

Breeding rice varieties with improved grain and nutritional qualityD.S. Brar¹, P.S. Virk¹, D. Grewal¹, I. Slamet-Loedin¹, M. Fitzgerald¹ & G.S. Khush²¹ International Rice Research Institute, Manila, Philippines² University of California, Davis, USA

Worldwide, 3 billion people depend on rice for more than 20% of their daily calorie intake. Like yield, rice grain quality has now become a primary consideration for producers and consumers. However, preference for grain quality is highly variable in different regions, countries and among different consumers. The grain consists of ≈80% starch and its quality is dependent on a combination of several traits, some of which are influenced by environmental factors. The major physical traits include grain shape, size, chalkiness, degree of milling, and head rice recovery, and chemical characteristics-amylose content, gelatinization temperature and gel consistency. A number of Quantitative Trait Loci (QTLs) have been identified and molecular markers for some of the traits are available. Starch biosynthesis, however, is a complex system involving as many as 18 genes including starch synthases, branching and debranching enzymes, which act in concert to affect starch structure and function at least at six organizational levels. Aroma carries a special place in rice and is controlled by 1 or 2 major genes, and molecular markers for three alleles are available.

To improve the nutritional quality, major focus is on developing rice varieties with Pro-vitamin A, high iron and zinc content in the polished grain. Pro-vitamin A enriched rice, Golden Rice, has been used to develop elite indica breeding lines, through marker assisted selection (MAS). Screenhouse and confined field tests have shown that these transgenic Golden Rice lines are similar in agronomic performance to IR64, PSBRc82 and BR29. Iron content is being increased using both conventional and transgenic approaches. Through conventional breeding, enhanced levels of zinc have been produced and QTLs are being mapped. We plan to pyramid genes for Pro-vitamin A, high iron and zinc content to develop micronutrient enriched rice.

Some of the priority areas for the genetic enhancement of grain quality include; (1) development of precise quantitative assays for different quality traits, (2) dissect complexity of the genetic control of eating and cooking quality characteristics, (3) discovery of genes known to enhance milling yield, head rice recovery and bran oil quality, (4) better understanding of the chemistry and genetics of cooking and eating quality traits of traditional varieties and of leading varieties like IR64, Basmati 370, Koshihikari, Khao Dawk Mali, (5) formulate selection indices to breed for improved grain quality, (6) develop varieties possessing slowly digestible starch (low glycemic index) that could assist in managing the global pandemic of diabetes. With the recent advances in analytical tools, molecular markers, applied genomics, proteomics and metabolomics, the scope for improving grain and nutritional quality in rice, and combining that with high yield, seems more promising than before.

Keywords

rice, grain, starch, nutritional quality, MAS, QTL.

Heat-induced oxidative stress and changes in protein profile in wheat cultivars

R. Mahla, S. Madan, R. Munjal & R.K. Behl

Department of Biochemistry, Department of Genetics & Plant Breeding, CCS Haryana Agricultural University, Hisar- 125 004, India

Wheat (*Triticum aestivum* L.) occupies an important place among cereals and it serves as a staple food for about 35% of the world population. Crop plants experience various stresses during their life cycle under high or low temperature, drought, and salinity conditions. Among these stresses, heat stress is getting alarming as a result of global warming. Therefore, research on the mechanism of high temperature stress in plants has the importance for future generations. The present investigation was aimed at studying the effect of heat stress and revival on antioxidative system and polypeptide pattern in the leaves of wheat seedlings. Four wheat genotypes, i.e., two tolerant (HW-2045 and WH-1021) and two susceptible (HS-277 and WH-147) were selected and the enzymes of antioxidant system, levels of antioxidant metabolites and pattern of polypeptide were observed. The production of H₂O₂ was higher in the leaves of susceptible and tolerant genotypes under heat stress conditions. However, its level was significantly higher in susceptible as compared to tolerant genotypes. There was enhancement in the activities of antioxidative enzymes, viz. CAT, POX, GR and APX in the leaves of tolerant and susceptible genotypes under heat stress. However, higher per cent increase was observed in tolerant genotypes. Heat stress increased the SOD activity in tolerant genotypes but activity declined in susceptible genotypes. On revival, the activities of the CAT, POX and GR declined in comparison to stressed seedlings but remained higher as compared to control. Accumulation of H₂O₂, which is a strong oxidant, led to disruption of cellular membrane integrity as obvious from increase in MDA content and an indicator of lipid peroxidation. Higher increase of H₂O₂ and MDA content was observed in susceptible genotypes which indicate more oxidative stress in the heat susceptible genotypes as compared to heat tolerant genotypes. On revival, accumulation of H₂O₂ and MDA content was reduced in all the genotypes but their level remained higher than their respective controls. A large number of studies have revealed a positive correlation between induction of HSPs and acquisition of thermotolerance. The most studied effect of heat shock treatment was on the induction of protective heat shock proteins which disappeared on removal of heat stress. In tolerant genotype WH-1021 under stressed conditions five polypeptide bands of MW 103.7, 92.2, 83, 65 and 26 kDa appeared in comparison to unstressed seedlings, while HW-2045 showed five bands of MW 103.7, 98.5, 79, 62 and 26 kDa under heat stress. Both the susceptible genotypes showed similar polypeptide bands of MW 80, 57.9, 45.7 and 34.4 kDa in response to high temperature. The better tolerance character of HW-2045 and WH-1021 during present investigation might be due to the induction of protective heat shock proteins and much higher activities of the enzymes involved in scavenging active oxygen species.

Keywords

wheat, thermo-tolerance, heat shock protein.