

Heredity



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ABOUT THE JOURNAL

Aims and Scope: *Heredity* is the official journal of the Genetics Society. The journal covers a broad range of topics within the field of genetics and therefore papers must address conceptual or applied issues of interest to the journal's wide readership. We encourage submissions on any study system but there should be a take-home message that focuses on broad general lessons that can be extended beyond single organisms. The journal particularly encourages submissions in the following areas:

- population genetics / genomics
- molecular evolution and phylogenetics
- genome architecture
- epigenetics
- ecological genetics
- functional genomics, transcriptomics, metabolomics and proteomics
- evolutionary genetics
- conservation genetics
- applied genetics
- quantitative genetics
- adaptation genomics
- crop and livestock genetics / genomics

Heredity's original articles cover new theory and primary empirical research that offers novel insights, using the latest advances in technological and analytical tools. We have recently added a 'computer notes' category, for which we invite submissions describing software packages that would be of interest for genetic analyses. The journal also encourages submission of reviews, mini-reviews and proposals for special issues on current topics.

There are NO CHARGES applicable to manuscripts published in *Heredity* unless the author wishes to publish Open Access.

Journal Details

Editor-in-Chief:

Professor Barbara Mable, University of Glasgow, Glasgow, Scotland

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heredity-journal@glasgow.ac.uk

Impact factor: 3.821 (2020 Journal Citation Reports, Science Edition, Clarivate Analytics, 2021)

Frequency: 12 issues a year

Abstracted in:

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EBSCO Discovery Service
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ARTICLE TYPE SPECIFICATIONS

ARTICLE DESCRIPTION	ABSTRACT	WORD LIMIT	TABLES/ FIGURES	REFERENCES (MAXIMUM)
<p>Original Article (Please see 'Preparation of Articles' below for further details) These are reports of current basic or clinical research. <i>Heredity</i> strongly encourages authors adhere to the reporting guidelines relevant to their specific research design. Any clinical trials submitted to <i>Heredity</i> must adhere to the registration requirements listed in the Editorial Policies.</p>	Max 250 words	7,000 excluding references	Maximum of 8 figures or tables	100
<p>Computer Note <i>Heredity</i> publishes notes of new or substantial updates to existing computer programs addressing an important problem in <i>Heredity's</i> broad range of topics within the field of genetics. The note should describe clearly the aim, design, main functions, as well as a brief summary of the input (data) and output (results) of the program. The authors may also include a section exemplifying the use of the software by analysing an empirical dataset, and/or a section comparing the performances of the new and existing software by analysing some simulated or empirical data. The software package should include executables for at least one computer platform (Windows, Mac, Linux) or source code, a user's manual, and one or more test datasets. At submission time, the package should be either deposited in a public domain to enable online access or submitted together with the computer note for assessment by referees.</p>	Max 250 words	7,000 excluding references	Maximum of 8 figures or tables	100
<p>Review Article A Review Article is an authoritative, balanced survey of recent developments in a research field. Review Articles should be structured around a clear and topical question/aim, plus incorporate a review of previously published literature from the past 5-10 years, describing the pros and cons of these studies. Normally, the review article will also present the author's opinion on how to approach the issue/situation being discussed and their thoughts on what is necessary to move the field forward in the future. Authors interested in submitting review articles to <i>Heredity</i> are encouraged to contact the editorial office in advance of submission to discuss their idea.</p>	Max 250 words	7,000 excluding references	Maximum of 8 figures or tables	120
<p>Perspective: A Perspective is intended to provide a forum for authors to discuss models and ideas from a personal viewpoint. They are more forward looking and/or speculative than Review Articles and may take a narrower field of view. They may be opinionated but should remain balanced and are intended to stimulate discussion and new experimental approaches. Perspectives are regularly commissioned however pre-submission enquiries are also welcome. Please contact the editorial office to propose an idea.</p>	No abstract required	3,000 excluding references	Maximum of 8 figures or tables	100
<p>Editorial (by Editor invitation only) Proposals for Editorials may be submitted; however, authors should only send an outline of the proposed paper for initial consideration.</p>	N/A	1,500	Maximum of 1 figure or table	10
<p>Commentary Commentary articles draw attention to recent advances in the field and may be based on papers published in <i>Heredity</i> or elsewhere. As with Reviews, most pieces are commissioned but the Editorial Office is happy to consider suggestions.</p>	N/A	1,000	Maximum of 1 figure or table	10

Special Issues

Special issues are comprised of a group of high quality, peer-reviewed manuscripts about a single specific theme / topic. Although the individual manuscripts are stand alone, they collectively make an important point by offering a comprehensive view, or by providing a diverse perspective. The number of manuscripts in a special issue is determined on a case by case basis.

Special Issues are commissioned only by invitation or upon consultation with *HDY* editorial staff. Please contact the Editorial Office (heredity-journal@glasgow.ac.uk) for preliminary inquiries about special issues. Usually, a person willing to be the Guest Editor of a special issue should initiate this process. This Guest Editor will act as the point of contact between *HDY* and the individual authors submitting manuscripts.

PREPARATION OF ARTICLES

Manuscripts should be double-spaced, with all margins at least 4 cm in width. Pages and lines should be continually numbered to aid cross-referencing. Any manuscript cited as 'in press' should be uploaded if possible. Papers based on thesis chapters normally require rewriting and drastic abbreviation before submission.

All manuscripts are subject to editorial review. Papers must be submitted exclusively to *Heredity* and are accepted on the understanding that they have not been, and will not be, published elsewhere. If accepted, papers become the property of The Genetics Society. Authors should ensure that a full copy of all submitted material, including illustrations, is retained. It is the author's responsibility to obtain permission to reproduce illustrations, tables, etc. from other publications.

Please note that original articles must contain the following components. Please see below for further details.

- Cover letter
- Title page (excluding acknowledgements)
- Abstract
- Introduction
- Materials and Methods
- Results
- Discussion
- Acknowledgements
- Author contribution statement
- Conflict of Interest
- Data archiving
- References
- Figure legends
- Tables
- Figures (uploaded separately)

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Please also include a Conflict of Interest statement, see [Editorial Policies](#) for more details.

Title Page: This should include the following, in sequence:

1. A succinct title.
2. Full names and addresses of all authors.
3. Name of corresponding author (to whom proofs and all correspondence will be sent) together with their full address, telephone and fax numbers, and e-mail address.
4. A running title of no more than 50 characters. Should not contain any abbreviations. Please note – the running head for a manuscript on all pages after the title page will be the shortened manuscript title followed by an ellipsis.
5. Word count for main text (excluding references, tables and figures).

Abstract: This should not exceed 250 words and should be provided on a separate page in the file, as well as on the online submission form. It is particularly important that the Abstract identifies the conceptual issue(s) addressed in the paper, as well as outlining the approach and the main findings. Please ensure that the conclusions consider a broad general message in addition to specific conclusions about the focal study system.

Graphical Abstracts (optional): A graphical abstract, which summarizes the manuscript in a visual way, is designed to attract the attention of readers in the table of contents of the journal. Files should be uploaded as a 'Figure' and be labelled 'Graphical abstract'. A standard file format (.tiff, .eps, .jpg, .bmp, .doc, or .pdf.) should be used, and the graphic should be 9 cm wide x 5 cm high when printed at full scale and a minimum of 300 dpi. All graphical abstracts should be submitted with a white background and imagery should fill the available width, whenever possible. Colour graphical abstracts are encouraged and will be published at no additional charge. Textual statements should be kept to a minimum.

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See example below:

MAJ was responsible for designing the review protocol, writing the protocol and report, conducting the search, screening potentially eligible studies, extracting and analysing data, interpreting results, updating reference lists and creating 'Summary of findings' tables. SBM was responsible for designing the review protocol and screening potentially eligible studies. She contributed to writing the report, extracting and analysing data, interpreting results and creating 'Summary of findings' tables. DIH conducted the meta-regression analyses and contributed to the design of the review protocol, writing the report, arbitrating potentially eligible studies, extracting and analysing data and interpreting results. NAL contributed to data extraction and provided feedback on the report. FRT and RAL provided feedback on the report.

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Authors are strongly encouraged to follow established minimum guidelines for the reporting of biological data, wherever appropriate. Guidelines for many relevant data types are available from MIBBI: Minimum Information for Biological and Biomedical Investigations (www.mibbi.org). Advice on good practice in data archiving is provided by Whitlock (2011).

DNA sequences published in *Heredity* must be deposited in a publicly available database, usually EMBL/GenBank/DBJ, and accession numbers must be included in the final version of the manuscript. Where public databases exist for other data types, such as microarray data (see www.ebi.ac.uk/Databases/microarray.html, for example), they must be used and the relevant reference should be included in the manuscript. Where no public database exists, authors must submit their data to the Dryad data repository (www.datadryad.org). On acceptance of an Original Article, the corresponding author will automatically receive an email with details of the steps necessary for submission to Dryad.

Dryad can accept data of any type. The data should be formatted for use in a relevant, readily available software package, ideally one which allows data export in a variety of formats (such as CREATE for population genetic data: <https://bcrc.bio.umass.edu/pedigreesoftware/node/2>). It is the corresponding author's responsibility to ensure that sufficient metadata (such as sample locations, individual identities etc.) are provided to allow easy repetition of analyses presented in the manuscript. We recognise that some information may be sensitive (such as identities of subjects or locations of endangered species). Such information can be excluded from the submission provided that this does not prejudice re-analysis of the data.

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References: These should be indicated chronologically in the text by the surnames of the authors with the year of publication. Citation by name and year can be given entirely in parentheses or by citing the year in parentheses after an author's name used in the text - examples below:

- Negotiation research spans many disciplines (Thompson 1990).
- This result was later contradicted by Becker and Seligman (1996).
- This effect has been widely studied (Abbott 1991; Barakat et al. 1995a, b; Kelso and Smith 1998; Medvec et al. 1999, 2000).

There should normally be no more than 100 references. The list of references should only include works that are cited in the text and that have been published or accepted for publication. Personal communications and unpublished works should only be mentioned in the text. Do not use footnotes or endnotes as a substitute for a reference list.

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Book: South J, Blass B (2001) *The future of modern genomics.* Blackwell, London

Book chapter: Brown B, Aaron M (2001) The politics of nature. In: Smith J (ed) *The rise of modern genomics, 3rd edn.* Wiley, New York, pp 230- 257

Website: Kassambara A. (2020) rstatix: pipe-friendly framework for basic statistical tests. <https://rpkgs.datanovia.com/rstatix/>

Online document: Cartwright J (2007) Big stars have weather too. IOP Publishing PhysicsWeb. <http://physicsweb.org/articles/news/11/6/16/1>. Accessed 26 June 2007

Dissertation: Trent JW (1975) Experimental acute renal failure. Dissertation, University of California

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Please submit supplementary figures, small tables and text as a single combined PDF document. Tables longer than one page should be provided as an Excel or similar file type. Please refer to the journal's Data Policies, outlined in the [Editorial Policies](#) section of these guidelines for additional options for such files, and which provides guidance on alternatives to supplementary files for data deposition, linking, preservation, and storage.

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- Statistical methods: For normally distributed data, mean (SD) is the preferred summary statistic. Relative risks should be expressed as odds ratios with 95% confidence interval. To compare two methods for measuring a variable the method of Bland & Altman (1986, *Lancet* 1, 307–310) should be used; for this, calculation of P only is not appropriate.
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