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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.

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Professor Barbara Mable, University of Glasgow, Glasgow, Scotland

#### **Editorial office:**

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**Impact factor:** 3.179 (*2018 Journal Citation Reports, Science Edition, Clarivate Analytics, 2019*)

**Frequency:** 12 issues a year

#### **Abstracted in:**

BIOSIS  
Current Contents/Agriculture, Biology & Environmental Sciences  
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EBSCO Biological and Agricultural Index

## ARTICLE TYPE SPECIFICATIONS

ARTICLE DESCRIPTION	ABSTRACT	WORD LIMIT	TABLES/ FIGURES	REFERENCES (MAXIMUM)
<b>Original Article</b> (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 <a href="#">Editorial Policies</a> .	Max 250 words	7,000 excluding references	Maximum of 8 figures or tables	100
<b>Computer Note</b> <i>Heredity</i> publishes notes of new or substantial updates to existing computer programs addressing an important problem in <i>Heredity</i> 's 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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- Materials and Methods
- Results
- Discussion
- Acknowledgements
- Conflict of Interest
- Data archiving
- References
- Figure legends
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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* **33**: 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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Dr Caron's work has been funded by the NIH. He has received compensation as a member of the scientific advisory board of Acadia Pharmaceutical and owns stock in the company. He also has consulted for Lundbeck and received compensation. Dr Rothman and Dr Jensen declare no potential conflict of interest.

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