Introduction
Potato is the only future food crop that can ensure, food and nutritional security to meet the demands of ever burgeoning population of the world, especially, for the developing countries like India. The crop is vulnerable to many pests and pathogens that impede its production. Late blight is among the most destructive potato diseases caused by fungus-like water mold oomycete Phytophthora infestans, which if left unchecked is capable of destroying the entire crop raised, with susceptible popular varieties within few days of infection. The disease was initially controlled with "Bordeaux mixture", an environmentally very unsafe chemical compound copper sulphate and calcium Hydroxide; later chemical agents based on manganese and tin became available. Finally these days, many fungicides including mancozeb, are extensively used in mixtures to prevent emergence of resistance, but the high costs and negative impact of these chemicals use, on human health and the environment brings into question the sustainable use of these crops in many situations. Besides, control through these fungicides, becomes dubious with emergence of new resistant strains of P. Infestans. So, breeding for resistance remains the only plausible alternative strategy to combat this notorious pathogen.

Breeding for resistance in potato, has had limited success due to difficulties in crossing cultivated potato to its wild relatives, which are the source of potential resistance genes. Resistance to late blight is mainly of two types; quantitative and qualitative. Race nonspecific resistance is broad spectrum, controlled by an unknown number of genes responsible for imparting quantitative resistances, whereas, specific resistance is qualitative, oligogenic and is determined by dominant R gene, which induces a hypersensitive response upon infection with races of P. infestans.

Initial efforts for breeding late blight resistant cultivars began nearly 100 years ago with the introgression of resistance from Solanum demissum, a wild hexaploid species indigenous to Mexico. So far, eleven such R genes have
been described from *S. demissum* (Malcolmson & Black, 1966). This type of resistance often called vertical resistance was introgressed into the cultivated potato extensively during early last century. However, *P. infestans* rapidly overcame such resistance and thus breeders lost interest in this type of resistance. But, now-a-days there is renewed interest in this type of resistance, as recent researches have shown that major and minor gene resistances are not different at molecular level, in fact it is same part of the genome that might be responsible for both the type of resistances (Gebhardt and Valkonen, 2001).

So far, eight major genes have been mapped *i.e.* R1 on chromosome 5 (Leonards-Schippers et al., 1992), R2 on chromosome 4 (Li et al., 1998), R6 & R7, R3a & R3b, R10 and R11 on chromosome 11 (El-Kharbotly et al., 1996; Huang et al., 2004; Bradshaw et al., 2006) and recently R8 have been mapped on chromosome 9 (Jo et al., 2011). Further four genes within this set have been cloned R1 (Ballvora et al., 2002), R2 (Lokossou et al., 2009) and R3a (Huang et al., 2005), R3b (Li et al., 2011). In addition, about twenty functional late blight R genes have also been cloned. Most of these R gene class are predicted to encode receptors with coiled coil (CC), nucleotide binding site (NBS), and leucine-rich repeat (LRR) domains. The cloning of these R genes further led to the development of molecular markers tightly linked to gene sequences paving the way for undertaking Marker Assisted Selection (MAS) to complement the conventional breeding programme.

In India, we have been fairly successful to contain this dreaded disease by application of fungicides, development and deployment of resistant varieties. But, the pathogens have already developed resistance to the fungicides currently in use and as far as the host resistance is concerned, it is a saga of continued battle between the pathogen and the host, eventually the pathogen overcomes the host resistance with the evolution of new matching virulence’s. As a result, globally no potato variety is able to withstand this onslaught for long and hence results in breakdown of resistance.

Since most of the major genes (R-genes) imparting resistance to late blight have been mapped to potato chromosomes in various labs, in different countries and the sequences of the cloned genes are available in public databases and the tightly linked markers reported to the R-genes by various
researchers, therefore, it is now possible to use this information for undertaking Marker Assisted Selection (MAS) in the conventional potato breeding programmes.

None of the laboratory in India has undertaken this type of work; so far, the screening techniques being used included the collection of most complex races of the *P. Infestans* from the field and used for screening and selection of resistant genotypes. However, we do not know the genetic background of the parental lines/ segregating progenies for the presence or absence of *R*-genes. This is the major gap, while planning the breeding programmes, since we do not know what is going on at the genetic level, hence attempts could not be made to pyramid all the known *R*-genes in one host background. But this challenge can be accepted now, since the *R*-genes are mapped and tightly linked markers are available to track them in the segregating populations.

Here, we report genotyping of indigenous and exotic potato germplasm collection of CPRI repository, through validation of molecular markers tightly linked to *R1*, *R2* and *R3a* genes in known late blight differentials, screening of potato genotypes for the presence of these genes and pyramiding these functional *R*-genes into single host background through marker assisted selection. The information, thus generated on the presence of *R*-genes in our breeding material will go a long way in planning the future strategies for combating this disease and having a durable product using host resistance by deploying different sources of resistance.

The study is an endeavour, 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.

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