Conclusions
Fine grain rice varieties Samba Mahsuri and Sona Mahsuri are highly susceptible to Xoo race Bxo1 a representative of Indian pathotype I.

Bacterial blight resistance genes in BJ1, IRBB5 and IRBB13 (near isogenic lines for xa-5 and xa-13) are ineffective against Xoo race Bxo1.

Presence of xa-13 resistance gene is critical for obtaining high level of resistance in pyramid lines.

The most effective BB resistance gene combination (xa-5, xa-13 and Xa-21) against the Xoo race Bxo1 in IRRI lines also proved effective in Samba Mahsuri background.

xa-13 resistance allele was found to be absent in both resistant variety Ajaya (IET8585) and moderately resistant cultivar BJ1.

Recessive resistance gene in Ajaya segregated independently of xa-5 gene in IRBB5.

The resistance gene in Ajaya was found to be monogenic recessive as indicated by the F2 segregating pattern.

An RAPD marker OPA121467 was found linked to the resistance locus in Ajaya at a distance of 5.0 cM.

ISSR marker UBC8152000 was found linked to the resistance locus in Ajaya at a distance of 10.5 cM.

The resistance locus in Ajaya was flanked by two SSR markers RM39130 at 14.5 cM and RM31150 at 17.7 cM on short arm of rice chromosome 5.

Although RFLP analysis could not detect any parental polymorphism, it led to the standardization of non-radioactive DNA labeling and detection system.
The markers identified in the present study can be successfully employed for Marker Assisted Selection (MAS) in rice breeding programmes.

Gene pyramiding through MAS resulted in the development of 28 resistant Samba Mahsuri lines homozygous for the 3 resistance genes (xa-5, xa-13 and Xa-21).

The combination of xa-5 + xa-13 genes showed a complementary gene interaction with a higher level of resistance against Xoo isolate Bxol.

Combining xa-13 gene pyramid with xa-5 + Xa-21 pyramid line in Samba Mahsuri background is the most efficient gene pyramiding scheme.

There was no yield penalty due to pyramiding of three BB resistance genes into Samba Mahsuri.

Five pyramid lines were selected based on grain length, grain breadth and grain yield per plant.