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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.

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Editorial office:

Sandra Huettenbuegel, University of Glasgow, Glasgow, Scotland

heredity-journal@glasgow.ac.uk

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ARTICLE TYPE SPECIFICATIONS

ARTICLE DESCRIPTION	ABSTRACT	WORD LIMIT	TABLES/ FIGURES	REFERENCES (MAXIMUM)
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 .	Max 250 words	7,000 excluding references	Maximum of 8 figures or tables	100
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.	Max 250 words	7,000 excluding references	Maximum of 8 figures or tables	100
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- Abstract
- Introduction
- Materials and Methods
- Results
- Discussion
- Acknowledgements
- Conflict of Interest
- Data archiving
- References
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Dickinson WJ (1991) The evolution of regulatory genes and patterns in *Drosophila*. In: Hecht MK, Wallace B, MacIntyre RJ (eds) *Evolutionary Biology*, Plenum Press: New York. Vol 25, pp 127–173.

Falconer DS (1989) *Introduction to Quantitative Genetics*, 3rd edn. John Wiley and Sons: New York.

Latta RG (1992) Inbreeding Depression and Mixed Mating Systems in *Mimulus*. MSc Thesis, University of Toronto.

Sano Y, Sano R (1990) Variation of the intergenic spacer region of ribosomal DNA in cultivated and wild rice species. *Genome* 3: 209–218.

Swofford DL, Selander RB (1989) *BIOSYS-1. A computer program for the analysis of allelic variation in population genetics and biochemical systematics*. Release 1.7. University of Illinois, Urbana, Illinois.

Wilde J, Waugh R, Powell W (1992) Genetic fingerprinting of *Theobroma* clones using randomly amplified polymorphic DNA markers. *Theor Appl Genet* 83: 871–877.

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- make inquiries of other titles believed to be affected;
- forward concerns to the author's employer or person responsible for research governance at the author's institution;

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- whether the cell line has recently been tested for mycoplasma contamination.

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Authors should use approved nomenclature for gene symbols, and use symbols rather than italicized full names (Ttn, not titin). Please consult the appropriate nomenclature databases for correct gene names and symbols. Approved human gene symbols are provided by [HUGO Gene Nomenclature Committee \(HGNC\)](#). Approved mouse symbols are provided by The Jackson Laboratory, [www.informatics.jax.org/mgihome/nomen](#). For proposed gene names that are not already approved, please submit the gene symbols to the appropriate nomenclature committees as soon as possible, as these must be deposited and approved before publication of an article

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