

Natural Variation Exploitation to Identify Genes of Insect Resistance

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ABSTRACT: *Herbivores are common and frequently severe restrictions on crop productivity. The use of insect-resistant crops for the management of insect pests in agriculture is an extremely efficient means, and understanding about plant resistance mechanisms and genes involved may significantly improve the creation of such crops. Plants have developed a variety of methods to deal with insect attacks which have led to natural variations in herbivorous insect resistance. The study of the molecular genetics and transcriptional backdrop of this polymorphism has made it easier to identify resistance genes and mechanisms leading to insect resistance. Molecular investigations are no longer limited to model plants with the advent of new technology. This review highlights the need to make use of the natural variations in insect resistance to enhance our understanding of resistance mechanisms and the genes involved. We will explain how this information may be used to offer sustained plant protection against insect pests in breeding projects. Furthermore, we address the present state of insect-resistance genetic research. We believe that the causes of insect resistance are still unknown at molecular level and that using new technology will help significantly to the creation of insect-resistant crop species.*

KEYWORDS: *Breeding, Herbivores, Insect-Resistance Gene, Natural Diversity, Natural Variation.*

1. INTRODUCTION

In agriculture, a wide variety of herbivorous insect species are significant pests, and many of them are primarily controlled via the use of pesticides. Alternative methods of insect control are required due to environmental concerns and the harmful effects of pesticides on beneficial insects such as pollinators and insectivorous insects. Alternative methods of insect control include Host plant resistance is one of the most efficient means of pest control available, and it is a highly viable alternative to the use of insecticides in many situations. For the purpose of developing insect-resistant cultivars, it is necessary to identify, describe, and categorize effective sources of resistance in order to go on with the process[1].

Despite the widespread occurrence of herbivorous insects in nature, deadly pests are only seldom seen. This is due to the fact that plants have a wide range of defenses against herbivorous insects that they may use to defend themselves. In terms of defense mechanisms, there is a great deal of diversity across plant species, which has been formed by variations in selection pressure throughout time. However, only a small portion of this natural variation has been used in agricultural production too far. Identifying natural diversity among crop plant relatives, or even within crop plant accessions themselves, may result in the development of resistant varieties of crop plants. The advent of sophisticated molecular genetic techniques has enabled genome-wide association studies to be conducted in order to unravel the biological variation that underlies variance in insect resistance in a systematic manner[2].

In order to introduce resistance characteristics into commercially significant farmed crops, such studies aid in the creation of molecular markers and the enhancement of marker-assisted breeding techniques in order to do so. Transgenic crops, on the other hand, may be used to add insect-resistance genes into crops already grown. Given the many political issues surrounding genetic modification technology, we shall restrict our discussion to traditional breeding methods in this study. Furthermore, the promise of transgenic methods, such as those employing, for example, Others have examined the literature on Bt-genes and RNAi constructs[3].

An examination of the possible utilization of natural variation to create insect-resistant crops, as well as the role that new biotechnological tools may play in this process, is the subject of this review. We begin by discussing the present state of research on natural variation at the molecular level, which includes both the genomic and transcriptome levels of analysis. We next explain how natural diversity in insect resistance may be used in agriculture, as well as providing an overview of the insect-resistance genes that have been discovered so far in the field of genetics. At the end of the paper, we suggest future avenues for study into the use of naturally occurring genetic variation to develop crops that are long-lasting and resistant to insect herbivores[4].

1.1 Insect Resistance:

Individuals from the same species may exhibit varying levels of resistance in the wild due to variations in their genetic composition. According to current thinking, genetic diversity is preserved through trade-offs between the advantages of decreased herbivory and the costs of resistance, as well as by variable selection pressures on various populations. For example, if a population is repeatedly infested by a specific herbivore, the resistance traits that are effective against this herbivore will be selected for, whereas a lack of natural selection could result in the loss of the resistance from the population as a result of the lack of natural selection. Different levels of resistance to specific herbivore species have developed as a consequence of differences in natural selection, resulting in the existence of populations with varying levels of resistance, ranging from sensitive to resistant. Variation may be produced by natural selection in wild populations, as well as by artificial selection during the process of domestication. In this review, for the purpose of simplicity, we will refer to variation as referring to variance across populations as well as variation among different types[5].

1.2 Variation in Plant Characteristics:

In general, plant resistance to insects may be based on direct and/or indirect defense mechanisms, which can either be present by nature or be induced by herbivore assault. Direct and/or indirect defense mechanisms can be present by nature or induced by herbivore attack. It is direct defense that is comprised of physical and/or chemical plant characteristics that by themselves interfere with the physiology and/or behaviour of the herbivore and are the primary determinant of plant resistance. It has been discovered that there is natural diversity in plant characteristics that are linked to direct defense in many plant species. This includes, for example, variations in trichome density or particular secondary metabolites in different plant species. Physical and chemical plant characteristics that attract natural enemies of herbivores and increase their efficacy in controlling herbivore populations are referred to as indirect defense. Herbivore-induced plant volatiles (HIPV) are the most significant chemicals that serve as signals in indirect defenses, and they have been found to differ across populations of accessions from the same plant species (i.e., accessions from the same plant species population). Although there has been documented variation in plant characteristics associated with direct and indirect defenses against herbivorous insects, there is little information about the genetic basis of these variations[6].

1.3 Variance at The Molecular Level:

Among genotypes, there may be significant variation in particular phenotypic characteristics, which may arise as a consequence of a mutation affecting a structural gene implicated in the trait or from variations in the expression of genes linked to the trait. These later variations are referred to as expression level polymorphisms (ELPs). It is possible that ELPs are triggered either by DNA polymorphisms in regulatory genes or by mutations in the promotor region of resistance genes themselves in theory. ELPs across *Arabidopsis thaliana* accessions have been shown to be correlated with variations in DNA sequences, indicating that DNA sequence polymorphisms have a substantial effect on gene expression. Besides variations in DNA sequences, variation at the transcriptional level may be affected by DNA methylation and the interference of short RNAs, among other factors. Additional copy number variation (CNV) has the ability to influence the amounts of gene expression in the body. CNVs, in contrast to whole-genome duplications, are tiny duplications and deletions that occur across the genome. Clearly, mutations alone are unable to predict whole-genome transcriptional variation, and analyzing sequence variation is just the first step in better understanding phenotypic variance[7].

1.4 Influence of Gene Expression On Resistance Characteristics:

Given that gene expression and post-transcriptional processing dictate whether proteins or secondary chemicals are generated, ELPs offer important preliminary insight into resistance mechanisms and the genes involved. Plant transcript levels have been monitored in various accessions of plants to identify ELPs using microarrays, next-generation RNA sequencing, and quantitative PCR technologies, all of which have shown to be effective tools for this purpose. The impact of variation in the transcription of genes and the expression of plant characteristics associated with direct insect defense has been investigated for a number of plant species, including In the case of *A. thaliana*. Aphid performance and glucosinolate concentrations in *Arabidopsis thaliana* could be linked because transcriptional variation in genes involved in the biosynthesis of glucosinolates, which are important defense compounds in the Brassicaceae, could be linked to glucosinolate concentrations and aphid performance[8].

ELPs in herbivore-responsive genes in *Nicotiana attenuata* have also been shown to be associated with the generation of defense chemicals as well as herbivore performance in the plant (Wu et al., 2008). However, it is important to recognise that nearly all of the research conducted to far have been studies that have examined the relationship between gene expression and insect resistance. A critical need exists for studies that provide direct evidence of the participation of specific genes, such as those that use mutants or lines carrying RNAi constructs that knockout gene functions; such studies are urgently required.

ELPs for genes producing proteins involved in the production of plant volatiles that result in variation in the attraction of natural enemies of the attacking herbivore have also been discovered, although with considerably less attention paid to them than transcriptional variation underpinning direct defense. For example, herbivore-induced expression of TPS23 (terpene synthase 23) in a maize variety resulted in the production of the volatile compound (E)- β -caryophyllene, which was found to be more attractive to herbivores' natural enemies when compared to a maize variety that did not induce the expression of TPS23. More recently, researchers discovered that there is heterogeneity in the herbivore-induced expression of genes involved in volatile production across *A. thaliana* populations. A parasitic wasp's discriminative behaviour has been shown to be associated with variations in the emission of the corresponding volatile chemicals from different *A. thaliana* accessions.

1.5 Use of Natural Diversity:

In the bulk of molecular research on plant responses to herbivorous insects, the model plant *Arabidopsis thaliana* is used as a test subject. It is not an agricultural species, but it has been chosen as a model plant because of its user-friendly features, which include a fast generation period and a relatively small genome. There are also many useful instruments available to aid in the conduct of (molecular) genetic studies, including whole-genome microarrays, single-nucleotide polymorphism arrays, and large mutant collections. Columbia-0, the *A. thaliana* accession that is most frequently utilized in plant–insect interaction research, is a good host for a wide range of herbivore species, including ants. As a consequence, investigating this particular *A. thaliana* accession does not result in the discovery of genes or their mechanisms of action in terms of efficient pest bug resistance. However, while there has been some evidence of diversity in resistance to insect herbivores across *A. thaliana* accessions, no significant sources of resistance have been found so far[9].

Using *A. thaliana* as a model organism, researchers hope to get a better knowledge of agricultural pest resistance. This is based on the premise that resistance mechanisms and the genes involved are conserved across species. However, one overlooked danger of transferring information from *A. thaliana* to crops is the possibility of differences in gene function and/or regulation as a result of plant ecology and consequent change in insect pressure, which is not taken into consideration. The plant species *Arabidopsis thaliana* has a very short life cycle (6–7 weeks), which allows it to avoid most insects. As a result, the regulation of a particular gene may be different from that of the homologue of that gene in a plant species that has to deal with many attackers over a much longer growing season, such as the related brassicaceous crop *Brassica oleracea* (6–7 months). Another danger associated with transferring information from *A. thaliana* to crops is the fact that some resistance characteristics are unique to the Brassicaceae and are not found in other plant species, which complicates the process.

As an example, brassicaceous plants generate glucosinolates, which have been shown to have a significant role in insect resistance; however, these chemicals are not produced by any other plant species. In light of these dangers, it is necessary to investigate naturally occurring insect resistance among crop wild relatives, or even among accessions of crop plants themselves, as a way of identifying sources of resistance unique to a plant species and incorporating them into contemporary crop plants. New breeding and selection methods, which have lately been evaluated by others, will improve the effectiveness of breeding programmes by increasing their genetic diversity[10].

2. DISCUSSION

Natural variation in insect resistance may be categorized as either qualitative or quantitative, based on the number of loci that are involved in the variance. Qualitative characteristics are often regulated by a single gene and function according to the gene-for-gene concept. A great deal is known about this form of resistance for plant–pathogen interactions, which involves recognition of an avirulence (Avr) gene product, i.e. effector protein, from the pathogen by a resistance (R) gene product in the host plant, as shown in the literature. As a result of this particular identification, a signal transduction cascade is triggered, which activates plant defenses and leads to

resistance. The presence of a very limited number of single dominant R-genes that confer resistance to phloem-feeding insects has been discovered in a number of different plant species.

These insect resistance genes, like the R-genes against diseases, are part of the nucleotide-binding, leucine-rich repeat (NBS-LRR) family of resistance genes, which also includes R-genes against parasites. There is, however, little information available on the R-genes that participate in plant–insect interactions, in contrast to the gene-for-gene interactions between plants and pathogens, in terms of how their products detect the attacking insect and which downstream reactions are triggered.

We now know which pathways are triggered by R-genes that give resistance to insect herbivores, which provides some insight into how they work. The wheat-hessian fly and medicago-bluegreen aphid interactions seem to be analogous to plant–pathogen interactions in that they both appear to include a hypersensitive response, which is a type of programmed cell death. According to the findings of a recent research, the preservation of cuticle integrity may be an essential component of wheat resistance to the hessian fly infestation. When it comes to resistance to the brown planthopper in rice, it seems to be due to the deposition of callose in sieve elements of phloem to prevent the insect from sucking up phloem sap, while the Vat gene in melon appears to confer resistance via improved sieve element wound repair. The next step will be to better understand the resistance mechanisms that operate downstream of insect R-genes, as well as to discover the insect-derived chemicals (effector proteins) that are responsible for activating the resistance response and that may be present in the insect saliva.

Plant susceptibility genes, in addition to plant R-genes, may be very helpful in the control of pests. Some herbivorous insects have the capacity to reduce the effectiveness of plants' defense mechanisms, which they may use to their own benefit. It is believed that these insects activate certain plant genes, referred to as susceptibility genes, in order to suppress or evade the defense that antagonizes insect performance, resulting in the vulnerability of the host plant to pests and diseases. When it comes to controlling plant-manipulating insects, knockdown of such susceptibility genes may be especially interesting. It has been shown that such a strategy may enhance resistance against certain infections, demonstrating its usefulness in disease management. Consequently, it is important to investigate if the possibility for using susceptibility genes to manage insect pests should be investigated.

In order to achieve increased persistence of resistance mediated by major genes, combining direct resistance with indirect defense characteristics, which may prevent or slow down the breakdown of direct resistance, would be an appealing supplementary approach. Several recent studies, including one conducted on *N. attenuata* plants in their natural environment, have demonstrated that the use of indirect defenses can be effective. For example, a recent study found a significant increase in predation rate following herbivore-induced changes in volatiles released by *N. attenuata* plants in their natural environment. The process of combining these two kinds of resistance may be complicated, but it is expected to result in the development of new combinations of resistance that are more lasting. After all, plants in the wild use both direct and indirect resistance, and pests are very uncommon in the wild as a result. Although a few studies have shown variation in indirect resistance characteristics, such as the impact of HIPVs on the attraction of natural enemies, our understanding of the molecular basis of this kind of resistance is still in its infancy, and further study is required.

Pest management that is long-lasting is typically achieved via a mix of techniques that include biological control and host plant resistance. A strategy that is focused on the integration of various techniques into integrated pest management (IPM) is required, with the components of the system being well-matched. Combining direct and indirect defenses in crops may make a significant contribution to the future development of integrated pest management.

3. CONCLUSION

There seems to be a great deal of diversity in the resilience of host plants to insects. In many plant species, insect resistance has been discovered, which has the potential to increase agricultural yields. However, only a limited number of instances have resulted in the cloning of the resistance gene. This group of R-genes that are efficient against herbivorous insects has been identified as being NBS-LLR type, which is comparable to resistance genes for diseases. However, in contrast to the vast amount of information available on plant–pathogen interactions, little is known about the effector proteins and pathways that are activated by the plant's detection of insects.

Evidence suggests that the downstream effects of R-genes that are effective against insects may vary from the downstream effects of R-genes that are effective against diseases. Genes providing insect resistance seem to be susceptible to being defeated in the same way as R-genes effective against infections are. This appears to be true for genes conferring insect resistance that are selected in agricultural settings. It seems that wild cousins of agricultural species, such as the tomato, have a high level of QTL-based resistance. However, none of these resistances have been successfully transferred into cultivated species, which is most likely owing to the complicated genetics of the cultivated species.

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