# **Reduced the Pomegranate Bacterial Blight Disease**

## Sumitra Saha \*

Department of Biotechnology, Bangladesh Agricultural University, Mymensingh 2202, Bangladesh

\*Corresponding author: Sumitra Saha, Department of Biotechnology, Bangladesh Agricultural University, Mymensingh 2202, Bangladesh, E-mail: mitrasu@bau.edu.bd

Received date: October 07, 2022, Manuscript No. IPRJPP-22-15334; Editor assigned date: October 10, 2022, PreQC No. IPRJPP-22-15334 (PQ); Reviewed date: October 20, 2022, QC No. IPRJPP-22-15334; Revised date: October 29, 2022, Manuscript No. IPRJPP-22-15334 (R); Published date: November 07, 2022, DOI: 10.36648/ iprjpp.5.6.125

Citation: Saha S (2022) Reduced the Pomegranate Bacterial Blight Disease. J Res Plant Pathol Vol.5 No.6: 125.

#### Description

Cowpea is well-known all over the world for its versatility, high protein content, and adaptability. However, the Xanthomonas axonopodis pv-caused bacterial blight disease has devastating effects on it. Vignicola or Xav Ten high-yielding cowpea varieties were tested for bacterial blight resistance in Bangladesh during two distinct cropping seasons. After phenotypic and molecular characterization, Xav bacteria were inoculated into seed and stems to evaluate the varieties. Nine disease-related qualitative and quantitative traits were used to evaluate the varieties morphologically, and nine SSR markers were used to investigate genetic variations. The development of the disease varied significantly between the varieties. The Kharif season had a significantly higher disease incidence than the Rabi season. In both seasons, Dark Green-1028, Felon local, and Dark Green-28 varieties were resistant. In contrast, BARI Felon-1 was extremely susceptible to susceptible in both seasons, with over 50% of infections. Additionally, the variety differences in plant height, leaf area, branch number, and leaf number were significant. In addition, Nei's gene diversity and polymorphism information content were found to be 0.4089 and 0.3658, respectively, in the molecular study. Compared to Dark Green-1028, Kegornatki exhibited the greatest genetic variation. The ten cowpea varieties were categorized into two main clusters by the UPGMA dendrogram. The results of this study showed that three high-yielding varieties, namely, Felon local, Dark Green-28, and Dark Green 1028 were better at morphomolecular characterization and were resistant to bacterial blight. As a result, these varieties can be incorporated into future cowpea breeding programs to produce cultivars capable of mitigating Xav's high pressures.

### **Pomegranate Bacterial Blight Disease**

In India, pomegranate is one of the most commonly grown fruit cash crops. For the beyond couple of many years, it has been noticed experiencing bacterial curse sickness, hampering the producers' financial advantages. The purpose of this study was to determine whether bacteriophage-based liquid formulations could be used to treat Pseudomonas sp.-induced pomegranate bacterial blight. For the bio control study, isolated two phages against the cause of pomegranate bacterial blight disease were utilized. Different liquid formulations based on phages were created and tested for a six-month shelf life at temperatures of 4°C and 30°C. The 0.5% whitening clay liquid formulation was found to maintain the most active phage titre among the studied formulations. Compared to standard streptocycline, the foliar spray of 0.5% whitening clay liquid formulation effectively reduced the pomegranate bacterial blight disease. In addition, in the greenhouse-like pot experiment, the preventative application of a 0.5% whitening clay liquid formulation based on phages produced promising results. Both biotic and abiotic factors have hampered rice production and productivity. Xanthomonas oryzae pv causes Bacterial Blight (BB). Oryzae is one of the major causes of biotic stress, resulting in a 20%-50% decrease in rice production. The most preferred method for managing BB disease is to use host plant resistance, and breeding disease-resistant varieties remains a cost-effective option. However, conventional methods alone make it difficult to cultivate rice varieties with long-lasting broad-spectrum resistance to BB. The cloning, characterization, and introgression of BB resistance genes into elite varieties has been made easier by modern biotechnological tools, particularly the use of molecular markers. From a variety of sources, at least 46 BB resistance genes have been identified and mapped thus far. 11 of these genes have been identified and cloned. By introducing two or more resistance genes into the target varieties, marker-assisted breeding continues to be the most effective method for increasing BB resistance. More than 70 rice varieties or hybrid rice parental lines have been improved for their BB resistance alone or in combination with genes/QTLs conferring tolerance to other stresses. Among the identified genes, xa5, xa13, and Xa21 are widely used in marker-assisted breeding. Through marker-assisted breeding, we examine developments in the identification and application of various resistance genes for the production of BB-resistant rice varieties.

#### **Backcross Breeding Programs**

Over half of the world's population relies on rice for their daily diet. Over the past few decades, significant efforts have been made to increase rice yields in order to guarantee food security. For instance, a compelling two-line crossover rearing framework was laid out in light of photoperiod-and thermo-delicate genic male-sterile lines, bringing about significant expansions in rice yield. Due to their lack of resistance to major diseases and insect pests, such as blast, bacterial blight, and brown plant hopper,

Vol.5 No.6:125

high-yielding two-line hybrid cultivars have, on the other hand, led to an excessive use of pesticides, resulting in environmental harm and increased production costs. Rice yield could be stabilized while also protecting the environment if two-line hybrid cultivars with superior resistance to major diseases and insect pests were bred. Rice's resistance to blast, bacterial blight, and brown plant hopper has been well-defined genetically. From both cultivated and wild rice, 25 blast resistance genes, 12 bacterial blight resistance genes, and 14 brown plant hopper resistance genes have been cloned. In marker-assisted backcross breeding programs, the blast resistance gene Pi2, the bacterial blight resistance gene Xa23, and the brown plant hopper resistance genes Bph14 and Bph15 have all been utilized extensively. However, linkage drag can transfer undesirable genes to rice, and unidentified genetic background effects can have a negative impact on agronomic traits, resulting in low yield or poor grain quality. Improved breeding lines can be produced using genomic breeding strategies that enable the

simultaneous introduction of multiple genes with minimal introgression segments to overcome these obstacles. Hybrid cultivars can achieve long-lasting resistance to diseases and insect pests using this method, which is an improvement over conventional pyramiding techniques. Foreground selection, which takes advantage of recombination events between target genes and flanking DNA markers to reduce the size of the donor segment containing the target gene, and background selection, which accelerates Recurrent Parent Genome (RPG) recovery, can be used to pyramid target genes that confer resistance to diseases or pests. A pyramided line with multiple or broadspectrum resistance to various diseases and pests is created as a result of these selection steps, which remove linkage drag and unidentified genetic background effects. By transferring two resistance genes, Bph14 and Bph15, through genomic breeding, five lines of the indica restorer rice Wushansimiao have recently developed brown plant hopper resistance.