

Instructions to Authors

Genes & Genetic Systems (GGS) is the official journal of the Genetics Society of Japan, which has been published bimonthly since 1918.

SCOPE

GGS covers a wide range of fields in genetics, including general genetics, molecular genetics, cell genetics, developmental genetics, behavioral genetics, ecological genetics, chemical genetics, epigenetics, cytogenetics, population genetics, evolutionary genetics, and molecular evolution. GGS also welcomes papers in the following fields, if they are related to genetics: genome-wide research, bioinformatics, systems biology, database, genetic bioresources, and technical advances (in both experimental and *in silico* methods).

CATEGORIES

- (a) Original papers.
- (b) Short communications.
- (c) Reviews and minireviews.
- (d) Meeting reports.

- All manuscripts (a-c) must be original and not previously published or submitted for publication elsewhere. Only manuscripts in English will be accepted.

- Short communications are short reports of the results of studies that are of sufficient interest to justify publication. They should not exceed five printed journal pages, and the text should not be divided into sections, such as Introduction, Results and Discussion.

- Reviews and minireviews are published on an invitation basis, and are managed by the Review Editor. However, GGS will also consider submissions without an invitation. Interested authors should contact the Review Editor or one of the Editors in the related field before submission. All reviews and minireviews are peer reviewed in the same way as original papers and short communications.

POLICY

Authors describing human research or animal experiments must indicate that the research was approved by a Review Committee at their institute, or state that the experiments were performed in accordance with accepted guidelines. Authors must include in the Methods section a brief statement identifying the institutional and/or licensing committee that approved the experiments.

Authors describing unique research materials, such as strains, gene clones, and computer programs, must agree to provide them at reasonable cost to researchers who request them.

For large-scale experiments, accessibility to raw data is necessary for publication. If public repositories are available, authors are expected to use these repositories. If not, the authors should provide the raw data as supplementary information.

All authors are required to disclose any association that poses a conflict of interest in connection with the submitted manuscript.

MANUSCRIPT SUBMISSION

1) Preparation of the manuscript

- (a) The manuscript should be typewritten double spaced. The manuscript should be arranged in the following order:
 - (i) Title page, (ii) Abstract, (iii) Main body, (iv) References, (v) Tables, (vi) Legends to Figures, and (vii) Figures.
- (b) The title page should comprise: (i) the title of the manuscript, (ii) name(s) of the author(s), (iii) academic

or professional affiliation(s), (iv) complete address(es) including street name(s) and number(s), (v) any footnotes referring to the above items, (vi) a running head (not exceeding 50 letters including spaces), and (vii) up to five keywords in alphabetical order (do not capitalize words unless they are proper names), (viii) name of the corresponding author, his/her address, telephone and facsimile numbers, and E-mail address.

- (c) The abstract should state the scope of the work and the principal findings in no more than 300 words. References should not be included.
- (d) Except for short communications, the main body should be divided into sections: Introduction, Materials and Methods, Results, and Discussion. The section titles should be written in centered, boldface, uppercase heading, such as **INTRODUCTION**. Each section, except for the Introduction, can be divided into subsections. The first paragraph of the subsection should begin with a left-aligned, bold face heading that starts with an uppercase letter and finishes without a period.
- (e) Each table should be on a separate sheet, and the tables should be placed at the end of the manuscript after the reference list. Tables should be provided with headings on the same sheet.
- (f) Figures should be prepared electronically and saved in one of following formats: "Word (.DOC or .DOCX)", "Power Point (.PPT or .PPTX)", "JPEG (.JPG)", "TIFF (.TIFF)", "EPS (.EPS)", or high resolution "PDF (.PDF)". The legends should be listed on a separate sheet(s).
- (g) References should be cited in the text by the author(s) and year, and listed at the end of the text with the names of the authors arranged alphabetically. Use of EndNote is highly recommended for the preparation of references (The "GGS style" for EndNote can be downloaded from the GGS author instructions home page, <http://gsj3.jp/ggs/intro.html>). Personal communications and unpublished data or reports should be mentioned in parenthesis in the text but should not be included in the reference list. In the reference list, please adhere to the formats in the following examples. For articles with more than ten authors, list the first ten names and then add "et al."

[Journal articles]

Tajima, F. (1989) Statistical method for testing the neutral mutation hypothesis by DNA polymorphism. *Genetics* **123**, 585–595.

Saitou, N., and Nei, M. (1987) The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Mol. Biol. Evol.* **4**, 406–425.

Sarojam, R., Sappl, P. G., Goldshmidt, A., Efroni, I., Floyd, S. K., Eshed, Y., and Bowman, J. L. (2010) Differentiating Arabidopsis shoots from leaves by combined YABBY activities. *Plant Cell* **22**, 2113–2130.

Sasaki, T., Matsumoto, T., Yamamoto, K., Sakata, K., Baba, T., Katayose, Y., Wu, J., Niimura, Y., Cheng, Z., Nagamura, Y., et al. (2002) The genome sequence and structure of rice chromosome 1. *Nature* **420**, 312–316.

[Books]

Steeves, T. A., and Sussex, I. M. (1989) *Patterns in Plant Development*. Cambridge University Press, Cambridge, UK.

Nakazaki, T., Naito, K., Okumoto, Y., and Tanisaka, T. (2008) Active transposons in rice. *In Rice Biology in the Genomics Era*. (eds.: Hirano, H.-Y., Hirai, A., Sano, Y., and Sasaki, T.), pp. 69–79. Springer, Heidelberg.

- (h) Authors are encouraged to submit supplementary

information. Supplementary information gives authors the opportunity to provide raw data, which would be impossible or impractical to include in the printed version. Supplementary information can include text, tables, and figures. The formats of the tables and figures should be the same as those of manuscript, but figure legends should be placed below the figures they refer to. Supplementary information files must be submitted in PDF format together with the main manuscript. Authors must indicate the number of supplementary information files in the cover letter. Supplementary information will be made available online after acceptance of the paper.

- (i) Genus or species names, names of genes, mathematical formulae, and other terms requiring special symbols should be appropriately indicated by the use of italics, boldface letters, superscripts, and subscripts.
- (j) Footnotes should be avoided whenever possible. If absolutely necessary, they should be numbered and placed at the bottom of the page in question.

2) Manuscript submission

Initial online submission: A manuscript and a cover letter should be submitted electronically via the website (<https://www.editorialmanager.com/ggs/>). You will receive an ID and a password with which you can monitor the progress of the paper during the review process.

Final manuscript submission: After the paper has been accepted for publication, the author is requested to send a final version of the manuscript to the Editor-in-Chief. The text should be prepared using MS Word (.DOC or .DOCX). Tables should be placed at the end of the text in the same file. Figures saved in the formats indicated in 1)-(f) and Supplementary information files (PDF format) should be sent as separate files. No file should exceed 10 Mb.

3) New nucleotide sequence data

New nucleotide sequence data must be submitted and deposited in the DDBJ/EMBL/GenBank databases, and an accession number must be obtained before the paper can be accepted for publication. Submission to any one of the three collaborating databanks is sufficient to ensure data entry in all. The accession number should be included in the manuscript, e.g., as a footnote on the title page. [Note: Nucleotide sequence data reported are available in the DDBJ/EMBL/GenBank databases under the accession number(s)---]. If requested by the author, the database will withhold release of data until publication. The most convenient method for submitting sequence data is via the World Wide Web at the following internet addresses: DDBJ via SAKURA (<http://sakura.ddbj.nig.ac.jp>), EMBL via WEBIN (<http://www.ebi.ac.uk/embl/Submission/webin.html>), GenBank via BankIt (<http://www.ncbi.nlm.nih.gov/BankIt/>), or by the stand-alone submission tool Sequin (<http://www.ncbi.nlm.nih.gov/Sequin/>).

For special types of submissions (e.g. genomes and bulk submissions), please use the contact information below to enquire about the availability of alternative submission systems.

Database Contact Information

DDBJ: Center for Information Biology and DNA Data Bank of Japan, National Institute of Genetics, Yata, Mishima, Shizuoka 411-8540, JAPAN; telephone: +81-55-981-6853; fax: +81-55-981-6849; e-mail: ddbj@ddbj.nig.ac.jp; WWW

URL: <http://www.ddbj.nig.ac.jp>

EMBL: EMBL Nucleotide Sequence Submissions, European Bioinformatics Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, U.K.; telephone: +44 1223 494400; fax: +44 1223 494472; e-mail: datasubs@ebi.ac.uk; WWW URL: <http://www.ebi.ac.uk>

GenBank: National Center for Biotechnology Information, National Library of Medicine, Bldg. 38A, Rm 8N-803, Bethesda, MD 20894, U.S.A; telephone: +1 301 496 2475; fax: +1 301 480 9241; e-mail: info@ncbi.nlm.nih.gov; WWW URL: <http://www.ncbi.nlm.nih.gov>

4) Microarray data submission to the international public gene expression databases

GGG now requires the submission of microarray data to one of the following public repositories: ArrayExpress (<http://www.ebi.ac.uk/arrayexpress/>), Gene Expression Omnibus (GEO) (<http://www.ncbi.nlm.nih.gov/geo/>), or CIBEX (<http://cibex.nig.ac.jp/>). An accession number for microarray data must be obtained before publication and should be included in the text of the manuscript.

5) Page charges

Members of the Genetics Society of Japan are requested to pay ¥4,000 for each printed page and an extra cost for color printing amounting to ¥10,000 per color figure, while nonmembers are requested to pay ¥8,000 for each printed page and an extra cost of color printing amounting to ¥30,000 per color figure. Page charges are waived for invited reviews.

6) Proofreading

Proofreading will be limited to the correction of typographical errors. Any additional cost incurred by the author making changes at the proofreading stage will be charged to the author.

7) Offprints

The minimum number of reprints that can be ordered is 100. A reprint order form and price list will be sent with the galley proof.

8) Copyrights

The copyrights for articles that appear in GGS are held by The Genetics Society of Japan. A Copyright Transfer Form will be sent with the galley proof.

9) Cover consideration

The cover of each issue will carry an inserted full-color illustration that is relevant to one of the articles published in the issue, the cost of which will be borne by the journal. A Cover Illustration will be solicited from any contributor whose manuscript is accepted for publication. Please send the illustration and a short caption (within 150 words) to the Editor-in-Chief of GGS.

10) Correspondence

Manuscripts and correspondence concerning editorial matters should be addressed directly to one of the editors of the discipline of the paper or to: Dr. Hiroshi Iwasaki, Editor-in-Chief, GGS, Institute of Innovative Research, Tokyo Institute of Technology, S2-7, 4259 Nagatsuta, Midori, Yokohama, Kanagawa 226-8503, Japan. E-mail: hiwasaki@bio.titech.ac.jp