Even after 160 years of Irish famine, potato late blight caused by *Phytophthora infestans*, persists to be a major threat for potato growers across the world. One of the most effectual and efficient way to control any plant disease is through host plant resistance. Although resistant varieties deployed with *R*-genes in case of potato late blight met with high rate of success initially, but increase in selection pressure on the pathogen, led to the development of matching virulence's and making them absolutely ineffective. Thus, breeders lost interest in this type of resistance and use of horizontal, race-non-specific general resistance conferred by minor genes, as a substitute of *R*-genes in potato breeding were preferred. However, this type of resistance is difficult to transfer in to cultivated potato due to its tetrasomic inheritance.

Thus, to confer broad spectrum race specific resistance, imparted by major genes through recognition of pathogen effectors is the ultimate goal of the breeders. These *R* genes, even if defeated, still provide partial resistance. With the advancement in plant molecular techniques, most of these *R*-genes have been mapped and cloned, tightly linked markers are available to track these genes which has widened the pragmatic applicability of gene pyramiding through marker assisted selection.

The present study was undertaken with aim to develop genotype(s) with pyramided group of *R*-genes for enhancing the resistance performance by combining two or more complementary *R*-genes and increasing durability of disease resistance. In the first part of research component, genotyping of indigenous and exotic potato germplasm collection of CPRI repository was done through validation of molecular markers tightly linked to *R1, R2* and *R3a* genes in a set of 21 known late blight differentials and screening of potato genotypes (179) for the presence of these genes. In the second part of the research, Hybridization among selected resistant parents possessing *R1, R2* and *R3a* genes was performed for pyramiding these genes in single genetic background through classical breeding method.

On the basis of marker screening of 158 genotypes, 17 genotypes were identified with *R1* gene, 18 genotypes were having *R2* gene and 41 genotypes possessed *R3a* gene. Besides, 17 genotypes had combinations of these genes. This population was phenotyped for late blight resistance by detached leaf method, revealing association between presence or absence of the marker.
Subsequently, 15 crosses were attempted for combining *R1*, *R2* and *R3a* genes in single potato host among these genotypes.

Berries obtained from five successful crosses i.e. HR 5-2 × K. Himsona, SM/92-338 × K. Girdhari, CP 4045 × CP 1945a, K. Jyoti × CP-4045, CP 4055× K. Kuber. F1 generation segregating progenies of 280 seedlings were raised and 220 plants which survived were used for MAS in identification of F1 clones, possessing major R-gene combinations for late blight resistance. 17 clones were identified with stacked *R1* and *R3a* genes inherited from the cross SM/92-338×Girdhari.

All the progeny clones were highly resistant except for the negative controls. Sizeable difference in the lesion area of the leaves was observed for all the genotypes as compared to the parents used in the cross., thus, expressing the effect of stacking major R-genes in single genotypic background. C-13, one of the Clones of CP4045×CP1945a was found with negative selection where *R2* gene was de-stacked from *R1* and recombinant progeny clone with *R1* and *R3a* gene was formed having better resistance phenotype. This significant increase in resistance level of progeny Clone due to rearrangement of genes corroborates the more efficient effect of *R3a* gene in comparison to *R2*. Further, apart from *R3a*, reorganization of genes during crossovers may have resulted in formation of new recognition as well as minor defence genes, the cumulative effect of which may have resulted in enhanced resistance.

This experimental design proved to be effective, because it allowed us to test the hypothesis whether or not pyramiding is a valid strategy and the conclusions drawn from this study are that stacking of race specific major genes adds to cumulative resistance, irrespective of the weak or strong effect of individual genes. The study is an endeavor, to reduce the dependency of conventional breeding programme through MAS on initial seedling screening in the laboratory and subsequent field screening for late blight resistance in the field. Potato breeding will benefit from combining individual R-genes, as the durability and level of resistance to late blight infection is expected to increase. Further, we will understand the type of resistance already deployed through resistant cultivars in the country and this will help in the future selection of parents in late blight breeding programmes.

The study is an example of hastening the conventional breeding process through MAS. Since, we adopted the classical breeding strategy to pyramid the R-genes, whole complex of other genes are likely to get combined in comparison to transgenic approach, where only the targeted sequence gets incorporated and chances of durable resistance is low, besides the safety regulations and public hitch in adopting genetically modified crops.