Molecular characterization and phylogenetic analysis of NBS-LRR genes in wild relatives of eggplant (*Solanum melongena* L.)

Sona S Dev*, P. Poornima and Akhil Venu

Department of Biotechnology,
St Peter’s College, Kolenchery, Koshi-682 311, Kerala, India.

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**ABSTRACT**

Eggplant or brinjal (*Solanum melongena* L.), is highly susceptible to various soil-borne diseases. The extensive use of chemical fungicides to combat these diseases can be minimized by identification of resistance gene analogs (RGAs) in wild species of cultivated plants. In the present study, degenerate PCR primers for the conserved regions of nucleotide binding site-leucine rich repeat (NBS-LRR) were used to amplify RGAs from wild relatives of eggplant (Black nightshade (*Solanum nigrum*), Indian nightshade (*Solanumviolaceum*)and Solanum mincanum) which showed resistance to the bacterial wilt pathogen, *Ralstonia solanacearum* in the preliminary investigation. The amino acid sequence of the amplicons when compared to each other and to the amino acid sequences of known RGAs deposited in Gen Bank revealed significant sequence similarity. The phylogenetic analysis indicated that they belonged to the toll interleukin-1 receptors (TIR)-NBS-LRR type R-genes. Multiple sequence alignment with other known R genes showed significant homology with P-loop, Kinase 2 and GLPL domains of NBS-LRR class genes. There has been no report on R genes from these wild eggplants and hence the diversity analysis of these novel RGAs can lead to the identification of other novel R genes within the germplasm of different brinjal plants as well as other species of *Solanum*.

**Key words:** Eggplant, Nucleotide binding site-. Leucine rich repeat, Resistance Gene Analogs.

**INTRODUCTION**

India is blessed by rich biodiversity and hence offers immense potential for studying the wild relatives of cultivated crops. These wild plants offer a diversity of traits including pathogen resistance for crop improvement. Studies should be focussed on major genes and defined characters present in these plants which may be absent in the cultivated gene pool. Eggplant (brinjal) aubergine, *Solanum melongena* L., an important solanaceous fruit crop is widely grown in Asia, Africa and the sub tropics, including India and Central America. However this poor man’s vegetable is susceptible to numerous soil-borne diseases leading to enormous loss in yield and quality. They have partial resistance to most of the soil-borne pathogens, but often at insufficient levels(Daunay et al., 1991). In order to combat the pathogen attack, farmers mostly depend on chemical fungicides which are expensive, cause environmental problems and health risks. Hence, the ideal strategy to combat these pathogens is to produce disease resistance in cultivated egg plants.

Cloning resistant genes, subsequent transformation and sequencing genomic DNA fragments amplified by degenerative PCR primers for conserved domains is one of the recent solutions for obtaining disease resistant plant varieties. Researchers have isolated disease resistant (*R*) genes from genomes of several plant species like *Arabidopsis thaliana*, *A lyrata*, rice cultivars, *Brachypodium*, woody species grape, poplar, cotton, apple, legume species, potato (*Solanum tuberosum*), tomato (*S. lycopersicum*) and pepper (*Capsicum annuum*) (Wei et al., 2016).

Most of the R genes belong to the nucleotide binding site-leucine rich repeats (NBS-LRR) class. Bacterial wilt, caused by *Ralstonia solanacearum*, is one of the most destructive diseases of eggplant especially in the tropical regions (Chandrashekara et al., 2012). There have been earlier reports of RGAs or R genes from other eggplants namely, *Solanum melongena*, *S aethiopicum* gr. Gilo, S linnaceanum, *Sintegrifolium*, *Ssisymbriifolium*, and *S khasianum*(Zhuang et al., 2012). But to the best of our knowledge, no research work on R genes was carried out in the three wild eggplants namely, Black nightshade (*Solanumnigrum*), Indian nightshade (*Solanumviolaceum*) and *Solanum incanum* (a species of night shade) which showed resistance to the bacterial wilt pathogen, *R solanacearum* in the preliminary investigation. Therefore, the main objective of this work was to characterize the diversity of NBS-LRR class of genes in these wild plants and to study their evolution with regard to the reported homologous R genes in other plant species. This could pave way for the
were collected from Aromatic and Medicinal plants resistance genes. Cluster analysis was carried out using set of NBS sequence analogs of the present study with other Analysis) Version 6.0 (Tamura (Timothy and Charles, 1994). A phylogenetic tree was predicted RGAs were analyzed using MEME software homologous sequences. The conserved motif structures of National Centre for Biotechnology Information (NCBI) settings was used for performing homology search through Eppendorf thermal cycler with initial denaturation at 94°C for 4 min, followed by 35 cycles of 94°C for 30 s, 55°C for 30 s and 72°C for 60 s with final extension of 72°C for 10 min. Amplified PCR products were electrophoresed in 1.5% w/v agarose gels stained with ethidium bromide. PCR fragments were excised under UV trans-illuminator and purified using NucleoSpin® Gel and PCR Clean-Up Kit. Cloning and sequencing of PCR products: Eluted purified PCR fragments of expected size were cloned into the vector pTZ57R/T using InstAcloneTM PCR Product Cloning Kit and transformed into competent Escherichia coli strain DH5α by following manufacturer’s instructions. The transformed colonies were screened and confirmed for the presence of insert by colony PCR. Plasmid DNA was isolated by NucleoSpin® Plasmid (NoLid) kit. Sequencing of the purified plasmid was done at SciGenom Labs Pvt Ltd, Kochi. Phylogenetic analysis of cloned sequences: The vector sequences and primer sequences were removed with GeneDoc 2.7 software and the region between P-loop and GLPL was taken for further analysis. The nucleotide sequences were translated to predicted amino acid sequence (Bikandi et al., 2004) and BLASTp algorithm with default settings was used for performing homology search through National Centre for Biotechnology Information (NCBI) (http://www.ncbi.nlm.nih.gov), to identify Rgenes as well as homologous sequences. The conserved motif structures of predicted RGAs were analyzed using MEME software (Multiple Expectation Maximization for Motif Elicitation) (Timothy and Charles, 1994). A phylogenetic tree was constructed using MEGA (Molecular Evolutionary Genetic Analysis) Version 6.0 (Tamura et al. 2013) to evaluate the set of NBS sequence analogs of the present study with other plants resistance genes. Cluster analysis was carried out using CLUSTALW(Thompson et al. 1997) based on the neighbor-joining tree (Jones Taylor-Thornton (JTT) model) with 1000 bootstrap replications.

RESULTS AND DISCUSSION

Solanum nigrum, Solanum violaceum and Solanum incanum are wild relatives of eggplant mostly prevalent in tropics showing resistance to bacterial wilt. Since there have been no earlier reports on the characterization of R genes in these plants, this study was undertaken. S nigrum constitute a minor food crop, with the shoots and berries not only being used as vegetables and fruits, but also for various medicinal uses. S violaceum and S incanum are also used as vegetables and for various medicinal treatments.

Identification and characterization of NBS-LRR fragment: The discovery of conserved motifs among the NBS-LRR class resistance genes opens the avenue for the use of PCR based strategy in isolating and cloning R gene family members and analogs using degenerate or specific primers. PCR amplification of nucleotide binding site-encoding genomic DNA regions of the wild eggplants in this study generated fragments of expected size Figure 1. These fragments were extracted from 1.5% agarose gel, purified and then cloned into pTZ57R/T vector. Fifteen recombinant clones from resistant type/cultivated species were selected for sequencing. Of these, six sequences had no match with R genes and had potential stop codons. The remaining nine sequences which had uninterrupted ORF were considered as RGAs. Homology matrix was done for the nine sequences and three sequences which have >50% homology with other sequences and highest identity to different NBS-LRR RGAs analyzed through BLAST were shortlisted. These were considered for further analysis and named as Sincanum(Smi), Snigrum (Sn), S violaceum (Sv). Protein sequences of the three nucleotide sequences were used for identity search with BLASTp algorithm which indicated that all these sequences had a high level of similarity to RGAs and R-genes of other

![Fig 1: PCR amplification of DNA samples of Solanum nigrum, Solanum violaceum and Solanum incanum using degenerative primers](image-url)
Plant species deposited in GenBank (Table 1). Nucleotide blast helped to identify the sequence diversity among the different varieties whereas protein level search and comparison helped to identify the conserved regions of the polypeptide chain. MEME motif identification software was used to detect conserved and relative motifs in RGAs and R genes of highly homologous species (Figure 2). Five major, conserved motifs (Kinase 2, RNBS-C, P-loop, GLPL and RNBS A-non TIR) were identified along the whole length of eggplant RGAs (Fig. 3) and this represented similarities of eggplant RGAs with the structural character of NBS domain of NBS-LRR R-genes. It was observed that the cloned sequences were highly similar to R genes or the RGAs identified in other plant species, especially solanaceous plants. Thus, these genes, especially those from the wild species, may encode resistance gene products of unknown specificity.

**Multiple amino acid sequence alignment of TIR and non-TIR-NBS-LRR RGAs in eggplant:** Multiple sequence alignment of RGAs isolated in this study with previously isolated RGAs by Reddy et al. (2015) and other known R genes of different plants, including *Solanum bulbocastanum, Lagenaria siceraria, Solanum melongena, Solanum tuberosum, Capsicum annuum, Solanum lycopersicum, Solanum tuberosum, Luffa aegyptiaca* also revealed various conserved motifs of NBS, including the highly conserved P-loop (GKTT), GLPL, RNBS-A, Kinase-2, RNBS-B and RNBS-C (Figure 4). This explains that the RGAs isolated in this study may be considered as NBS-LRR class of resistance genes. The three isolated RGA analogs also had an aspartic acid (D) or aspartate (N), suggesting their resemblance to TIR type NBS-LRR class of R-genes.

**Table 1:** Similarity search between eggplant RGAs and GenBank accessions carried out using the BLASTp algorithm.

<table>
<thead>
<tr>
<th>Eggplant</th>
<th>Plant species</th>
<th>Description</th>
<th>Identity</th>
<th>e value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sm</td>
<td><em>Lagenaria siceraria</em></td>
<td>NBS-LRR resistant protein (AEV46136.1)</td>
<td>67</td>
<td>3e-43</td>
</tr>
<tr>
<td></td>
<td><em>Solanum melongena</em></td>
<td>NBS-LRR protein (AHL69098.1)</td>
<td>88</td>
<td>5e-70</td>
</tr>
<tr>
<td></td>
<td><em>Solanum tuberosum</em></td>
<td>PREDICTED : TMV resistance protein N-like (XP006359566.1)</td>
<td>85</td>
<td>4e-55</td>
</tr>
<tr>
<td>Sn</td>
<td><em>Solanum bulbocastanum</em></td>
<td>Putative resistance protein (AFD18779.1)</td>
<td>75</td>
<td>3e-75</td>
</tr>
<tr>
<td></td>
<td><em>Capsicum annum</em></td>
<td>Resistance protein RGAo6 (AEV76889.1)</td>
<td>69</td>
<td>6e-66</td>
</tr>
<tr>
<td></td>
<td><em>Solanum lycopersicum</em></td>
<td>Resistance protein homolog (AAD08712.1)</td>
<td>69</td>
<td>4e-68</td>
</tr>
<tr>
<td>Sv</td>
<td><em>Solanum tuberosum</em></td>
<td>PREDICTED: LOW QUALITY protein: uncharacterized protein (LOC102590743) (XP015159498.1)</td>
<td>83</td>
<td>2e-75</td>
</tr>
<tr>
<td></td>
<td><em>Luffa aegyptiaca</em></td>
<td>NBS-LRR resistance protein (AEV46141.1)</td>
<td>69</td>
<td>1e-75</td>
</tr>
</tbody>
</table>

**Fig 2:** Conserved amino acid motifs identified within the eggplant RGAs NBS domains through MEME software analysis. The black line represents the length of different eggplant RGAs and coloured boxes represent the motifs along the length of each eggplant RGAs.
Phylogenetic analysis of eggplant RGAs: MEGA 6.0 (Tamura et al. 2013) software was used to analyze evolutionary relationship among eggplant RGAs of present study with already characterized known resistance genes from different plants. The phylogeny was constructed using neighbor joining method along Jones Taylor-Thornton (JTT) model with 1000 bootstrap replications. The region between P-loop and GLPL was identified for analysis and it is present in both TIR and non-TIR-NBS-LRR of resistance genes. Sequences were classified into two major types - non-TIR and TIR sequences (Fig.5). Non-Toll-interleukin receptor type genes SMRGA3, SVRG A2, SMRG A4 and SMRG A5 (Reddy et al., 2015) were grouped together in a separate class. The wild species of eggplant in this study along with other closely related plant species belonged to the TIR type due to the presence of highly conserved motif aspartic acid (D) and aspartate (N) at the end of Kinase 2 domain. Multiple sequence alignment with other known R genes in different plants showed significant homology with P-loop, Kinase 2 and GLPL domains of NBS-LRR class.
genes. A class of protein conferring resistance to several strains was found in TIR NBS-LRR class of R gene products of R solanacearum (Deslandes et al., 2002). This reinforces the possibility that the newly cloned eggplant RGAs can also function as R. solanacearum resistant genes.

CONCLUSION

Plant RGAs are a large group of potential R-genes that have conserved domains and structural features which have specific roles in host-pathogen interactions. Studies on R-genes and RGAs identification and characterization will assist marker development, cloning of plant resistance genes and resistance breeding (Sekhwal et al., 2015). However the mechanism and physiology of the action of NBS–LRR protein has not been fully understood. Information on more R-gene sequences is necessary to delineate more structural domains, which is the basis for the search of RGAs in any crop plant (Totad et al. 2005). The diversity among the novel RGAs characterized in this study may lead to identification of different R-genes within the germplasm of different brinjal plants as well as other species of Solanum. Two more potential R genes from wild eggplants (S torvum and S surattense) under investigation, which will provide a better understanding of the role of potential R genes and facilitate the utilization of wild species for eggplant breeding. Novel primer sets can also be designed for analysis of brinjal wild relatives to target novel genomic resources for the genetic improvement of this crop.

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REFERENCES


