

Title (en)

MQM MAPPING USING HAPLOTYPED PUTATIVE QTL-ALLELES: A SIMPLE APPROACH FOR MAPPING QTL'S IN PLANT BREEDING POPULATIONS

Title (de)

MQM-KARTIERUNG MIT HAPLOTYPISIERTEN PUTATIVEN QTL-ALLELEN: EIN EINFACHER ANSATZ ZUR KARTIERUNG VON QTL'S IN PFLANZENZUCHTPROGRAMMEN

Title (fr)

CORRELATION DE MQM AU MOYEN D'ALLELES DE QTL PUTATIFS HAPLOTYPES: SOLUTION SIMPLE POUR CORRELER QTL DANS DES POPULATIONS DE CULTURE DE PLANTES

Publication

**EP 1265476 A2 20021218 (EN)**

Application

**EP 00989407 A 20001221**

Priority

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Abstract (en)

[origin: WO0149104A2] Methods for mapping a phenotypic trait to a corresponding chromosomal location are provided. Statistical methods which correlate pedigrees with multiple genetic markers, the haplotype, to determine identical-by-descent (IBD) data are employed to map phenotypic traits. The statistical models provided are a HAPLO-IM+ model, a HAPLO-MQM model, and a HAPLO-MQM<+> model. These statistical methods are applied to map traits determined alternatively by single genes or by quantitative trait loci. Methods of marker assisted selection (MAS) using a variety of genetic markers are provided. Plants selected by MAS using the methods are provided. Additionally, methods for cloning nucleic acids corresponding to phenotypic traits that are in linkage disequilibrium with genetic markers are provided, and for transducing them into plant cells are provided. Transgenic plants transduced with the cloned nucleic acids corresponding to phenotypic traits, e.g. QTL, are provided.

IPC 1-7

**A01H 1/04**; **A01H 5/00**; **C12Q 1/68**

IPC 8 full level

**A01H 1/04** (2006.01); **C12N 15/82** (2006.01); **G16B 20/10** (2019.01); **G16B 20/20** (2019.01); **G16B 20/40** (2019.01)

CPC (source: EP US)

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Citation (search report)

See references of WO 0149104A2

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