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A REVIEW

Association mapping : a useful tool

■ **HEMANT SAHU, JAIRAM AMADABADE AND NAMRATA DHIRI**

SUMMARY

Future advances in plant genomics will make it possible to scan a genome for polymorphisms associated with qualitative and quantitative traits. Association mapping, also known as linkage disequilibrium mapping. Association mapping has the promise of higher mapping resolution through exploitation of historical recombination events at the population level that may enable gene level mapping on non-model organisms where linkage-based approaches would not be feasible. Association mapping utilizes ancestral recombinations and natural genetic diversity within a population to dissect quantitative traits and is built on the basis of the linkage disequilibrium concept. One of the working definitions of linkage disequilibrium (which here on will be referred to as LD) is the non-random co-segregation of alleles at two loci. In contrast to linkage-based studies, LD-based genetic association studies offer a potentially powerful approach for mapping causal genes with modest effects. The commonly used LD measure, D or D^1 (standardized version of D). Besides D, a various different measures of LD (D^1, r^2, D^2, D^*, F, X and¢) have been developed to quantify LD. Softwares packages measuring LD, such as "graphical overview of linkage disequilibrium" (GOLD), power marker, and TASSEL (Trait Analysis by association Evolution and Linkage) are available. Applications of AM has been extended from model plant arabidopsis to field crops. The increasing number of AM studies in crop species indicates the potential of this approach in all plant species in near future.

Key Words : Linkage disequilibrium, Association mapping, Genetic diversity, Polymorphism

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MEMBERS OF THE RESEARCH FORUM

Author to be contacted :
HEMANT SAHU, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, RAIPUR (C.G.) INDIA

Address of the Co-authors:
JAIRAM AMADABADE, Department of Genetics and Plant Breeding, G.B. Pant University of Agriculture and Technology, PANTNAGAR (UTTARAKHAND) INDIA

NAMRATA DHIRI, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, RAIPUR (C.G.) INDIA