habitat, the nutrient requirements of European sea bass are 48-52% crude protein and 14-16% crude fat during the fry period and 43-45% crude protein and 18-20% crude fat during the growth period (Oliva-Teles, 2000; Ghisaura et al., 2014). However, there are no studies on the optimum protein values that should be used in the diets of freshwater European sea bass fry. Understanding the interactions between growth performance and food consumption of European sea bass fry kept in freshwater is important for the success of aquaculture. For this purpose, in this study, the effects of using feeds with different protein contents on the survival and growth rates of European sea bass fry adapted to freshwater were investigated.

## MATERIALS AND METHODS

### Fish and experimental plan

Sea bass fry, which are widely cultivated in Türkiye, were used in the study. The study was carried out at Ege University Center for Research on Laboratory Animals, Aquaculture Research Laboratory. The fish used in the experiment had an average live weight of  $1.0 \pm 0.03$  grams and were obtained from a private hatchery (Akvatek, Çandarlı-Izmir) and transferred to the experimental unit with a fish transport tank. Three experimental groups were formed in the study. Accordingly, the fish were stocked in 9 cylindrical conical polyester tanks with a volume of 120 liters, each group was stocked with 35 individuals/tank with 3 replicates for a total of 315 individuals. The salinity in the experimental tanks was gradually reduced from 38 ppt to 0 ppt over 4 days.

The experimental system used in the study was a recirculated aquaculture system (RAS) and a sand filter, protein skimmer, biological filter and UV filter were used for water filtration. The current capacity of the system was maintained by adding freshwater to the system. Water flow rates were set at 2 l/minute so that 100% of the total volume was changed in one hour. Water temperature was kept between 21.4-22°C and dissolved oxygen between 7.1-7.3mg/l. Lighting was set to 12 hours day and 12 hours night. Water parameters (temperature, dissolved oxygen, pH and

salinity) and daily mortality rates were measured and recorded every morning before feeding started. YSI P1100 model multi-parameter device was used for the measurements.

The study was initiated with the adaptation of the fish to freshwater. The study lasted 75 days and biometric measurements (body weight and total length) of the fish were measured at the beginning of the experiment, on the 25th, 50th and 75th days. Visceral and hepatosomatic index values were measured and calculated at the end of the experiment.

### Feed and nutrition

The fish adapted to freshwater were fed with 3 different proteins (45, 50, 55%) and 18% fixed lipid ratios. Feed groups and their nutrient contents are given in Table 1.

**Table 1.** Ingredients and nutritional values of the feeds used in the study

	45CP (45/18%)	50CP (50/18%)	55CP (55/18%)
<b>Ingredients</b>			
Fish Meal (65.5% CP)	33	46.5	59
Soybean Meal (48% CP)	23	23	15.5
Wheat Meal (15% CP)	3	3	0
Corn Gluten Meal (66% CP)	10	10	12
Sun Flower Meal (35.18% CP)	15.5	3	0
Fish Oil (Anchovy)	14.5	13.5	12.5
Vitamin Mix*	0.4	0.4	0.4
Mineral Mix*	0.3	0.3	0.3
Methionin	0.1	0.1	0.1
Binder	0.2	0.2	0.2
Total	100	100	100
<b>Chemical Composition (%DM)</b>			
CP % (min)	45.26	49.73	54.57
CF % (min)	18.29	18.21	18.16
CS % (max)	3.2	2.72	2.04
DM % (min)	92.9	90.83	90.41
Ash % (max)	12.4	10.56	10.48
ME Kcal/kg**	4308.79	4568.19	4892.73
DE Kcal/kg***	4290.05	4370.93	4400.72
NFE %****	13.75	9.58	5.16
P/E***** (mg protein/Kcal DE)	105.49	113.56	123.82

\*Commercial premixes were used for European sea bass fry feeds. Vitamin A 15000 IU/Kg, Vitamin D3 2500 IU/Kg, Vitamin E 350 mg/Kg, Vitamin K 20 IU/Kg, Vitamin C 350 mg/Kg, P 1.5%, Ca 1-3%, Se 0, 1%.

\*\*Metabolic Energy (ME) = 0.239.  $[10 \cdot (CP \cdot 0.9 \cdot 18.64 + HY \cdot 0.9 \cdot 39.57 + NFE \cdot 0.88 \cdot 17.17)]$  (Kcal/kg)

\*\*\*Digestible Energy (DE) = 0.239.  $[10 \cdot (CP \cdot 0.9 \cdot 23.66 + HY \cdot 0.9 \cdot 39.27 + NFE \cdot 0.88 \cdot 17.17)]$  (KCal/kg)

\*\*\*\*Nitrogen Free Extractives=  $100 - (\%CP + \%HY + \%HK + \%HS + \%Moisture)$

\*\*\*\*\*Protein Energy Ratio=  $(\%CP/SE(Kcal/100g)) \times 1000$

The raw materials used in feed production were purchased from a company producing commercial fish feed. The feeds were produced as a pellet form by using a meat grinder in the Fish Nutrition and Feed Technology Laboratory. After drying, they were ground to 0.8-2mm in diameter in accordance with the size of the experimental fish.

The experimental groups were named as 45CP group (45% CP/18% HY), 50CP group (50% CP/18% HY) and 55CP

group (55% CP/18% HY). Feeding was made 3 times a day at a rate of 4% of the total body weight at the beginning of the experiment and 3% of the total body weight from the second half of the experiment due to the increase in the body weight of the fish. Feed amounts were recalculated after body weight measurements every 25 days, taking into account survival rates. Feed amounts given to the experimental tanks were recorded daily in order to determine the feed utilization rates.

Depending on the feeds, the growth performance of the fish was evaluated according to the following formulas (Halver, 1976; Metailler, 1986; Hoşsu et al., 2005; Mritunjoy et al., 2022).

Live weight gain(g)=Final weight(g)-Initial weight(g)

Feed conversion ratio (FCR)=(Total feed consumed(g))/(Body weight gain(g))

Specific growth rate (SGR,%day<sup>-1</sup>)=[Ln(Final weight(g))-Ln(Initial weight(g))]/(Trial duration(days))×100

Protein efficiency ratio (PER)=Weight gained(g)/Crude protein consumed

Condition factor (CF)=(Total live weight(g))/(Total height(cm))<sup>3</sup>×100

Visceral index (VSI)=(Visceral weight(g)/Body weight(g))×100

Hepatosomatic index (HSI)=(Liver weight(g)/Body weight(g))×100

### Statistical analysis

Live weight gain, growth performance (CF, FCR, SGR and Survival), VSI and HSI values of fish fed with diets produced with different protein and fixed fat ratios were statistically tested by analysis of variance (ANOVA). When significant differences among the variables were detected, Tukey's honestly significant difference (HSD) test was used to determine variables were different. Significance levels were set at  $P<0.05$ . The SPSS ver. 25 statistical programs were used to evaluate data.

### RESULTS

During the 4-day adaptation period, European sea bass fry showed normal behaviour, swimming and feeding activities. No mortality was observed during the freshwater adaptation period.

Since the experimental tanks operated in a closed-water system, no big changes were observed in water temperatures. Accordingly, the average water temperature was determined as  $21.8\pm 0.1^{\circ}\text{C}$ . During the experiment, the lowest water temperature was  $21^{\circ}\text{C}$  and the highest water temperature was  $22.4^{\circ}\text{C}$ . The average dissolved oxygen value was 7.2mg/l, with a minimum of 6.8 and a maximum of 7.7mg/l. The pH was 7.3 on average, and nitrite, ammonia and phosphorus values were observed at appropriate values.

There was a statistical difference between the 45CP group and the 55CP group in terms of body weight gain, while there was no difference between the 50CP group and other groups ( $P>0.05$ ). The highest live weight gain was observed in the

55CP group with  $5.84\pm 0.03\text{g}$ , while the lowest weight gain was observed in the 45CP group with  $5.73\pm 0.09\text{g}$ . In the 50CP group, the weight gain was  $5.8\pm 0.08\text{g}$ . SGR rates were similar for all three groups and there was no statistical difference between the groups ( $P>0.05$ ). While there was no statistical difference between the 45CP and 55CP groups in terms of FCR, the 50CP group showed a statistically lower FCR rate than the other groups ( $P<0.05$ ). While there was no statistical difference between the 45CP and 50CP groups in PER values, the 55CP group was statistically different from the other 2 groups ( $P<0.05$ ). It was observed that the PER value was inversely proportional to the protein value in the feed (Table 2).

When survival rates were evaluated, no difference was found between the groups (Table 2).

**Table 2.** Comparison of growth and development performance between groups

	45CP	50CP	55CP
Initial body weight (g)	0.97±0.19 <sup>a</sup>	1.01±0.19 <sup>a</sup>	1.01±0.22 <sup>a</sup>
Final body weight (g)	6.71±1.24 <sup>a</sup>	6.81±0.94 <sup>ab</sup>	6.86±1.30 <sup>b</sup>
Live weight gain (g)	5.73±0.09 <sup>a</sup>	5.8±0.08 <sup>ab</sup>	5.84±0.03 <sup>b</sup>
SGR	1.94±0.04 <sup>a</sup>	1.89±0.01 <sup>a</sup>	1.91±0.02 <sup>a</sup>
FCR	1.36±0.05 <sup>a</sup>	1.29±0.03 <sup>b</sup>	1.37±0.04 <sup>a</sup>
PER	1.63±0.06 <sup>a</sup>	1.55±0.3 <sup>a</sup>	1.32±0.08 <sup>b</sup>
Survival %	97 <sup>a</sup>	96 <sup>a</sup>	97 <sup>a</sup>
CF	1.25±0.03 <sup>a</sup>	1.23±0.07 <sup>a</sup>	1.22±0.02 <sup>a</sup>
VSI	11.37±0.9 <sup>c</sup>	12.33±0.3 <sup>b</sup>	13.26±0.5 <sup>a</sup>
HSI	1.52±0.05 <sup>a</sup>	1.91±0.04 <sup>b</sup>	1.98±0.1 <sup>b</sup>

CF values were similar for all groups ( $P<0.05$ ). VSI values were statistically different between all groups; ( $P<0.05$ ). HSI values of the 45CP group were statistically different from the other 2 groups, while there was no difference between the 50CP and 55CP groups ( $P<0.05$ ).

### DISCUSSION

Survival rates determined during adaptation to freshwater showed that European sea bass can adapt to freshwater without any problems within 4 days. Dendrinou and Thorpe (1985) reported that European sea bass fish can be adapted to a minimum of 0.5 ppt water, death occurs at 0 ppt, and feed intake and growth decreases as salinity decrease. However, in many other studies, in agreement with our study, the direct or gradual transfer of European sea bass fish to freshwater has been reported to be successful (Cataudella et al., 1991; Venturini et al., 1992; Varsamos et al., 2005; Kokou et al., 2019).

Many studies have reported different survival rates in European sea bass fry kept in freshwater, indicating that there are different physiological capacities in adaptation to freshwater within the same species (Dendrinou and Thorpe, 1985; Allegrucci et al., 1994; Jensen et al., 1998; Nebel et al., 2005; Giffard-Mena et al., 2008). Considering the results obtained in the study, the survival rate of all groups is quite high with 97%, but it is lower than the 100% value reported by

Eroldoğan and Kumlu (2002). It has been reported by various researchers that European sea bass in the Mediterranean region have genetic differences and therefore their adaptation to environmental conditions is different (Caccone et al., 1997; Allegrucci et al., 1997). The difference in survival rates may be due to the fact that the experimental fish in our study and the study of Eroldoğan and Kumlu (2002) were European sea bass taken from different regions of Türkiye. Thus, more studies should be carried out on this subject.

In general, growth rate is positively correlated with protein levels in feed in many species. However, in some studies, it has been reported that fish change their feed intake due to the effect of salinity and this has an effect on growth. Fish growth is reduced or unaffected when fish are fed lower or higher feed protein than the optimum level (Talukdar et al., 2019; Kim and Lall, 2001). In such a situation, there is no protein synthesis, and there is a decrease in protein conversion efficiency, depending on the percentage of protein catabolized (Deng et al., 2014). In addition, although there is high protein in the feed, an insufficient non-protein energy source in the feed also decreases growth performance. (Winfree and Stickney, 1981). The carbon chains constituting amino acids due to the increase in the protein ratio in the feed are used in energy production. In addition, the amino parts cannot be used and must be excreted from the body. In addition, giving too much protein disrupts the amino acid balance and deamination is observed. This leads to increased nitrogen excretion and energy loss and protein efficiency decreases (Hoşsu et al., 2005). It has been reported that there is a negative correlation between protein efficiency ratio (PER) and feed protein level and feed protein/energy level ratio for almost every growth period of European sea bass. (Kousoulaki et al., 2015). In our study, it was observed that PER values decreased as the protein content of the feed increased. This may be due to the increase in nitrogen excretion in freshwater due to protein content.

Oliva-Teles (2000) reported that the optimum protein/energy ratio of European sea bass diets is higher than that of trout and sea bream and that feeds should contain 45 to 50% protein and a minimum of 9-12% lipids. Furthermore, the optimal DP/DE ratio for European sea bass fry was recommended to be 21-22 mg DP/kJ DE (0.525 kcal/kg) (Peres and Oliva-Teles, 1999). Saleem et al. (2022) reported that feeds containing 42% protein and 17.4% protein were suitable for the growth of European sea bass raised in seawater. The protein contents of the feeds used in the study were within the limits given in the above literatures. The fat ratios used in the feed are the ratios used in commercial feeds and are slightly higher than those given in the literatures. In future studies, different fat and energy contents should be tried to increase feed efficiency.

It has been reported that increasing the fish meal ratio in the feed causes an increase in SGR and FCR in European sea bass adapted to freshwater (Shalaby et al., 2023). In addition, it has been reported that decreasing the fish meal ratio and adding salt to the feed increases feed intake, SGR and FCR values (Cnaani et al., 2012). In the study conducted by Rimoldi

et al. (2015), the addition of 3% salt to a diet containing only 10% fishmeal resulted in feed intake, SGR and FCR values similar to those of fish fed a diet containing 30% fishmeal. Therefore, in future studies, it will be important to try to reduce the utilization rate of fish meal by using salt in the diet of fish adapted to freshwater. Also, osmoregulation capacity may differ according to fish developmental stages and new studies should be conducted to include the whole production period (Bernardino and Fernandes, 2016).

The value of the viscerosomatic index increases as a result of visceral fat accumulation. Lovell (1989) reported that when fish are fed a high protein diet, excessive fat accumulation in the visceral cavity and tissue is reported due to an imbalance in the digestible energy/crude protein ratio. The highest HSI and VSI values obtained in the group fed low protein diets may be attributed to an imbalance in the P/E ratio due to the conversion of carbohydrates from raw materials into liver glycogen and lipid, thus increasing liver weight, and not as a result of freshwater rearing (Brown et al., 1992). As observed in this study, higher HSI and VSI values indicate poorer growth compared to the other groups. According to the condition factor data obtained in our study, it was observed that the VSI and HSI differences observed in the internal organs and liver did not cause a morphological difference. This shows that the feeds used were suitable in terms of nutrition and feeding rates.

## CONCLUSION

According to the results obtained, at the end of 75 days, there was no significant difference between the groups fed with feed containing 45% protein and feed containing 50% protein. Accordingly, it was observed that European sea bass fish can be adapted to freshwater at the fry stage and can be fed with feeds containing lower protein ratios than the currently used commercial feeds, and this will not have a negative effect on the growth of the fish. This will help to reduce the cost of production.

In addition, the cultivation of European sea bass in freshwater will make a great contribution to the development of aquaculture. The fact that European sea bass is not affected by water temperature increases as much as trout and can live in higher water temperatures will enable the utilization of freshwater resources that cannot be used for trout production during hot periods and remain empty.

## AUTHORSHIP STATEMENT

All authors contributed to the idea and design of the study. Material preparation and research was carried out by (Kutsal Gamsız), (Ali Yıldırım Korkut) and (Aysun Kop). The writing and editing of the manuscript was done by (Kutsal Gamsız), (Ali Yıldırım Korkut) and (Aysun Kop) and all authors have read and approved the manuscript.

## CONFLICT OF INTEREST

The authors declare that there are no conflicts of interest or competing interests.

## ETHICS APPROVAL

Approval was obtained from Ege University Animal Experiments Ethics Committee (25.12.2019/2019+-116).

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## DATA AVAILABILITY STATEMENT

Data sets generated and/or analyzed during the current study will be provided by the corresponding author upon request of the editor or

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# First record of alien gastropods *Epitonium aranea* Bonfitto, 2018 and *Stosicia annulata* (Dunker, 1860) (Mollusca) from the Mediterranean Sea

## İki yabancı gastropod türünün [*Epitonium aranea* Bonfitto, 2018 ve *Stosicia annulata* (Dunker, 1860) (Mollusca)] Akdeniz'den ilk defa kaydedilmesi

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**Abstract:** In a benthic material taken from the Levantine coast of Türkiye, *Epitonium aranea* Bonfitto, 2018, a species previously known from the Red Sea only, and *Stosicia annulata* (Dunker, 1860) distributed in Japan Sea, Persian Gulf and Central and East Indian Ocean were recorded for the first time from the Mediterranean Sea. Along with two unknown species from the region, herein have also been dealing with *Melanella* sp., *Oscilla virginiae* Peñas, Rolán and Sabelli, 2020 and *Zafra pumila* (Dunker, 1860) which are poorly known species from the area, and some remarks of the taxonomy and distribution of the studied taxa are discussed.

**Keywords:** Mollusca, alien species, Mediterranean Sea, new record, Turkish coast

**Öz:** Türkiye'nin Levant Denizi kıyılarından alınan bir bentik materyalde, daha önce sadece Kızıldeniz'den bilinen *Epitonium aranea* Bonfitto, 2018 ile Japon Denizi, Basra Körfezi ve Orta ve Doğu Hint Okyanusu'nda dağılım gösteren *Stosicia annulata* (Dunker, 1860) türleri Akdeniz'de ilk defa bulunmuştur. Bu çalışmada, bölgeden bilinmeyen bu iki türün yanı sıra, *Melanella* sp., *Oscilla virginiae* Peñas, Rolán ve Sabelli, 2020 ve bölgeden az bilinen yumuşakçalar arasında yer alan *Zafra pumila* (Dunker, 1860) türleri de bulunmuş olup, incelenen türlerin taksonomik ve dağılım özellikleri tartışılmıştır.

**Anahtar kelimeler:** Mollusca, yabancı tür, Akdeniz, yeni kayıt, Türkiye kıyıları

## INTRODUCTION

The Mediterranean Sea, which is a semi enclosed ecosystem, is one of the prominent hotspots of marine bioinvasions on earth (Rilov and Galil, 2009) and most of the known species in this ecosystem are assessed to have successfully established, being recorded for multiple times (Zenetos et al., 2022).

The alien species being successfully established in an introduced area may restructuring established food webs, importing new diseases and competition with native organisms for food and space. Other ecological changes may occur when the invading organisms reproduce with native species, altering the gene pool (Occhipinti Ambrogio, 2001). Invaders are also capable of colonizing every ecosystem on earth, changing the ecological relations within communities, altering evolutionary processes, and causing dramatic changes in native populations, including extinctions (Mack et al., 2000). Gastropods, which are in the majority among the alien species, cause a multitude of environmental and socioeconomic impacts in many habitats, represent a major threat to native plants and animals. They also consist one of the significant problems in agriculture, resulting in economic losses by reducing the yield (Kesner and Kumschick, 2018).

Regarding the housed alien species number, there are

significant differences among the Mediterranean basins. Eastern Mediterranean, being close to the Suez Canal, which is one of the main pathways for entering of alien species, includes highest number species, where the taxa with Indo-Pacific origin dominated. The lowest alien species diversity occurs in the western Mediterranean, where fouling and ballast water of ships seem to be the main vector for transportation of alien species (Zenetos et al., 2012; Galil et al., 2018).

Among the Mediterranean countries, Türkiye is one of the most impacted one. İskenderun Bay, which is found in close distance to the Suez Canal and the dense maritime traffic occurring due to the oil transportation from the Ceyhan Oil Terminal, attracts attention as a hotspot area of the region from where was reported 77 alien species (Bitlis Bakır et al., 2012). Çınar et al. (2021) reported 539 species belonging to 18 taxonomic groups, 404 of which have been estimated as established ones, including the list of alien species distributed on the Turkish coasts by the end of 2020. In terms of the number of species, molluscs rank first with 123 species. The number of alien molluscs has been increased from 105 species (Çınar et al., 2011) to 123 for a period nearly one decade. *Epitonium vaillanti* (Jousseau, 1912) recorded from the Turkish Levantine coast (Öztürk et al., 2023a), *Phosinella digera* (Laseron, 1956) found on the Turkish Levantine coast

(in Taşucu) and *Circulus octoliratus* (Carpenter 1856) recorded from Taşucu and İskenderun Bay (Levantine coast of Türkiye) (Ovalis and Mifsud, 2019; Öztürk et al., 2023b) should be added to the last published checklist (Çınar et al., 2021). *P. digera* and *C. octoliratus* have been overlooked in the recently published checklist by Çınar et al. (2021).

In the present study is dealing with two new record gastropod species for the Mediterranean Sea (*E. aranea* and *S. annulata*), recorded in the İskenderun Bay (Levantine coast of Türkiye), along with some other poorly known alien species.

## MATERIALS AND METHODS

The material was sampled from off Konacık Sütunlu Liman (Colonnade Port) (İskenderun Bay), eastern Levantine coast of Türkiye. Konacık Sütunlu Liman is located within the borders of Konacık village (Arsuz-Hatay) and is in a distance approximately 8 km from Arsuz district center (Figure 1). On the coast of Konacık village there are the ruins of an ancient port city from the Hellenistic period, and for this reason, it was called the “Colonnade Port” by the local people.



Figure 1. Map of sampled area and locality

The benthic material, in which the species dealing with herein were found, was sampled from a depth of about 48 m (36°23'46"N- 35°50'19"E) on August 23, 2022 (Figure 1). The material was muddy sand with shell fragments and sea urchin skeletons and was fixed with 4% formaldehyde. In the laboratory, the material was washed with tap water on a 0.5 mm mesh and then sorted under a stereomicroscope. Both living individuals and empty shells were identified and counted. In the present study, only the alien gastropods have been taken into consideration. The nomenclature of the studied species is given according to WoRMS (World Register of Marine Species).

The studied specimens of each species, with individual catalogue numbers, are deposited in the museum collections

of the Faculty of Fisheries (ESFM), Ege University, İzmir/Türkiye.

## RESULTS AND DISCUSSION

The examination of the sampled benthic material revealed 16 specimens and 5 shells belonging to nine alien mollusc taxa, from which four species are within the subclass Caenogastropoda [*Epitonium aranea* Bonfitto, 2018; *Melanella* sp., *Stosicia annulata* (Dunker, 1860) and *Zafra pumila* (Dunker, 1860)] and five species are from the subclass Heterobranchia [*Leucotina natalensis* Smith, E. A., 1910; *Cingulina isseli* (Tryon, 1886); *Oscilla virginiae* Peñas, Rolán and Sabelli, 2020; *Pyrgulina pupaeformis* (Souverbie, 1865) and *Pyrunculus fourierii* (Audouin, 1826)]. According to the recent publication by Zenetos et al. (2022), including the alien species distributed in the Mediterranean Sea, *E. aranea* and *S. annulata* were recorded for the first time from the Mediterranean Sea. On the other hand, *O. virginiae* and *Melanella* sp. are new records for the Turkish mollusc fauna as reported by this study. Among the other taxa, some are well known species such as *L. natalensis*, *C. isseli*, *P. pupaeformis* and *P. fourierii*. All the previously known species were recorded from the Turkish Levantine coast, except for *L. natalensis* and *P. fourierii* which were also reported from the Aegean coast of Türkiye.

Some taxonomic, ecologic, and distributional features of newly recorded or poorly known species are given below.

### Taxonomic account

#### Epitoniidae Berry, S. S., 1910

#### *Epitonium aranea* Bonfitto, 2018 (Figure 2)

*Epitonium aranea*; Bonfitto, 2018: 119-129, fig. 4, A-K

**Material examined:** 1 specimen (ESFM-GAS/2022-01).

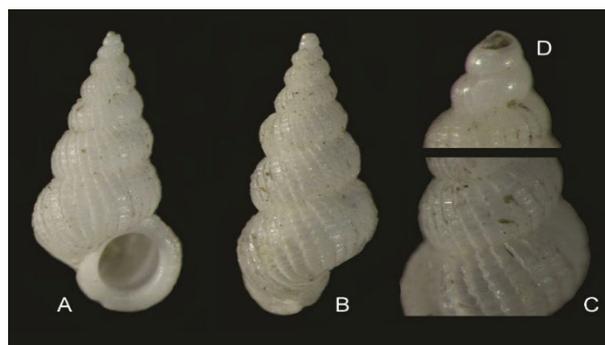


Figure 2. *Epitonium aranea*: ventral (A) and dorsal (B) views of the sampled specimen, axial ribs under magnification (C) and the protoconch of the specimen (D). (A=B=4.3 mm)

**Remarks:** The type locality of the species is the Red Sea (off Yemen), found on muddy sand at 76 m depth (Bonfitto, 2018: 124). The species is with a glossy protoconch of about 3.5 whorls and is characteristic having a reticulated sculpture of regular meshes caused by the crossing of axial ribs and spiral threads. Axial ribs (23 on the body whorl) are thin, stripe-

like, and sinuous (Figure 2). Aperture oval, outer lip thick and columella auriculate.

**Distribution:** The species was hitherto known from its type locality (Red Sea) only (Bonfitto, 2018). The present record is the first one for the Mediterranean Sea. The location, where the species was found, being in the close distance to the Suez Canal, it is suggested the species to have penetrated the Mediterranean by this pathway.

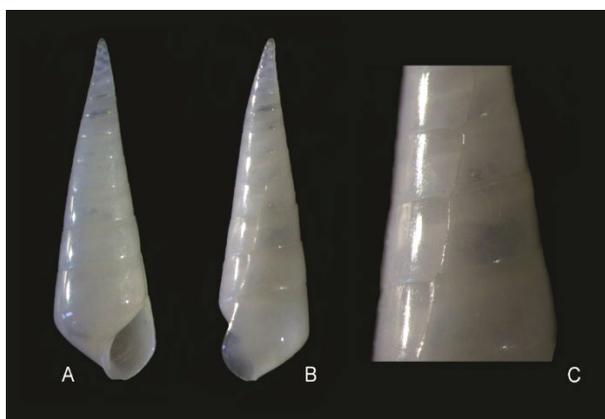
**Eulimidae** Philippi, R. A., 1853

*Melanella* sp. (Figure 3)

*Melanella* sp. 2; Mbazios et al., 2020: 35, fig. 7a.

*Melanella conoidea*; Manousis et al., 2021: 39, fig. 5e.

**Material examined:** 1 specimen (ESFM-GAS/2022-02).



**Figure 3.** *Melanella* sp.: ventral (A), lateral (B) and incremental scars (C) views of the found specimen (A=B=6.3 mm)

**Remarks:** The shell in grey-white colour, conical, shiny and consists of 11 flat teleoconch whorls. Apical part sinuous. Incremental scars evident. The species is characteristic with subangulated body whorl and angulated outer lip of the aperture. By its shell shape and characteristics of the body whorl, the specimen looks very similar to that of *Melanella conoidea* (Kurtz and Stimpson, 1851), which is a species distributed along the Atlantic coasts from North Carolina to Uruguay at depths between 0-538 m (Rosenberg et al., 2009: 643), but more specimens need to be studied to understand whether we are dealing with a known species or a new undescribed one.

A similar specimen was reported by Mbazios et al. (2020: 35, fig. 7A) as *Melanella* sp. 2, which specimen was compared by the authors to *Parvioris ibizenca* (Nordsieck, 1968), *Melanella conoidea* (Kurtz and Stimpson, 1851) and fossil records of Chirli (2009) and, although existence of some differences, the specimen was found quite similar to *Melanella conoidea* and *M. lactea* (Grateloup, 1838). After a while, a similar specimen was identified as *Melanella conoidea* by Manousis et al. (2021: 39, fig. 5e). The authors were also in opinion that the specimen considered by Mbazios et al. (2020) as *Melanella* sp. 2 was a *Melanella conoidea* (Manousis et al., 2021: 32).

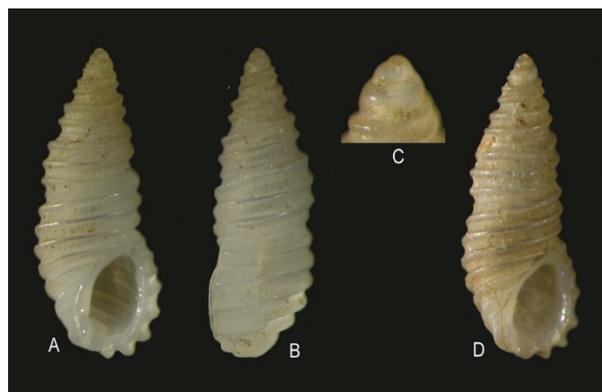
**Distribution:** *Melanella* sp. is distributed along the Hellenic (Mbazios et al., 2020; Manousis et al., 2021) and Turkish coasts (the present study).

**Zebinidae** Coan, 1964

*Stosicia annulata* (Dunker, 1860) (Figure 4)

*Rissoina annulata*; Dunker, 1860: 235 (not figured).

**Material examined:** 2 specimens (ESFM-GAS/2022-3).



**Figure 4.** *Stosicia annulata*: ventral (A, D) and dorsal (B) views of the sampled specimens and the protoconch (C) of the specimen A (A=B=3.4 mm; D=3.4 mm).

**Remarks:** The type locality of the species is Japan coasts (WoRMS).

Shell thick, consists of about 4 teleoconch whorls and a smooth protoconch of nearly 3 whorls (Figure 4C). On the whorls strong spiral ribs with canalculated interspaces. On the body whorl 6 ribs, 3 ribs on the penultimate whorl and two ribs on the initial whorls. Aperture ovoid, outer lip thickened. In whitish colour.

**Distribution:** The species is known to be distributed in Japan Sea to Kyushu (Okutani, 2000: 160), Persian Gulf and Gulf of Oman (Bosch et al., 1995: 48), western Indian coast, Indochina, Central and East Indian Ocean (Mukhopadhyay, 2015: 92-93). Its report in the present study is the first one for the Mediterranean Sea.

**Pyramidellidae** Gray, 1840

*Oscilla virginiae* Peñas, Rolán and Sabelli, 2020 (Figure 5)

**Material examined:** 2 shells (ESFM-GAS/2022-04).

**Remarks:** The type locality of *O. virginiae* is Aqaba (Jordan), 5-15 m (Peñas et al., 2020).

Shell minute, solid and consists of 4 teleoconch whorls with spiral ribs on. On the first two whorls there is two ribs, of which adapical one is wider. On the third whorl the upper rib bifurcates and on the body whorl they become three ribs, of which the upper two ribs being closer to each other. One of the shells (A) was with eroded protoconch and the other shell (B) has a protoconch with submerged nucleus. No visible axial elements. Aperture oval-shaped, an evident tooth on the columella

and thin outer lip. The differences of the species from the similar ones (*C. isseli*, *Oscilla galilae* and *Miralda* sp.) were clarified in the study by Albano et al. (2021: 46).

**Distribution:** Red Sea (Jordan and Egypt coasts) (Peñas et al., 2020) and eastern Mediterranean Sea (Israeli coast) (Albano et al., 2021). The present record is the second one from the Mediterranean Sea.

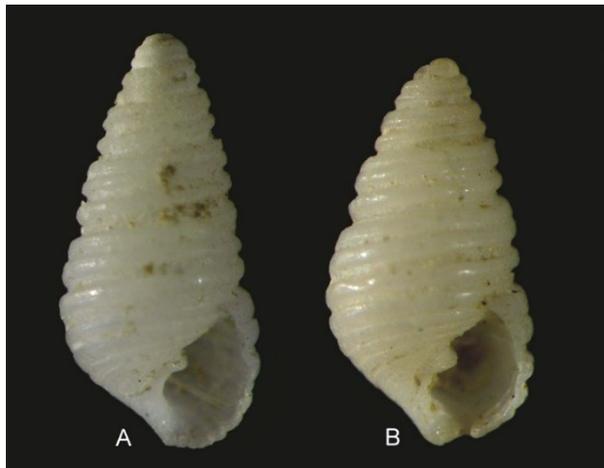


Figure 5. *Oscilla virginiae*: ventral views of the sampled shells (A=2.9 mm; B=2.3 mm).

**Columbellidae** Swainson, 1840

*Zafra pumila* (Dunker, 1860) (Figure 6)

*Columbella pumila*; Dunker, 1860: 224 (not figured).

**Material examined:** 2 specimens (ESFM-GAS/2022-05).



Figure 6. *Zafra pumila*: ventral (A) and dorsal (B) views of one of the sampled specimens (A=B=4.0 mm).

**Remarks:** The type locality of the species is Decima (Japan) (Monsecour and Köhler, 2006).

In the Mediterranean Sea, the species was first recorded from the Turkish Levantine coast in June 2010 (Öztürk et al., 2015). According to Monsecour and Köhler (2006), the

specimens belonging to the species may be of two-colour morphs: one is brown overall and the second one in yellowish colour with two narrow brown spiral bands on the body whorl and one spiral band on the spire whorls, nearer to the lower suture. Along the Turkish Levantine coast both colour morphs have been recorded (Figure 6A, B and Öztürk et al., 2015 fig. 5 A, B, C). Recently, 7 specimens of *Z. pumila* was also found in Taşucu (Tisan Bay) (Levantine coast of Türkiye) in a sandy substrate taken at 8 m depth (Panayotis Ovalis, pers. comm.).

**Distribution:** *Zafra pumila* is widespread in the Indo-Pacific area. The species is also distributed along the shoreline from the Red Sea south to Natal (South Africa), and on the Japanese and Polynesian coasts (Monsecour and Köhler, 2006). Since June 2010 it also occurs in the Mediterranean Sea (Öztürk et al., 2015).

The other alien species detected in the present study (*L. natalensis*, *C. isseli*, *P. pupaeformis* and *P. fourierii*) are widely distributed in the Mediterranean and have been assessed as established species (Figure 7). All above-mentioned species are distributed on the Levantine coast of Türkiye (Çınar et al., 2021), except for *L. natalensis* and *P. fourierii*, which are also distributed along the Turkish Aegean coast (Öztürk et al., 2017).

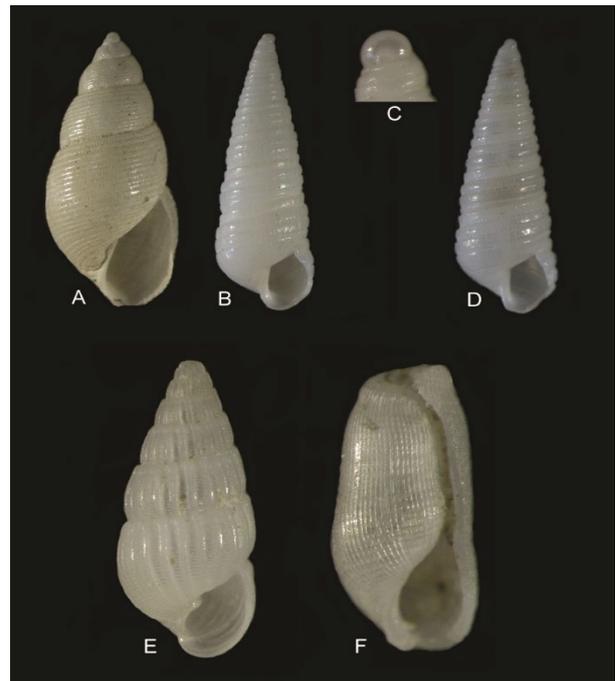


Figure 7. The alien species detected within the present study and widely distributed in the Mediterranean Sea. A. *Leucotina natalensis*; B. *Cingulina isseli*; C. protoconch of the specimen B; D. *C. isseli*; E. *Pyrgulina pupaeformis* and F. *Pyrgunculus fourierii* (A=7.2 mm; B=5.9 mm; D=5.5 mm, E=3.7 mm and F=2.3 mm)

The penetration of non-indigenous species into the Mediterranean Sea is a process that has been going on for years, although it has increased in last decades depending on

many factors such as widening of the Suez Canal, intensive marine transport, and rapid climate warming.

In a recent study by Zenetos et al. (2022), comprising the alien species in the Mediterranean Sea reported to the end of 2021, 1366 alien taxa were examined, of which 751 species are assessed as established, 232 taxa as casual, and 70 species were evaluated as questionable ones. However, the number of alien species in different groups also varies depending on the years, and the establishment success or status of some species can be changed in a shorter period, due to their adaptation to the environmental conditions in the recipient ecosystem. For example, after the year 2020 only, 21 more mollusc species have been assessed to be in established status in the Mediterranean (Zenetos et al., 2022). The same fact is also valid for the Turkish coasts, where some species such as *Pseudorhaphitoma iodolabiata* (Hornung and Mermod, 1928), *Circulus novemcarinatus* (Melvill, 1906), *Zafra pumila* (Dunker, 1860) and *Varicopeza pauxilla* (Adams, A., 1855) which have been increased to the established rank for a period nearly one decade (since 2012), being recorded for multiple times from different localities on the Turkish Levantine coast (Bilal Öztürk, pers. data). On the other hand, out of 230 alien mollusc taxa known from the Mediterranean Sea (Zenetos et al., 2022), 123 species were also detected on the Turkish coasts, which number was increased by 23% since 2011 (Çınar et al., 2021). Their number is varied according to the seas and most species (113 species) are known from the Turkish Levantine coast, whereas the lowest number species

(3 species) were detected along the Turkish Black Sea coast. With the species dealing with herein, is being added two more species to the Mediterranean mollusc fauna and four species to the Turkish marine mollusc inventory.

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#### AUTHOR CONTRIBUTIONS

Bilal Öztürk: Designing of the study, identification of the investigated species, writing of the draft, submission, writing-review, and editing. Murat Recevik: Sampling and sorting of the materials.

#### CONFLICTS OF INTEREST

The authors declare that there are no conflicts of interest or competing interests.

#### ETHICS APPROVAL

No specific ethical approval was necessary for the study.

#### DATA AVAILABILITY

For any questions the corresponding author should be contacted.

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# A new oligochaeta record for Türkiye, *Rhyacodrilus falciformis* Bretscher, 1901 (Annelida: Naididae: Rhyacodrilinae)

## Türkiye Oligochaeta faunası için yeni kayıt, *Rhyacodrilus falciformis* Bretscher, 1901 (Annelida: Naididae: Rhyacodrilinae)

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**Abstract:** The aim of this paper is to contribute to the aquatic Oligochaeta fauna of Türkiye. The study area selected for this research is Karasu Stream, located in the Black Sea Region of Türkiye, in the province of Sinop. Benthic macroinvertebrate samples were collected on a monthly basis between February 2013 and January 2014 from 10 selected stations in the study area. As a result of the study, *Rhyacodrilus falciformis* Bretscher, 1901 is reported as a new record for the Oligochaeta fauna of Türkiye. Besides being recognized as a new record species, this record also extends the species' distribution area to the Asian part of Türkiye. Additionally, this study provides detailed information on the biological, ecological, and morphometric characteristics, as well as the distribution of *R. falciformis*, identified as a new record for the fauna of Türkiye.

**Keywords:** Oligochaeta, Rhyacodrilinae, new record, Karasu Stream, Sinop, Türkiye

**Öz:** Bu makalenin amacı, Türkiye'nin sucul Oligochaeta faunasına katkıda bulunmaktır. Bu araştırma için seçilen çalışma alanı, Türkiye'nin Karadeniz Bölgesi'nde, Sinop ilinde bulunan Karasu Çayı'dır. Bentik makroorganizma örnekleri, Karasu Çayı'nda 10 istasyondan Şubat 2013 ile Ocak 2014 arasında aylık olarak toplanmıştır. Araştırma alanında tespit edilen, *Rhyacodrilus falciformis* Bretscher, 1901, Türkiye'den ilk kez bildirilmektedir. Türkiye Oligochaeta faunası için yeni kayıt olarak tanınmasının yanı sıra, bu araştırma ile türün dağılım alanı Türkiye'nin Asya kısmına kadar genişlemektedir. Ayrıca, bu çalışma, Türkiye faunası için yeni bir kayıt olarak tanımlanan *R. falciformis*'in biyolojik, ekolojik ve morfometrik özellikleri ile dağılımı hakkında detaylı bilgiler de sağlamaktadır.

**Anahtar kelimeler:** Oligochaeta, Rhyacodrilinae, yeni kayıt, Karasu Çayı, Sinop, Türkiye

## INTRODUCTION

The Oligochaeta order in freshwater ecosystems comprises approximately 1100 known species (Martin et al., 2008). The family Naididae is one of the most significant groups of aquatic Oligochaeta. Rhyacodrilinae is a subfamily within the family Naididae, and its representatives are commonly found in rivers and marine environments. The genus *Rhyacodrilus*, now placed in the family Naididae from Tubificidae, is a cosmopolitan and large genus (Ohtaka, 1995). There have been 54 valid species of *Rhyacodrilus* identified worldwide (Martin et al., 2023). Globally, 20 genera are recognized within this subfamily (Martin et al., 2023).

However, from Türkiye, only five species belonging to this subfamily have been reported so far: *R. coccineus* (Vejdovsky 1876) in Gümüş River by Öntürk and Arslan (2003); in Tunca River by Çamur-Elipek et al. (2006); in Balıkdanı Wetland by Arslan et al. (2007); in Lake Uluabat by Kökmen et al. (2007); in Porsuk River and in the Trace Region by Arslan and İlhan (2010); in Trace Region-Taş et al. (2012); in Tuzla Stream by Odabaşı et al. (2018); *Branchiura sowerbyi* Beddard, 1892 in

Buldan Dam Lake by Balık et al. (2004); *Monopylephorus irroratus* (Verrill, 1873) in Hazar Lake by Şahin and Baysal (1972); *Epirodilus moubayedii* Giani and Martinez-Ansemil (1981) in Balıkdanı Wetland by Arslan et al. (2007); and *Bothrioneurum vej dovskyanum* Štolc, 1886 in Karamenderes Stream by Odabaşı et al. (2017) have been reported from different parts of Türkiye.

The objective of this study is to report *R. falciformis* Bretscher, 1901 as a new record for the Oligochaeta fauna of Türkiye. In addition, this record also contributes to the knowledge of the species distribution by extending its range to the Asian part of Türkiye.

## MATERIALS AND METHODS

Between February 2013 and January 2014, samples were collected from 10 stations in Karasu Stream, located in the Black Sea Region of Türkiye, at monthly intervals (Figure 1).

The kick sampling method was used to collect zoobenthic

samples from a 1 m<sup>2</sup> area at each station, with a 5-minute collection standard (kick-net mesh size: 180 µm) (Letovsky et al., 2012). After fixing the samples with 4% formaldehyde in the study area, they were transported to the laboratory and washed again through a 180 µm sieve. Oligochaeta samples separated from the debris were preserved in 70% alcohol with CMCP 10 solution for identification. Species identification was carried out

using Timm's (1999 and 2009) keys.

Digital photos of the species were taken using a digital camera (Camedia, C-7070, Olympus) connected to compound and stereo microscopes. The specimens are housed in the Museum of the Faculty of Fisheries, Ege University. All measurements are given in parentheses.

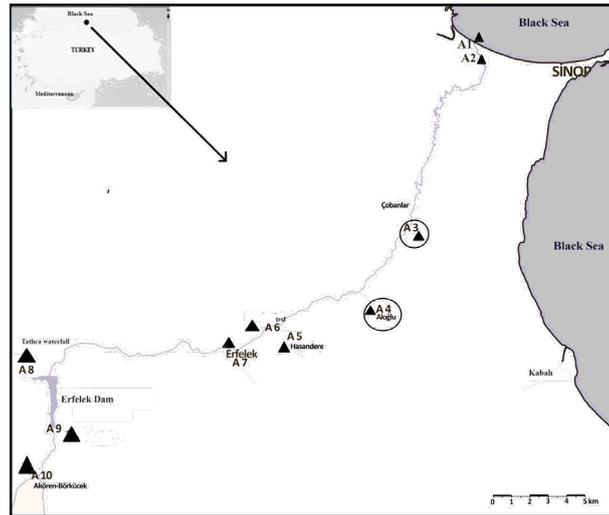


Figure 1. Sampling stations and map of the study area (Çil et al., 2021)

## RESULTS

As a result of the samplings, *R. falciformis* was found at only two stations (Stations A3 and A4) (Figure 2, Figure 3).



Figure 2. Station 3 (A3)



Figure 3. Station 4 (A4)

The ecological, biological, and morphometric characteristics, as well as the distribution, of the Oligochaeta species determined as a new record for the fauna of Türkiye are explained in detail below.

***Rhyacodrilus falciformis* Bretscher, 1901 (Figure 4 and 5)**

### Material

A total of 15 specimens were obtained, and they were found only at two stations in the study area (Station 3=A3: Karasu Stream 41°57'59.24"N, 35°01'26.45"E, and Station 4=A4: Tributary of Karasu 41°54'45.10"N, 34°59'33.17"E) (Figure 1). One individual was obtained from Station 3 in February, while 11 were collected from Station 4 in February and 1 in March.

### Description

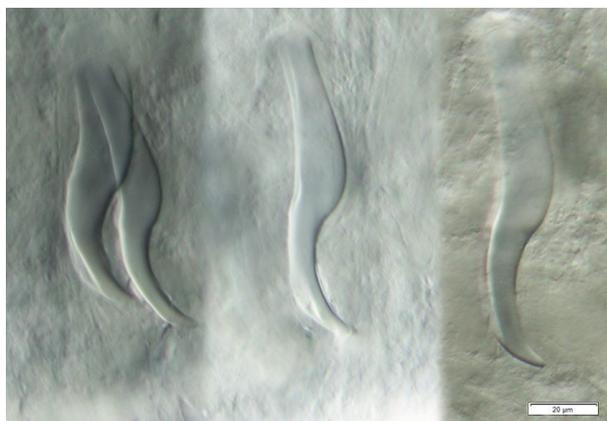
Total length = 8-10 mm, Number of segments = 38-48

The anterior and posterior locomotory chaetae are similar, with upper teeth 2-6 in anterior bundles and 1-2 in posterior bundles, measuring 72-81 µm in length. Near the male pores (XI), single large sickle-shaped penial chaetae are usually hidden inside the body with a simple tip, measuring 94-148 µm in length and 12-14 µm in thickness. The presence of abundant large coelomocytes in the body cavity gives the living worm a white color, similar to enchytraeids (Timm, 1999).

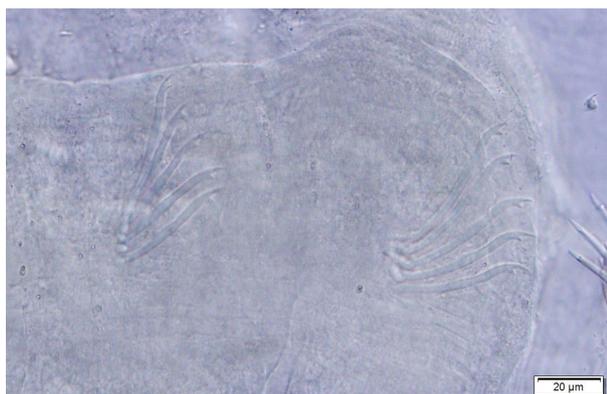
### Diagnosis

Total length = 5.75-9.25 mm, Number of segments = 31-45

The anterior and posterior locomotory chaetae are similar, with upper teeth 2-6 in anterior bundles and 1-2 in posterior bundles, measuring 57.5 µm-61 µm in length. Near the male pores (XI), single large sickle-shaped penial chaetae are usually hidden inside the body with a simple tip, measuring 96-117 µm in length and 18.5 µm-22.5 µm in thickness.



**Figure 4.** *Rhyacodrilus falciformis*, genital area (XI, ventral segment) showing large modified penial setae



**Figure 5.** *Rhyacodrilus falciformis*, anterior dorsal setae III-IV with distinct longer distal tooth

#### Differential characteristics

*R. falciformis* shows similarities with *Bothrioneurum vej dovskyanum* Štolc, 1886, but *B. vej dovskyanum* bears sensory prostomial pits and only the foremost chaetae have

considerably longer upper teeth, while the teeth become progressively equal in subsequent preclitellar segments.

The sickle-shaped penial setae of this species are a distinctive feature. A similar species described from France (*R. pigueti*) has larger penial chaetae of 150 µm and is more straight compared to the sickle-shaped penial chaetae of *R. falciformis* (Martinsson et al., 2013).

In this study, the penial setae of *R. falciformis* vary in length from 96-117 µm, which falls within the normal range for this species (100-140 µm: Martinsson et al., 2013).

Although penial setae are normally between 94-148 µm long (Kasprzak, 1979, 1981; Timm, 2009), Martin and Boughrou (2012) have shown penial setae of approximately 175 and 200 µm (Table 1).

#### Environment

This species can be found in groundwater, springs, clean lakes, and in soil (van Haaren, 2002).

#### Habitat

*R. falciformis* inhabits freshwater. Karasu Stream originates in Boyabat district, passes along through Erfelek town (Sinop Province) and pours into the Black Sea (Figure 1). This approximately 80 km long stream provides drinking water to the surrounding settlement areas together with the Erfelek Dam.

Station 3 (A3): This stream, which passes through the middle of a village surrounded by forest, is closely associated with agricultural activities and animal husbandry. The water flow rate at this station shows significant changes throughout the year. The bottom structure of the stream consists of stones, gravel, and sand.

Station 4 (A4): This station has a rich riparian zone and merges with the Karasu Stream. The main source of pollution at this station is the domestic waste discharged from nearby settlement areas.

#### Distribution

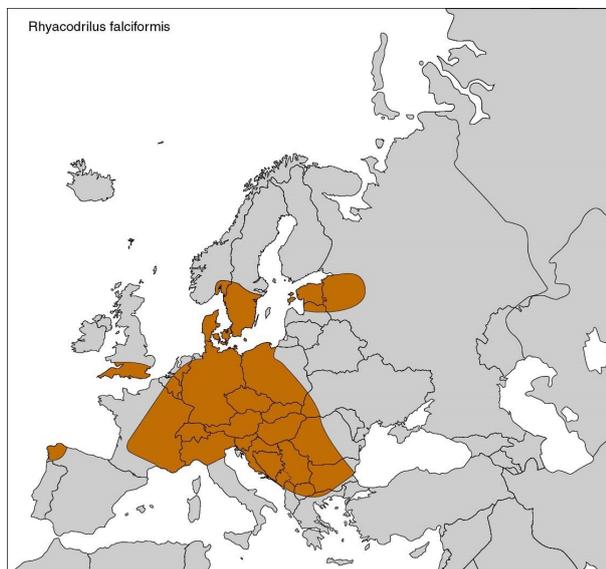
Europe, possibly introduced in North America (Timm, 2009).

**Table 1.** Penial setae lengths according to literature

References	Region	Length penial chaetae (µm)
Piguet (1906) as <i>R. lemani</i>	Lake Geneva	124
Michaelsen (1908) as <i>Taupodrilus lemani</i>	Germany	116
Piguet and Bretscher (1913); Piguet (1913)	Switzerland	138
Hrabě (1935)	Bohemia and Moravia	117.6
Čhekanovskaya (1962); Brinkhurst (1963)	Europe	138
Hrabě (1981)	Czech Rep	128-140
Kasprzak (1979, 1981)	Poland	94-148
Timm et al. (1996)	Sweden	100-122
Martin and Boughrou (2012)	Maghreb	~175 (fig no 58C) and ~200µm (fig no 58D)
Unpublished measurements (van Haaren, T.)	Netherlands	100-130 (n=7)
This study	Türkiye	(78-)96-117

## DISCUSSION

The main distribution area of *R. falciformis* is in Central Europe (van Haaren, 2002) (Figure 6).



**Figure 6.** Distribution map of *Rhyacodrilus falciformis* Bretscher, 1901 in Europe (van Haaren, 2002).

*R. falciformis* Bretscher, 1901, is a rarely encountered groundwater species. This genus was first described in 1900 from materials collected from the Swiss Alps (Bretscher, 1901). Subsequently, it was rediscovered from samples collected at Geneva Lake in France (Juget, 1967) and from the Pieniny Mountains in the southern part of Poland (Kasprzak, 1979). According to van Haaren (2002), the distribution of *R. falciformis* in Europe is as follows:

Records of *R. falciformis* are from the following locations: Holland (Verdonschot et al., 1992), Susaa River in Denmark (Berg, 1948), source of the Fulda River, and Schlei in Germany (Wachs, 1967; von Bülow, 1957), Vättern Lake in Sweden (Brinkhurst and Jamieson, 1971), Geneva Lake in Switzerland (Brinkhurst, 1964; Brinkhurst and Jamieson, 1971), South Dorset in England (Ladle and Bird, 1980), Jantra and Struma rivers in Bulgaria (Uzunov and Kapustina, 1993), Tambre River and Porto do Cabo in the Iberian Peninsula (Martínez-Ansemil and Giani, 1980; Martínez-Ansemil, 1984; Martínez-Ansemil and Collado, 1996), source of the Adige basin in Italy (Di Chiara Paoletti and Sambugar, 1996), Estonia (Timm, 1999), Dyje River in Czechoslovakia (Wolgemuth and Schenkova, 1999), Poland (Dumnicka, 2001), and various locations in France including Annecy Lake, Argens River (l'Eau Salée), Geneva Lake, and the (subterranean) underflow of the upper Rhône, as well as the southern and western foothills of the Carpathian mountains in caves along the Hungarian/Slovakian border (Brinkhurst and Jamieson, 1971; Giani and Martínez-Ansemil, 1981; Juget, 1984; IUCN, 1998; Dumnicka, 2001). There are also records from Scandinavia (Milbrink, 1978) and Norway (Bremnes and Sloreid, 1994) and in Magnesian Limestone Plateau of County Durham, UK (Standen et al., 2009).

Recently, Martinsson et al. (2013) described a slightly different new species from France, *R. pigueti* sp. n., and successfully distinguished it from *R. falciformis* using DNA barcoding, based on the shape of the penial chaetae. In *R. falciformis*, the penial chaetae are sickle-shaped, while in the new species, they are straight and somewhat spoon-shaped.

In North America, *R. falciformis* is extremely rare. According to Timm (2009), this species was possibly introduced to North America. It was first recorded from Airport Creek in British Columbia (Brinkhurst, 1978), and since then, it has been documented from Cascade Cave (Vancouver Island), the Hudson River in New York, Fraction Run in Illinois, and Montana (Brinkhurst, 1986; Wetzel, 1992; Kathman and Brinkhurst, 1998). The collection of *R. falciformis* from Mystery Cave expands its range southward and is the second report of this species from a cave in North America (Wetzel and Taylor, 2001).

Apart from the distribution of *R. falciformis* in these continents, Martin and Boughrouss (2012) reported that *R. falciformis* has also been collected in the upper courses of the Oued Aïssi River in Algeria by Lounaci (1987).

## CONCLUSION

Numerous studies have been conducted on freshwater oligochaeta species in different regions of Türkiye, yet to date; there have been no verified records of the stygophilous species *R. falciformis*. With this study, it has been confirmed that the distribution of *R. falciformis* extends to the Asian part of Türkiye. Ongoing research on the oligochaeta fauna in Türkiye is expected to yield more records regarding the distribution of this species and other oligochaeta species that were previously unrecorded in the country's biodiversity records.

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## AUTHOR'S CONTRIBUTION

Melek Zeybek Yünlü, Eylem Aydemir Çil and Seray Yıldız conceived the idea and developed the experimental protocol. Seray Yıldız and Ton van Haaren have organized the assignments and data related to the species. All authors contributed critically to the draft and gave the final approval for publication.

## CONFLICT OF INTEREST

The authors declare no conflict of interest.

## ETHICS APPROVAL

No specific ethical approval was necessary for this study.

## DATA AVAILABILITY

The data supporting the conclusions of this paper are available in the main paper.

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