

FINAL REPORT

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

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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.

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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.