International Journal of Plant Sciences (2006) **1** (2) : 349-351

A Review:

Use of molecular markers for wheat grain quality improvement

A.S. THORAT*[1], S.S. THORAT[2] AND B.B. THORAT[1]
[1] Dept. of Bio Technology, College of Agriculture Beed – 431 122 (M.S.) India
[2] Dept. of Food Microbiology College & Food Technology, MAU Parbhani - 431 402 (M.S.) India

(Accepted : May, 2006)

SUMMARY

Wheat is used in the preparation of different food products like bread, biscuits, noodles, pasta, cakes, pastries and confectioneries. The quality of these end products largely depend on characters like grain size, grain protein content (GCP) and flour color. The consumption of nutritionally sound and processed food is increasing day by day in India. However, suitable wheat varieties specifically for industrial uses are not available, the demand for which is increased at the rate of 5-7 per cent per annum. For this purpose special quality of wheat grain as per specific product is required, hence there is a need to put an emphasis on development wheat varieties to meet the quality requirement of various end products. Little attention has been paid for the improvement of quality traits mainly because of its complexity nature of inheritance. The molecular marker technique has opened up new avenues for the improvement of such complexity traits. The work so far done on the following aspect has been reviewed in this article.

Key words : Wheat, Grain quality, Molecular markers.

WHEAT AND MOLECULAR MARKERS

Wheat is segmental allopolyploid (2n=6x=42) containing three distinct but genetically related homologous genome A, B and D. The haploid DNA content of breat wheat genome is approximately 1.2x 10 bp (Arumunganathan and Earl, 1991) with an average of 810 chromosome 10mm. The average wheat chromosome is 25 fold longer than the average rice chromosome (Moore *G.*. 1995) Thus three wheat chromosomes are equal to the haploid maize genome and one half of a average wheat chromosome equal to a haploid maize genome and one half of an average wheat chromosome equal to a haploid rice genome (Gill and Gill 1994).

The wheat genome consists of more than 80% of repetitive sequences, which makes molecular marker analysis and gene isolation technology challenging. The wheat genes are spread in the genome like island in a large ocean of repetitive elements. Progress of identifying molecular markers in wheat has been comparatively slow due to its large genome size and low level of polymorphism at the molecular level. In spite of these difficulties, significant progress has been made in construction of complete RELP maps of the wheat genome.

Various molecular markers have been developed till date and they can be grouped in to the following three categories.

1. Hybridization based DNA markers such as restriction fragment length polymorphism (RFLPs), and oligonucleoted fingerprinting.
2. PCR-based DNA markers such as Random Amplified Polymorphic DNAs (RAPD). Simple Sequence Repeats (SSRs) or microsatellites, Sequence-Tagged Sites (STS), Amplified Fragment Length Polymorphism (AFLPs), Inter-simple Sequence Repeat amplification (ISA), Cleaved Amplified Polymorphic Sequences (CAPS), Amplicon Length Polymorphisms (ALPs) and
3. DNA chip and sequencing-based DNA marker such as Single Nucleotide Polymorphisms (SNPs).

Each marker system is associated with some advantages and disadvantages. The choice of marker system is dictated to a large extent by the intended application, convenience and the cost involved.

MOLECULAR MARKERS

1) Hybridization based Molecular Markers

a) Restriction Fragment Length Polymorphism (RELP)

Among the various molecular markers developed to date RELPs were developed first and were initially used for human genome mapping. Later these markers were adopted for mapping plant genomes including bread whear (Liu and Tsunewalki 1991) and durum wheat (Blanco *et al*. 1998). In wheat Chao *et al.* (1989) first used RELP marker to developed genetic maps of wheat homeologous group 7 chromosomes. A number of agronomically important gene and QTLs related to be linked with RELP marker. In wheat RELP markers have been developed for the following grain traits *viz.*, pre-harvesting sprouting tolerance (Anderson *et al.* 1993), grain protein content (Balanco *et al.*, 1996), kernel hardness (Nelson *et al.*, 1995), flour colour and milling, yield (Parker *et al.*, 1997)and amylase content (Araki *et al.*, 1999).

RELP analysis however has some limitation. It is time consuming and labor intensive. Further, because of the low frequency of RELP in wheat this approach has been relatively less useful in this crop. This low frequency is some time attributed to the polyploidy nature, high proportion of repetitive DNA and large genome size of wheat.

2) PCR based molecular markers

The advent of the polymerase chain reaction (PCR) by K. Mullis in mid 1980's revolutionized molecular genetic.

*Author for correspondence