

Molecular Analysis Of Wild Barley (*Hordeum Spontaneum*) Germplasm

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Abstract

Ninety wild barley accessions and 11 cultivated barley lines were fingerprinted using restriction fragment length polymorphisms (RFLP), amplified restriction fragment length polymorphisms (AFLPs), microsatellite (SSR) and resistance gene analogue polymorphisms (RGAPs). The results will be analysed using Jaccards dissimilarity coefficient, unweighted paired group averages (UPGMA) algorithm and principal component analysis (PCA). This will provide the starting point for the application of Advanced Backcross Quantitative Trait Loci (AB-QTL) analysis in barley which offers the potential to identify new genes from *H. spontaneum* which can substantially improve the agronomic, physiological and malting quality attributes of Australian barley varieties.

This paper has been withdrawn for submission in an alternative conference