FINALREPORT



UHS10485

Quantifying uncertainty in genetic map construction

PROJECT DETAILS

| PROJECT CODE: | UHS10485 |
|----------------|--|
| PROJECT TITLE: | QUANTIFYING UNCERTAINTY IN GENETIC MAP CONSTRUCTION |
| START DATE: | 25.02.2013 |
| END DATE: | 20.06.2014 |
| SUPERVISOR: | DR IAN WOOD (LECTURER) AND DR EMMA HUANG (SENIOR RESEARCH SCIENTIST) |
| ORGANISATION: | UNIVERSITY OF QUEENSLAND |
| CONTACT NAME: | IAN WOOD |

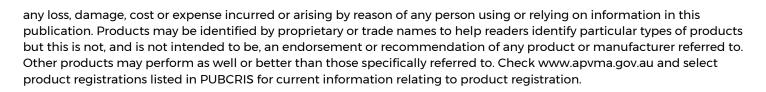
Summary

This work has led to a paper which has been accepted subject to editor acceptance of revisions for a special issue of the journal Genetics on multi-parental populations. The paper is entitled 'Characterizing uncertainty in high-density maps from multiparental populations', with authors Daniel Ahfock, Ian Wood, Stuart Stephen, Colin R. Cavanagh and B. Emma Huang. Daniel and Ian are in the School of Mathematics and Physics, University of Queensland, St Lucia and Stuart, Colina and Emma are with CSIRO. Genetics is a leading international genetics journal, which was ranked A* (top level) in the 2010 Excellence in Research for Australia (ERA) journal rankings.

Daniel also gave a talk at the Conference of the Australasian Region of the International Biometric Society in Mandurah, Western Australia (WA) in December 2013, which was awarded best student presentation.

Report Disclaimer

This document has been prepared in good faith on the basis of information available at the date of publication without any independent verification. Grains Research & Development Corporation (GRDC) does not guarantee or warrant the accuracy, reliability, completeness or currency of the information in this publication nor its usefulness in achieving any purpose. Readers are responsible for assessing the relevance and accuracy of the content of this publication. GRDC will not be liable for



Copyright

Grains Research and Development Corporation. This publication is copyright. Apart from any use as permitted under the Copyright Act 1968, no part may be reproduced in any form without written permission from the GRDC.

Old or Archival Reports (Projects that concluded in 2007 or earlier)

The information contained in these older reports is now several years old, and may have been wholly or partially superseded or built upon in subsequent work funded by GRDC or others. Readers should be aware that more recent research may be more useful for their needs. Findings related to agricultural chemical use are also potentially out of date and are not to be taken as a recommendation for their use.

Conclusions

A new methodology has been developed which provides guidelines for sample sizes necessary for accurate genetic mapping, and offers hypothesis tests and confidence intervals for simultaneously assessing marker order instability and distance uncertainty in estimated genetic maps. These can be used by geneticists with any type of genetic map, but are particularly suited to agriculturally relevant species for which field trials have been conducted with multi-parental populations, with the requisite genotyping throughout. The utility of the approach was demonstrated on bread wheat.

Recommendations

Using this methodology, genetic map construction can now be accompanied by estimates of the uncertainty of the map at the inter-marker level. The guidelines on sample size can lead to experiments which provide very accurate maps, which can then be used for further analysis, such as quantitative trait loci (QTL) mapping.

Other Research

There is much scope to incorporate the uncertainty derived from this methodology in follow-on analysis, such as QTL mapping, to improve the accuracy of the reporting and improve rates of detection of such loci. There is also scope to extend the accuracy of the methods.