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Integrating conventional and molecular approaches for improvement of Basmati rice

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Basmati rice from the Indian subcontinent is unique in its grain and cooking quality characteristics which fetches premium price in the international markets. The traditional Basmati cultivars are tall, prone to lodging, photoperiod and temperature sensitive and very low yielding. Genetic improvement of Basmati rice at Indian Agricultural Research Institute, New Delhi through classical breeding approaches has led to development of a number of high yielding Basmati rice varieties, wherein the duration of Traditional Basmati rice varieties has been reduced from 160 days to 115-140 days with enhancement of productivity from 2.5 tons/ ha to 6-8 tons/ ha (Singh et al., 2011). Country's forex earning from export of Basmati rice has gone up from US \$ 5.6 million in 1990-91 to US \$ 2.70 billion in 2011-12, of which the contribution of IARI varieties is more than 70 per cent.

Basmati rice varieties in general are highly susceptible to several biotic stresses such as bacterial blight (BB), blast and brown plant hopper (BPH). A large number of genes conferring resistance to these biotic stresses have been identified and mapped with tightly linked molecular markers. However, all these genes are available in non-Basmati sources and their transfer to Basmati background impairs the grain and cooking quality traits of Basmati rice varieties. Under these circumstances, marker assisted backcross breeding (MABB) provides a great opportunity for precise transfer of desirable donor segment while minimizing the linkage drag. Development and release of Improved Pusa Basmati 1 in 2007, developed by marker assisted pyramiding of genes xa13 and Xa21 for resistance to BB in the background of Pusa Basmati1, is a landmark (Gopalakrishnan et al., 2008). Currently we are using MABB for transferring genes for resistance to BB (xa13 and Xa21), blast (Piz5 and Pikh) and BPH (Bph 3, Bph 13, Bph 18,

Bph20 and Bph 21) into Basmati rice varieties Pusa Basmati 1121 and Pusa Basmati 6. The parental lines of superfine grain aromatic rice hybrid Pusa RH 10 namely, Pusa 6A, Pusa 6B and PRR 78 have already been improved for resistance to BB (Basavaraj et al., 2010) and blast by transferring genes xa13+Xa21 and Pikh +Piz5, respectively (Prabhu et al., 2009). In addition, a major QTL for salt tolerance (Saltol) is being transferred to Pusa Basmati 1121, which is widely grown in Haryana, the state having problem of salinity owing to underground brackish water. In order to develop genetically enhanced donor sources for resistance to biotic (BB, blast and BPH) and abiotic (Salt tolerance, drought tolerance and phosphorus uptake) stresses in Basmati background, we are developing isogenic lines for major resistance genes/QTLs for respective stresses in the background of Pusa Basmati 1 (Singh et al., 2011). Further, QTL mapping using RIL population has resulted in identification of several novel QTLs for grain and cooking quality traits (Guleria et al., 2011). Molecular markers are also being routinely used for establishing variety/hybrids identity and authentication of genetic purity of hybrid seed lots. The progress made on all these aspects will be discussed.

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