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Review Article

Resistance Genes of *Oryza sativa* for Protection against *Xanthomonas oryzae* pv. *oryzae*, the Causative Agent of Bacterial Leaf Blight

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Rice (*Oryza sativa*) is a major staple crop around the world, particularly in developing regions such as Africa and Asia. Attack of the rice crop by pathogens has the capacity to greatly diminish crop yield with major agricultural, economical and human consequences. *Xanthomonas orzyza* pv. *oryzae* (*Xoo*), the causative agent of bacterial leaf blight, has the ability to cause substantial crop loss, up to 80% worldwide. Genetic sources of resistance have long been considered the most sustainable method of disease control, both from an environmental and agricultural perspective. This review considers the discovery, evolution, characterization and utilization of resistance genes (R genes) in rice against *Xoo.* R genes for *Xoo* are plentiful and exist at multiple loci throughout the rice genome due to multiple gene duplication and transposition events. The presence of multiple gene loci makes gene pyramiding and resistance stacking accessible and fruitful applications in breeding for resistance. Biotechnological approaches to take advantage of R gene function have also begun to take root. However, a more global and concerted effort to study the multiple varieties and climates in which rice is grown is required in order to truly attain food security and find sustainable resistance.

Keywords: R genes; Rice; *Oryza sativa*; *Xanthomonas oryzae*; Bacterial Leaf Blight

Introduction

Rice (*Oryza sativa)*, is a staple food crop for a majority of the world's population. In developing regions of Asia, and also in Africa, rice plays an even more crucial role in agricultural systems. For many communities, rice is the main source of caloric intake and farmers rely on their fields not only for profit, but also for sustenance. However, a multitude of diseases plague rice crop yield every year, bacterial leaf blight being the most devastating. This disease causes substantial loss, averaging from 20%-30% but severe cases can result in loss up to 80% of total yield (Perumalsamy *et al*., 2010).

Xanthomonas oryzae pathovar (pv.) *oryzae* (*Xoo*), the causative agent of bacterial leaf blight, is a gram negative bacterial pathogen infecting the xylem of the rice plant, causing lesions of the leaves and eventual plant death. Upon infection, *Xoo* secretes several factors, which both cause infection as well as trigger host resistance. There are several races of *Xoo*, all of which secrete race-specific effectors into the xylem to trigger individualized response and cause infection. These effectors are targeted to the host cell nucleus where they bind to specific genes, host susceptibility genes, and activate transcription to alter the host environment to benefit the pathogen. The bacteria also release factors which bind and activate transcription of genes which activate resistance response, known as resistance genes (R genes) (Hummel *et al*., 2012).

As reviewed by Bent (1996), R genes are a common phenomenon in plant-pathogen interactions in which the plant recognizes effectors from the pathogen and activates specific responses to these signals. This is often referred to as gene-for-gene resistance - a specific gene in the host is activated due to the presence of a specific gene product from the pathogen. Pathogens, such as *Xoo*, are constantly evolving to have effectors unnoticeable by the plant, while the plant evolves to recognize a greater spectrum of effectors. The result is the coevolution of an innate, genetic resistance system in rice specific towards *Xoo* infections. The factors that activate *Xoo* resistance genes are known as avirulence factors, reducing the virulence of the pathogen as they are recognized by the host. As mentioned above, once the bacterial avirulence factors bind to the host gene, they activate a series of downstream events that lead to host resistance. Ultimately the signaling pathway may cause hypersensitive response, localized cell death to limit bacterial spread throughout the rest of the plant, or cause other changes which reduce pathogen success. Since each race of *Xoo* produces unique virulence and avirulence factors, R genes have evolved to provide resistance to individual races of *Xoo*. In light of the destructive nature of the bacterial leaf blight pathogen, farmers continually seek methods of disease control to protect their crops from infection and subsequent yield loss. Traditional plant breeding takes advantage of innate immunity to develop resistant lines bred to accommodate R genes. Host resistance, as compared to chemical control, has not only proven to be the most effective control method, but also is a more economically and environmentally sound way to combat bacterial leaf blight. However, with new races consistently emerging, broader and more comprehensive resistance must be pursued in order to prevent super-races of *Xoo*, which can overcome all genetic sources of resistance, from becoming prevalent.

Current research has identified up to thirty-five R genes in the rice genome specific for *Xoo*. These genes have become a focus of study for many scientists looking to improve rice resistance to this pathogen. Many of these genes have been finely mapped to multiple loci across the rice genome and their modes of action characterized. Also, study of these genes has led to a greater understanding of their

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evolution and function within rice species. The R gene family responsible for *Xanthomonas* resistance has been discovered to be a multigene family with genes located at multiple loci throughout the rice genome. All genes associated with *Xoo* resistance have been named with a *Xa* prefix followed by a specific number assigned upon discovery. The knowledge gained thus far in the field has already been applicable in developing rice lines with increased resistance towards *Xoo* infection. Pyramided genes in hybrid rice lines produced more efficient resistance, both broader in scope and more sustainable against selective pressures. Biotechnologists have also begun to take advantage of R genes through gene silencing and genetic engineering, and the results are encouraging. Further investigation into R gene resistance is a promising field with immense potential to help insure global food security by supporting the health of an essential crop.

Evolution of *Xoo* Resistance Multigene Family

The rice *Xa* gene family is characterized by encoding for receptor-like kinases with a leucine-rich repeat (RLK-LRR) domain (Wang *et al*., 2006). The RLK-LRR domain is a common motif found among plant R-genes and is prevalent throughout the plant kingdom in various species, including rice, *Arabidopsis*, tomato and tobacco. Across species, there is a strong similarity in the structure, function and mechanism of the LRR motif (Zhao *et al*., 2009). This suggests an evolutionary link between the resistance gene families across species as well as conservation in function crucial for survival. In rice, there are RLK-LRRs specific to bacterial leaf blight resistance, but this motif can be functional against a wide range of pathogens. The rice LRR resistance gene family, *Xa*, have undergone evolutionary development in response to the selection pressures of new races of *Xoo*. The evolution of these genes has created specificity in resistance against the multiple races of *Xoo* which have emerged. Through examination of DNA sequences and gene product structure of multiple members of the *Xa* family, several evolutionary trends for their differentiation have been proposed.

Song and coworkers (1997) sequenced and analyzed seven family members of rice resistance genes against *Xoo* all of which are related to known R gene *Xa21*. This analysis found 15 transposable-like elements such as terminal inverted repeats, duplication of target sequences and sequences similar to known transposable elements within the family members. While most of transposable elements were within non-coding regions, two were found to be in open reading frames of two different family members. These elements resulted in truncated proteins varying in function and structure from each other and the precursor protein. A change in structure may lead to a change in function, providing diversity in resistance towards *Xoo.* The insertion and recombination of these transposable elements is a promising mechanism for diversification of the characteristic receptor kinase.

Additionally, Song's group identified a highly conserved (HC) G-C rich 233bp region of *Xa21* present in all sequenced family members. The similarity of the amino acid sequence encoded by the HC region is nearly 100%. The HC region appears to provide an excellent area for recombination as demonstrated by family member *F* which contains an abrupt change in nucleotide sequence 120bp downstream of the start codon. The precise break point between *F* and *Xa21* is located within the HC region and was determined to be a non-random event because the coding region was not altered, maintaining the receptor-kinase open reading frame. Three other family members were determined to have a break point within the HC region, suggesting this locus is a likely site of recombination and subsequent gene product differentiation. The authors also provide evidence suggesting the HC region facilitated intergenic recombination leading to duplication and divergence of the *Xa21* family members. The HC region encodes for domains I and II of the receptor kinase. These domains have also been identified in receptor-like kinases with the LRR motif in other plant species, however the nucleotide sequence is not conserved between species.

In summary, the overall model proposed by Song and coworkers for the evolution of the *Xa21* gene family begins with duplication and divergence from a common progenitor receptor kinase gene. This is followed by unequal recombination between family members to further expand the gene family. Recombination within the conserved HC region allowed for unique promoter and coding sequence combinations which could alter gene expression. A large duplication expanded the *Xa21* gene family and integration of transposon-like elements has allowed the further diversification and addition of new members. Evolution of R genes is crucial for plant survival as pathogens concomitantly evolve virulence factors.

Multiple Gene Loci Confer Resistance to *Xoo*

The R genes in the rice genome encode different proteins, have a characteristic response to infection, vary in their mode of action and provide differential levels of resistance depending on genetic background. Some of the genes are dose dependent, some are dominant, and others recessive, some may be developmentally controlled while others are constitutively expressed. The great diversity of genetic function is testament to the evolution of R genes in rice over time as a way to combat the development of new races of *Xoo*. Selections of interesting and important R genes which have thus far been characterized and studied are explored below.

With the vast number of R genes being unearthed from the rice genome, it is sometimes difficult to differentiate a novel gene from a previously discovered one. Prior to further analysis, R genes *Xa3* and *Xa26* were thought to be discrete genes. However, upon analysis by Xiang and colleagues (2006), these genes were determined to be the same. Both R genes were identified by the production of an LRR receptor-kinase like protein, as is characteristic of the *Xa* multigene family. Two rice lines, each containing one of the genes in question, were compared and each demonstrated a dominant resistant phenotype segregating in the expected 3:1 ratio. While it is not unlikely that multiple R genes are dominant, further results suggested they were, indeed, the same gene. In a rice line containing *Xa3* only, *Xa3* was found to co-segregate with a tightly linked genetic marker of *Xa26*. This would imply the two genes are located at the same locus. However, since the generation of two disparate gene products from the same locus is very rare, they may be the same gene. DNA fingerprinting of the *Xa3* rice line showed the same number of copies of *Xa26* genes as in the *Xa26* rice line.

When comparing the lesion appearance of rice lines with either *Xa3* or *Xa26*, lesion patterns were identical when interacting with *Xoo*. These patterns were not seen in other plants without these R genes, suggesting the lesion phenotype is unique to these genes, and therefore may be characteristic of only one gene. The genes were confirmed not to be alleles of each other. Compiling the preceding evidence - the similarity in function, location and expression of the *Xa3* and *Xa26* R genes, the authors concluded *Xa3* and *Xa26* are the same gene and will be denoted as *Xa3/Xa26*.

The *Xa3/Xa26* gene was subsequently determined to be part of a multigene family including two additional functional genes, *MRKa* and *MRKc* and the pseudogene *MRKd,* clustered in tandem on rice chromosome 11(Cao *et al*., 2007). *MRKa, MRKc,* and *Xa3/Xa26* function together to provide full resistance to *Xoo.* Individually, these genes could not maintain resistance when isolated and regulated by their native promoters. *MRKa* could confer partial resistance when isolated and constitutively expressed. On the other hand *MRKc* could not provide resistance when regulated by its native or a constitutive promoter. However, when *MRKa* was constitutively expressed along with normal expression of the other genes in the family, there was an observed increase in resistance, suggesting a dosage effect of *MRKa* in disease resistance. The associated *MRK* genes are not themselves R genes, but act synergistically with *Xa3/Xa26* and *Xa21* to produce a resistant phenotype (Century *et al*., 1999). Complex interactions between multiple gene families within the R gene class further expands the diversity and specificity of R genes in relation to the variety of races of *Xoo*.

The genetic background in which the R gene resides is also responsible for the expression and effectiveness of resistance response to *Xoo* infection. Two primary rice varieties grown in Asia are *japonica* and *indica,* each containing a distinctive genetic composition. Zhou and coworkers (2009) demonstrated that the *Xa3/Xa26* gene provides a higher level of resistance to *Xoo* infection in the *japonica* background versus *indica.* The increased resistance was discovered to be the result of increased expression of the *Xa3/Xa26* gene through the effect of four quantitative trait loci identified in *japonica.* Furthermore, epistatic and digenic interactions discovered within both genetic backgrounds were indicated to impact expression of *Xa3/Xa26*. Different overall gene expression in *indica* and *japonica* is the major factor in the observed divergent activity of *Xa3/Xa26* in each line. The native genes expressed may code for products in another signal transduction pathway, which may indirectly regulate resistance genes. This, in turn, may lead to an increase or decrease in expression of the R gene product resulting in differential resistance between rice varieties. The influence of genetic backgrounds was shown to function throughout all stages of plant development.

Therefore, the functionality of some rice resistance genes is affected by multiple loci throughout the genome. Resistance to *Xoo* infection is not isolated within a particular loci, region or chromosome where the R gene is located but is a dynamic interaction between the R genes and the host genome. Because of these complex interactions, when feasible, R genes should not be studied as discreet units but instead in the context of the genome as a whole.

Recessive genes, such as the *xa5* resistance gene, have an important role in rice disease resistance. In a study by Iyer-Pascuzzi and coworkers (2008), the *xa5* resistance gene was shown to be completely recessive even though its mode of inheritance was once disputed. Traditional crosses resulted in *Xoo* infection susceptibility co-segregating with the dominant *Xa5* allele in the expected 3:1 ratio. The dominant *Xa5* allele is considered a susceptibility gene as only one copy is required to diminish resistance against *Xoo.* The observed segregation pattern demonstrates the *xa5* allele must be present in the homozygous state to obtain a resistant phenotype, confirming its identity as recessive. This data also suggests *Xoo* susceptibility is an active process rather than just an absence of resistance. In this instance, the dominant allele codes for a required receptor for bacterial infection. Much like the dominant *Xa3/Xa26* gene discussed above, the genetic background of the rice line affects the resistance of plants containing the *xa5xa5* genotype. In *xa5*-mediated resistance, bacterial multiplication is prevented more strongly in *japonica* rice lines as compared to *indica* lines. However, other characteristics of *xa5* defense, such as restriction of bacterial movement and inheritance of the allele did not seem to be affected by the genetic background. The resistance granted by the recessive allele may be due to other secondary defenses which may be induced by *xa5* expression. Once again, the action of R genes is shown to be highly interactive and dependent on the genetic constitution of the host genome and must be carefully observed in a variety of genetic environments.

Other recessive genes have been identified and finely mapped to particular locations within the rice genome. By fine-mapping the exact location of these genes, they can be further exploited for use in developing resistant crop lines for famers. Using specific restriction fragment length polymorphism genetic markers, recessive R gene *xa13* was mapped to a 14.8 kb DNA fragment on the long arm of chromosome 8. This gene was determined to be recessive, only conferring resistance when present in the homozygous state (Chu *et al*., 2005). Recessive gene *xa24* was localized using simple sequence repeat (SSR) markers to a 71 kb fragment on the terminal end of the long arm of chromosome 2, a completely different locus than *xa13.* This gene was shown to contribute whole-growth-stage resistance to several different races of *Xoo* when present in the homozygous condition (Wu *et al*., 2008). A more recent mapping of recessive resistance genes is the fine mapping of *xa34(t)* which is defined to a 204 kb region near the centromere of chromosome 1 using SSR markers. This gene was proven to be discrete from all other previously known R genes and displayed the expected 3:1 recessive phenotype segregation characteristic of a recessive allele (Chen *et al*., 2011). R genes are a highly variable multigene family present at multiple loci, in multiple states and with varying expression patterns, all of which are crucial to resistance against *Xoo*. The presence of multiple sources of resistance gives breeders a wide range of genes available for application in resistant lines.

The library of R genes continues to expand as novel genes are continually discovered and mapped throughout the rice genome. This characteristic of the *Xa* R gene family has proven to be beneficial in developing hybrid resistant rice to control bacterial leaf blight. Also, the above research emphasizes the importance in considering all genetic factors influencing resistance genes. This research has shown the

effect of multiple genes families, differing genetic backgrounds and methods of regulation all are critical in determining the functionality of *Xoo* resistance conferred by a particular R gene. Scientists working towards developing resistant lines for farmers must be aware of the several confounding effects in disease resistance. A broad scope must be used when designing methods to increase crop vitality.

Developmental Control and Potential Modes of Action

One particularly interesting characteristic of some R genes found in rice is their developmental regulation. While some genes are constitutively expressed throughout the life of the plant, some genes reveal differential expression and resistance depending on the developmental maturity of the plant. The changes in expression further testify to the complexity in the gene-for-gene interaction which has evolved among the *Xanthomonas* R gene family in rice.

Resistance genes *Xa21* and *Xa3/Xa26* are two examples of genes conferring different levels of resistance depending on plant developmental stage. In plants containing the *Xa21* R gene, each consecutive leaf which developed had an increased resistance to infection. Full resistance was not obtained until the ninth or tenth leaf, with resistance increasing as development progressed (Century *et al*., 1999). In plants with the *Xa3/Xa26* genotype, lesion length, which can be measured as a representative of infection severity, decreased as plants matured suggesting resistance increases throughout development (Zhao *et al*., 2009). Originally, *Xa21* developmental regulation was thought to be independent of gene expression (Century *et al*., 1999). However, further analysis discovered both *Xa21* and *Xa3/Xa26* were more highly expressed as plants mature, implicating a correlation between development and gene expression. As the plant develops, genes are more highly expressed and resistance increases leading to highly resistant adults (Zhao *et al*., 2009). This also means seedlings could be more susceptible to *Xoo* and more care for disease control should be taken during this vulnerable stage.

Pathogenesis-regulated (PR) genes are also involved in resistance, though they cannot confer complete resistance on their own. These genes have also been shown to be developmentally regulated. The mechanism by which *Xa21* grants resistance is related to the expression of these PR genes and presence of their gene products. In plants containing the *Xa21* gene, higher expression levels of PR genes were found and accompanied by increases resistance. This suggests an interaction between the *Xa21* and PR genes to confer resistance. Characteristic of the developmental control observed in both PR genes and *Xa21*, resistance was found to be strongest in adult leaves (Ponciano *et al*., 2006).

The *Xa21* gene encodes a receptor-like kinase that acts in the resistance pathway for *Xanthomonas* (Wang *et al.*, 2006). This protein is only present and active in the adult leaf stage, again supporting developmental regulation (Park *et al*., 2010). The LRR domain is evolutionarily conserved throughout the family and confers race-specific resistance to *Xoo*. The juxtamembrane region of this domain is responsible for specificity and also contains the kinase activity required for functionality (Zhao *et al*., 2009). The knowledge of the effect of development on resistance granted by R genes could further understanding of entire resistance mechanisms. Once these mechanisms are more fully understood, they could potentially be used, modified and harnessed in applications to increase resistance to *Xoo*.

Applications

Understanding the structure, evolution, expression and confounding effects of resistance genes has opened up a new wealth of information which can be used to develop new methods for protecting rice from bacterial leaf blight. Developing highly resistant lines with innate resistance has proven to be the most successful way to protect this vital crop from unnecessary loss. Several methods have been created to develop bacterial leaf blight resistant rice lines. However, with rapid and constant evolution and increasing variety of *Xanthomonas* races, new resistant lines and novel methods need to continually be sought. Several methods ranging from traditional breeding to emerging biotechnology have been used with success.

Rice lines with only one resistance gene often become susceptible to new pathogen races that evolve in response to selection pressure. Therefore, pyramiding methods incorporating multiple genes into a single rice line have proven to be more genetically stable against new races of *Xoo* compared to monohybrid lines. Successful pyramiding of *Xa7* and *Xa21* resulted in a rice line with increased resistance compared to a plant with only a single resistance gene (Zhang *et al*., 2006). If at least one dominant allele was present at each locus, there was an increase in *Xoo* resistance. However, the two genes were demonstrated to be incompletely dominant. If the genes were present in a heterozygous state, there was a slight decrease in resistance compared to resistance in a homozygous dominant. Nonetheless, the hybrid lines showed drastic increase in resistance compared to monohybrid lines, even in the heterozygous state. The pyramided line also expressed resistance towards a larger spectrum of pathogens, suggesting an interacting additive effect in which the multiple genes present together can confer resistance to pathogens not attainable when each gene is expressed individually. Pyramiding of genes should help rice lines sustain resistance as evolutionary pressures from new races of *Xoo* emerge because of the "two hits" required to overcome the dihybrid resistance background.

The benefits only increase when you add a third resistance gene. Functional marker analysis, which uses phenotypic signals to select for the desired genotype, recently showed the increased effectiveness of a pyramided line containing three R genes, *xa5, Xa13,* and *Xa21* (described in Perumalsamy *et al*., 2010). Hybrid lines with at least two of the genes present in a homozygous state showed the highest levels of resistance. In lines with the *Xa21* gene present in the heterozygous condition and *xa5* and *xa13*, both recessive, present in the homozygous condition, there was moderate resistance. Thirty triply pyramided *xa5*, *Xa13*, *Xa21* genetic lines were developed with 12 of the 30 having an increase in grain yield along with increased resistance. This is particularly significant for agriculture as there are often cases in which resistance is accompanied with less desirable agronomic traits. Additionally, in lines pyramided with only two R genes, the disease lesion increased 21 days post induction. This was not seen in the triply pyramided line, suggesting more sustained resistance when the third gene was

present. The above data suggest that more efficient, resistant and profitable crops could be developed through pyramiding multiple resistant genes into individual rice lines and traditional breeding methods.

Gene silencing has also been proposed as an effective method to add resistance to rice lines. Traditionally, single recessive genes are overlooked in pyramiding plans since they have to be present in the homozygous condition, which is more difficult to achieve than a heterozygotic or homozygotic dominant genotype. However, gene silencing provides a way to utilize these genes more efficiently. Artificial microRNA (amiRNA) technology has been developed to silence the dominant allele of *xa13*, allowing the recessive allele to be unmasked thereby expressing the resistant phenotype, mimicking a homozygous state. This silencing conferred a higher degree of resistance to the rice line without affecting other essential traits, such as fertility (Li *et al*., 2012). This technology opens the possibility of developing resistant lines by using recessive R genes and without having to pyramid multiple genes into one plant.

Hummel and coworkers (2012) show that besides gene silencing, genetic engineering of the R gene promoter can also effectively promote resistance towards *Xoo*. Many R genes have been classified as executor genes and are turned on in the presence of a transcription-activator like effector (TALE) released from the pathogen by binding to a specific effector binding element (EBE) to initiate the resistance response. Different races of bacteria release different TALEs and different R genes have specific EBEs. By fusing new EBEs to the promoter of *Xa27*, gene transcription could be initiated by bacterial races other than the races that normally activate *Xa27*. Therefore, the *Xa27* gene will respond to a greater spectrum of pathogens, triggering resistance. Also, the addition of the EBEs resulted in resistance against a pathovar of *Xanthamonas* which is the causative agent of bacterial leaf streak, for which no R genes have yet been identified. This method creates a single gene with the expanded spectrum of traditionally pyramided lines but is less time-consuming and laborious than creating multigenic lines. Several EBEs could be added to a single promoter, greatly increasing the number of pathogens which initiate resistance. While this method appears to be extremely promising, broadening the spectrum to other diseases along with various races of *Xoo*, there may be some limitations which are yet unknown. The number of EBEs that can be added may be restricted by distance between gene and promoter. Also, it has proven somewhat difficult to direct the exact insertion point of the EBEs and therefore may require extensive trial and error. Addition of the EBEs also runs the risk of an EBE being added to a promoter of regulatory or synthetic elements. These genes may then be induced by the TALE out of context causing unintended expression and unwanted effects that may prove disadvantageous or dangerous. This method is promising, but investigation should proceed with care as further progress is made. Frequent and thorough testing should be performed on all resistant lines produced via this method before being released for cultivation to insure there are no unwanted consequences.

Xanthomonas and Food Security

A majority of the research on *Xoo* resistance has focused on Asian varieties of rice and against Asian species of bacterial leaf blight; this focus is logical since rice is the main grain consumed in this region. However, rice is also becoming a staple crop in Africa, which has a unique strain of *Xoo* endemic to the area. Bacterial leaf blight is posing a significant threat to the sustainability of the rice crop in Africa. It has been shown in the Asian varieties the benefits of inbred host resistance compared to other methods of control, yet no systematic breeding strategy nor is biotechnological application being pursued to fight against *Xoo* in Africa (reviewed in Verdier *et al*., 2012). R genes *Xa4*, *xa5*, and *Xa7* have been shown to provide resistance against African *Xoo*, but there has been no pursuit to use these genes to develop resistant African rice lines. While traditional pyramiding of these genes may be used to increase resistance, biotechnology may provide a more efficient method to do so. With the food security crisis worsening and affecting a majority of Africa, biotechnological approaches should be pursued on African rice lines. However, these technologies must be applied locally and adapted to the current problems, local constraints and priorities in the African cultural context.[12]

Conclusion

There has clearly been extensive work elucidating the details of genetic resistance again bacterial leaf blight in rice. Work has been, and is currently, identifying, mapping, characterizing and developing *Xoo* R genes to obtain a full spectrum of resistance to this devastating disease. These discoveries have already begun to benefit farmers and their patrons through the development of hybrid lines and biotechnological advances working towards a more sustainable crop. As explained above, there are numerous factors impacting the resistance granted by these genes, and a complete understanding of the resistance dynamic would result in a better equipped scientific community.

Rice is an essential food source for a large portion of the population, and if its health can be supported through methods supported by study of resistance genes, research must continue. The global food crisis has the potential to escalate as global warming and overpopulation worsen. Developing host resistance using R genes has already been shown to be the most effective and environmentally friendly method of disease control. Further investigation into how *Xanthomonas* R genes can be used to create sustainable resistance against bacterial leaf blight is necessary for the security of a staple crop capable of feeding the world.

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