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Molecular Markers Used in Wheat Breeding

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SUMMARY

For the identification and utilization of potential genotypes, evaluation of germplasm is an important step in plant breeding. The development of molecular marker technologies during the last twenty years has revolutionized the genetic analysis of crop plants. These markers are being used for improving the efficiency of traditional plant breeding by facilitating indirect selection through molecular markers linked to genes for the traits of interest and fastening the process of variety development program, specifically in gene pyramiding which is otherwise very difficult to do.

INTRODUCTION

In recent years, significant progress has been made in the use of molecular markers in plant breeding. The development of molecular marker technologies during the last twenty years has revolutionized the genetic analysis of crop plants. Molecular markers closely linked to numerous traits of economic importance have been developed and in many cases have been used for indirect selection for the linked traits. Use of linked DNA markers for indirect selection of quantitative traits is expected to be more effective than direct selection because these markers are not influenced by the environment and can be scored at all stages of plant growth. Molecular markers also allow gene pyramiding for characters like disease resistance which is very difficult in conventional breeding.

Molecular Markers

MAS is a strategy in which selection is based on molecular markers, selection through markers is purely on genetics bases thus it is more reliable. Moreover MAS reduces the time period to develop a variety where convention method takes 8-10 years to develop a suitable variety while MAS can decrease the time to 5-6 years by allowing direct selection based on genotype of the plant. As the selection is through marker, selection intensity of breeder increases and requires less resources and less plant material for further generation thus molecular markers saves time and cost both. Microsatellites or simple sequence repeats (SSRs), which cover the entire genome and show high levels of polymorphism (Röder *et al*., 1998) are suitable for tagging and mapping agronomically important genes in wheat. Today, molecular markers are the best tools used to determine the level of genetic diversity among plants and can provide detailed characterization of genetic resources (Mir *et al*., 2012). The essential requirements for MAS in a plant breeding program is that markers should co-segregate with the desired trait, means to screen large populations and it should be available with high reproducibility across laboratories. Moreover, molecular markers should be economical to use and user friendly. Breeders use molecular markers to increase the precision of selection for best recombinants and transgressive segregants in the F_2 and segregating generations. Molecular marker aided selection methods resulted in significant improvement in breeding efficiency by reducing trial and error aspect of breeding process and also save time and cost.

Results and Discussion

In the present investigation, overall size of PCR amplified products were ranged from 100 bp (Xgwm437, Xwmc216) to 500bp (Xgwm374). Similarly, Abbas *et al*. (2008) obtained amplified DNA fragments that varied in size ranging from 250bp to 1000bp and Manifesto *et al*. (2001) obtained amplified DNA fragments that varied in size from 115bp to 285bp. Mukhtar *et al*., 2015 reported xpsp3000 has band size of 260bp.

In the present study, polymorphism was observed among parental genotypes and different populations of the cross DBW17 x WH1105. The NTSYS-PC UPGMA tree cluster analysis clearly grouped F_3 individuals in two major groups at a similarity coefficient of 0.54. Major group I consisted of DBW17 and the major group II had WH1105. Cluster as well as PCA analysis clearly indicated that the F_3 population were scattered between both the two parental genotypes.

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