Marker assisted selection and applications of mas.

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Commentary

In livestock selection systems, marker assisted selection (MAS) provides for more precise selection of specific DNA polymorphisms linked to measurable changes in economically significant traits. For qualities that are lowly heritable or determined postmortem, the rate of genetic improvement gained by MAS may be significantly greater than that produced through selection based on EPD values. Marker assisted selection (MAS) is an indirect selection process in which a trait of interest (e.g. productivity, disease resistance, abiotic stress tolerance, and quality) is selected based on a marker (morphological, biochemical, or DNA/RNA variation) linked to the trait of interest (e.g. productivity, disease resistance, abiotic stress tolerance, and quality), rather than the trait itself. This method has been studied in depth and is being proposed for plant and animal breeding. As a result, MAS has the potential to dramatically improve animal breeding efficiency. According to previous research, there are three stages to the development of MAS programmes. The detection phase comes first, then the evaluation, and finally the implementation step. DNA polymorphisms are utilised as direct or linked markers to detect specific allele frequencies within QTL segregating populations during the detection phase. During this step, markers linked to QTLs are found, and the amount of QTL allele effects and the QTL's position throughout the genome can be estimated. Linked markers are evaluated in target populations during the evaluation phase to see if QTL separated within the population. Finally, in order to create a genotypic database, predicted linked markers from a population are utilised inside families and direct markers are used across families during the implementation phase.

Applications of MAS

The use of MAS in disease resistance selection: MAS provides for highly precise disease resistance selection that is unaffected by environmental influences. A large number of samples must be searched for the genes that confer disease resistance. It is feasible to distinguish between lines that are resistant and vulnerable to that disease. The use of MAS in breeding and selection: MAS stands for multi-agent selection using genetic marker information. MAS is useful for highly heritable traits with big effects, which are already fixed in commercial lines with near-optimal alleles. The economic benefit of MAS in dairy cattle was documented by Ruane and Colleau (1996) and Spelman and Garrick (1997). Multiple Ovulation Embryo Transfer (MOET) technology and progeny testing are used in MAS. The true genotype of an animal can be inferred using information about genes located at QTL. The data at QTL helps to improve the accuracy of breeding value estimation. In breeding strategies, genes having stronger genetic effects at QTL can be exploited more specifically. Evaluation of

breeding material with the help of markers There are various applications in which DNA marker data may be beneficial for breeding prior to crossing (hybridization) and line development, such as cultivar identity, assessment of genetic diversity and parent selection, and confirmation of hybrids. These tasks have traditionally been carried out via visual selection and data analysis based on morphological criteria.

Cultivar identification/purity assessment

In order to take advantage of heterosis, significant levels of genetic purity are required in cereal hybrid development. SSR and STS markers were employed to validate purity in hybrid rice, which was a lot easier than the traditional "grow-out tests," which entail growing the plant to maturity and evaluating morphological and floral traits.

Heterosis research

DNA markers have been utilised to define heterotic groups that can be exploited to exploit heterosis in hybrid crop development, particularly in maize and sorghum (hybrid vigour). The creation of inbred lines for the purpose of developing superior hybrids is a time-consuming and costly process. Unfortunately, based on DNA marker data, it is not yet possible to predict the exact level of heterosis, however there have been cases of paternal lines being assigned to the appropriate heterotic groups. It's also been suggested that smaller subsets of DNA marker data, together with phenotypic data, could be used to select heterotic hybrids.

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