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Breeding Approaches for Disease Resistance in Crop Plants: A Review

Shivam Maurya¹*; Mahabeer Singh²; Sunil Kumar¹; Lalita Lakhran¹; Naresh Kumar¹; Satyadev Prajapati¹ ¹Ph.D Scholars, Department of Plant Pathology, SKN Agriculture University, Jobner, Rajasthan, India. ²Professor and Head, Department of Plant Pathology, SKN Agriculture University, Jobner, Rajasthan, India.

*Corresponding Author(s): Shivam Maurya

Ph.D Scholar, Department of Plant Pathology, SKN Agriculture University, Jobner, Rajasthan, India. Email: mauryashivam662@gmail.com

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Abstract

Present day agriculture has disturbed the age-vintage stability of host-pathogen system resulting diseases arise at regular interval leading to significant loss to the agricultural production, that is predicted to be 10-25% or much less in the course of everyday years however might also additionally enlarge as much as 100 % in the course of epidemic. Broadly, there are breeding tactics followed for disease resistance, which incorporates molecular and molecular one. Conventional method consists of pure line, pedigree, backcross, recurrent choice and interspecific hybrids through which numerous resistant sorts were developed. However, after someday there may be surprising outbreak of diseases because of non-stop sowing of those sorts, which ends up with inside the development in molecular biology and with the invention of trait-connected markers, it paved a new pathway to appearance a new nook to expand sorts that are disease resistant. Molecular method includes gene pyramiding through which or greater genes imparting resistance to different varieties of diseases is introgressed in a specific variety, gene deployment and multiline sorts which include heterogeneous populace shaped with the aid of using mixing the cultivars to vary with inside the ability of disease resistance and decreases the charge of epidemic improvement. With the help of makers in marker assisted breeding the usage of foreground, recombinant and historical past choice several linked markers are diagnosed which gives resistance towards disorder like in wheat stem rust, leaf rust etc. With the improvement of greater superior technology transgenic techniques got here into life wherein gene silencing is achieved through RNA, mediated silencing strategies and numerous fungal, viral and bacterial diseases has been controlled.



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Introduction

Disease resistance is regularly described as reduction of pathogen increase on or with inside the plant. It denotes much less disease development in a genotype than that with inside the susceptible range and is a relative attribute. Generally, the price of reproduction is significantly decreased which limits the unfold of disease. Plants are nearly usually proof against certain pathogens however at risk of different pathogens; resistance is typically pathogen species-unique or pathogen strain-unique. The first mentioned work concerning disease resistance is of Theophrastus for the duration of the third B.C. who cultivated varieties differed within side the cap potential to keep away from disorder. Later, de Barry 1861 first mounted the parasitism of stem rust of wheat. Erikson in 1894 confirmed that pathogen morphologically comparable differed from every different of their cappotential to attack different associated host species. But the important milestone got here with the work of Flor in 1956 who gave gene for gene hypothesis. With the time numerous researchers additionally got here and targeted on development of excessive yielding range with adequate grain excellent however to allow excessive yield diseases have to be managed. As we recognize that after a range is launched its location will increase and covers huge location however hence if it new virulent race of pathogen additionally develops and is the bust length for crop for this reason cultivar failure happens and main to heavy economic loss which opens a huge scope for the plant breeder. As we recognize that after a range is launched its location will increase and covers huge location however hence if it new virulent race of pathogen additionally develops and is the bust length for crop for this reason cultivar failure happens and main to heavy economic loss which opens a huge scope for the plant breeder to look for the brand new method to plot concerning this field. One of the powerful way to govern them is find of resistant varieties however earlier than the use of any method to start with one have to recognize at which level diseases are inflicting economic losses and secondly, with the aid of using software of which measures they may be managed. Some of them were managed with the aid of using elimination of its exchange host, volunteer plant or through, chemical biological and cultural practices like bacterial blight of rice but effective control has not been obtained [1].

Conventional breeding

The most effective technique of disease control is using disease resistant plant varieties. This may be particularly costeffective, and growers want now no longer spend some thing to manipulate the diseases. Several genes are involved in conferring disease resistance in plants. Several types of genetic resistance were reported. These resistances are defined here. Epistasis, additive impact, and interactive impact of clusters of resistance genes were reported. Molecular markers related to resistance genes had been evolved and they are now used for choice of resistant plants from segregating populations of crosses. Various strategies of breeding for disease resistance are defined.

Types of disease resistance

Disease resistance may be labeled into fundamental kinds: the host both resists the establishment of a successful parasitic relationship through proscribing the infection site and the contamination process, or it resists the following colonization and reproduction of the parasite following successful contamination. The first kind of resistance affects disease onset through lowering the quantity of effective initial inoculum. The different kind of resistance impacts the plain infection charge and the quantity of disease that sooner or later develops within side the vegetation [2]. The first kind of resistance may be called "vertical resistance," "qualitative resistance," "race-specific resistance," "specific resistance," "major-gene resistance," "monogenic resistance," "whole resistance," or "actual resistance." The resistance is "vertical" due to the fact the resistance is precise to races of the pathogen and is prone to different races (a race is a taxon of pathogens, especially characterised through specialization to distinct cultivars of one host species). The resistance is "qualitative" due to the fact the disease symptom is sort of absolutely suppressed, usually through improvement of a hypersensitive pinpoint fleck reaction. It is called "race-precise/ precise resistance" due to the fact the resistance is precise in opposition to races of the pathogen. It is called "fundamentalgene resistance" due to the fact the resistance is ruled through a major gene. Major genes are genes which have big, wonderful phenotypic expressions displaying clear Mendelian segregation. The resistance is likewise called "monogenic resistance" due to the fact it is ruled by a unmarried gene. It is called "whole/ actual resistance" due to the fact the resistance is expressed through whole suppression of disease symptom improvement. The second kind of resistance is called "quantitative resistance," "horizontal resistance," "race-nonspecific resistance," "nonspecific resistance," "minor gene resistance," "polygenic resistance," "standard resistance," "partial resistance," or "discipline resistance." It is called "quantitative resistance" due to the fact the resistance is primarily based totally on the quantity of ailment symptom improvement, quantified through distinct infection kinds including necrotic flecks, necrotic and chlorotic regions with constrained sporulation, sporulation with chlorosis, plentiful sporulation without chlorosis, lesion size, lesion area, etc. It is called "horizontal resistance" due to the fact this resistance is in opposition to numerous races of the pathogen. It is called "race-nonspecific/nonspecific resistance" due to the fact the resistance isn't always precise to a specific race most effective. It is called "minor gene resistance" due to the fact the resistance is governed through minor genes. Minor genes have small outcomes at the expression of the phenotype for resistance and display quantitative segregation. This resistance is likewise called "polygenic resistance" due to the fact it's miles ruled through numerous genes. It is called "standard/partial/ field resistance" due to the fact this resistance is most effective partial and field tolerant. Although those definitions are attractive, there are numerous exceptions to this extensive classification. Pre-infection elements may also play a function in a few quantitative/horizontal resistance, and sporulation isn't always affected in a few qualitative/vertical resistance [2]. Separate fundamental and minor genes might not exist. Whether fundamental or minor, both type of gene is inherited the identical manner and is able to displaying comparable outcomes. The diploma of expression is changed through environmental contribution to a big extent. Further, what works as a prime gene in a single genetic historical past should paintings as a minor gene in any other historical past. Expression of resistance (fundamental or minor) genes can be stimulated or changed through different resistance genes in a distinct genetic historical past. When many fundamental genes specific together, they characteristic precisely like minor genes. Genetic resistance may also range relying on host age and environmental elements. Seedling resistance works while vegetation are young, and grownup plant resistance works while the vegetation are mature. The wheat stem rust resistance gene Sr25 from Thinopyrum elongatum is incredibly powerful within side the seedling stage of the wheat plant, however loses its effectiveness to some extent in grownup wheat plants which might be close to maturity. The stem rust resistance gene Sr2 is exceptional expressed in grownup wheat vegetation [3]. The modifications in host body structure throughout maturity might have contributed to this kind of resistance. Seedling resistance can be primarily based totally on fundamental genes, while grownup plant resistance is usually polygenic. However, exceptions also are common. Adult plant resistance of the durum wheat cultivar Glossy Huguenot is managed through a single dominant gene [4]. Temperatures may also adjust the expression of a few resistance genes. The wheat stem rust resistance genes Sr6, Sr12, Sr15, Sr17, Sr22, Sr34, and Sr38 are usually greater powerful at temperatures under 20°C. Genes Sr13 and Sr23 usually display greater effectiveness at better temperatures [3]. Two types of resistance genes were recognized: recessive genes and dominant genes. A recessive gene is a gene this is phenotypically take place within side the homozygous state; however is masked within side the presence of its dominant allele or dominant gene. Usually the dominant gene produces a useful product, while its recessive does not. The ordinary phenotype is produced if the dominant allele is present, and the mutant phenotype seems most effective within side the absence of the dominant allele, i.e., while the recessive gene is homozygous. For example, wheat stem rust resistance genes Sr2 and Sr17 are recessively inherited, while all different Sr genes display dominant inheritance [3].

Interaction between resistance genes

Plants are endowed with numerous disease resistance genes. The interaction among those genes might also additionally vary. Epistasis, additive outcomes and interactive outcomes of clusters of resistance genes were pronounced. Epistasis is typically discovered while or extra wheat stem rust resistance Sr genes are gift together. Only the gene conditioning the bottom infection type is expressed. An additive impact of resistance genes is discovered in lots of plants. The wheat stem rust resistance genes Sr7a and Sr12 have been discovered to interact, ensuing in extensively better tiers of resistance than that conferred through both gene appearing alone [3]. An interactive impact of positive genes has additionally been pronounced. A gene conferring resistance to at least one disease might also additionally interact with a gene conferring resistance towards any other unrelated disease and enhance or suppress the movement of the latter gene. Some suppressors that inhibit the expression of applicable resistance genes can be present on chromosomes. Suppressors on chromosomes 1D and 3-d have been pronounced to save you the expression of stem rust resistance genes present on chromosomes 1B, 2B, and 7B in wheat. The wheat cultivar Thatcher and the backcross derivative 'Canthatch' have been susceptible to numerous stem rust races due to a suppressor on chromosome 7DL that inhibited the expression of applicable resistance genes. Thatcher traces owning the leaf rust resistance gene Lr34 have been extra immune to stem rust than Thatcher. In Thatcher and backcross derivatives, Lr34 inactivates the 7DL suppressor [5]. Fast rusting to stem rust turned into pronounced in traces sporting leaf rust resistance genes Lr28 and Lr32, suggesting that those genes would possibly have suppressed the movement of stem rust resistance genes.

Common breeding methods for disease resistance

The most common technique of breeding for disease resistance is pedigree choice. In this technique, crosses are made among parents (one with the resistance trait and some other with precise agronomic traits) and the individual plant life is decided on for resistance from the F2 generation. These choices are allowed to supply seed for the following generation. The choice manner is repeated in every technology, and a better percentage of resistant plant life is acquired in every successive technology till homozygosity is acquired. In the majority populace choice technique, early segregating generations, generally F2 to F5, are bulked collectively without choice. In later generations, while maximum plant life are homozygous, man or woman plant life are decided on for resistance and their progenies are evaluated for resistance as within side the pedigree technique. In backcross breeding, the hybrid derived from a cross among the donor plant (with the resistance trait) and a recurrent parent (susceptible, however with precise agronomic characters) is crossed again to the recurrent parent and the progeny are screened for the disease resistance trait by inoculation with the pathogen or by the usage of molecular markers tagged to the resistance genes. The selected individuals are crossed once more to the recurrent parent and the process is repeated. The selection procedure is repeated in every generation, and as a result, it's far called "recurrent selection." After numerous cycles, plants are acquired which can be almost equal to the recurrent parent, with the exception that genes for resistance were added [6]. The advent of molecular markers enables to overcome main boundaries of backcross breeding. If the gene(s) to be transferred are marked by tightly related molecular markers, segregating populations of plant life may be screened on the seedling stage-earlier than the trait is expressed-for the presence of the resistance genes. Because the molecular markers may be used to mark Quantitative Trait Loci (QTLs) in addition to main genes, there aren't any boundaries to the varieties of resistance that may be manipulated with the aid of using the backcross selection.

Breeding for disease resistance using major genes

Breeding techniques for major gene disease resistance contain identity of resistance genes and incorporating them into high yielding, however susceptible types through pedigree/ backcross breeding. Identification of disease resistance genes is executed with the help of traditional genetic evaluation using easy inheritance studies and tests of allelism. The matching avirulence/virulence check and the gene linkages also are beneficial approach to pick out resistance genes. Several disease-resistant types had been evolved to take advantage of predominant gene resistance. More than forty loci for resistance to wheat stem rust had been recognized and targeted as Sr genes. Most of the targeted Sr genes had been derived from Triticum aestivum. However, some of genes had been derived from different Triticum spp., Secale cereale, and Thinopyrum elongatum. Several cultivars had been evolved the use of those genes. Gene-for-gene hypothesis works some of the predominant gene resistances. According to Flor [7,8] a gene for resistance within side the host corresponds to a gene for avirulence within side the pathogen. No resistance happens until a resistance allele is gift within side the host at the side of a corresponding avirulence gene within side the pathogen [9]. Several races exist in every pathogen, specifically within side the case of biotrophic pathogens, and those races include exceptional avirulence genes. Hence, predominant gene resistance, that's unique in opposition to particular races, breaks down quickly each time new races occur. For example, 239 races of the wheat leaf rust pathogen, Puccinia triticina, were detected from 8 wheat-developing areas of the USA from 1984 to 1999 [10]. Puccinia recondita f. sp. tritici race 104-1,2,3,6,7,9,11 with virulence. Virulence for the wheat leaf rust resistance gene Lr26 have become big in Australia in 1997. This resulted within side the withdrawal from cultivation of the wheat cultivar Mawson, which possesses Lr26. Barley types resistant to the powdery mildew pathogen Blumeria graminis f. sp. hordei had been evolved via way of means of incorporating diverse resistance genes, inclusive of Va6, Va7, Va8, Va9, Va12, Vh, Va3, Va13, and V(Me). Virulences to these kind of genes had been detected within side the populace of the pathogen in Lativia [11]. Breeding for resistance that exploits major genes frequently results within side the evolution of an identical virulence in the pathogen populace, main to an obvious breakdown of resistance. This leads to "boom-bust" cycles, wherein varieties possessing powerful resistance are grown on an increasing acreage (boom) till an identical virulence evolves and spreads in the pathogen populace (bust) [12]. Hence, strong genes, which show resistance to many races, must be used for breeding for predominant gene resistance. The wheat stem rust resistance gene Sr26, that's derived from Thinopyrum elongatum, indicates resistance to all stem rust cultures received worldwide [3]. The wheat leaf rust resistance gene Lr19 shows resistance to the leaf rust cultures collected worldwide, except those from Mexico.

Pyramiding of genes

Combining one-of-a-kind genes in a single plant is called "pyramiding of genes." A pyramid may be built with most important genes and minor genes. Pyramiding different resistance genes right into a genotype will facilitate in growing long lasting resistant varieties. Liu et al. [13] advanced powdery mildew resistant wheat types with the aid of using molecular marker-facilitated pyramiding of various genes. Genes (Pm) for resistance to powdery mildew (Erysiphe graminis f. sp. tritici) have been recognized in wheat at greater than 30 loci. Molecular markers tightly connected to approximately 10 of those Pm genes have been recognized. Three of those genes, Pm2, Pm4a, and Pm21, have been used for marker-facilitated pyramiding. The following is the process accompanied with the aid of using Liu et al[13]. For pyramiding: First, Near-Isogenic Strains (NILs), 'Yang 93- 111' (Pm4a), 'Yang 94-143' (Pm2), and 'Yang 96 (487)' (Pm21) have been advanced with the aid of using six to 9 backcrosses with the local inclined cultivar 'Yang 158' because the recurrent parent. These strains have been proved to consist of Pm4a, Pm2, and Pm21, respectively, with the aid of using synthetic inoculation and with appropriate RFLP markers. The NILs had morphological and agronomic attributes, which might be just like their recurrent parent 'Yang'. To pyramid the resistance, crosses have been made among the NILs, i.e., 'Yang 93-111' (Pm4a) 'Yang 94-143' (Pm2), 'Yang 94-143' (Pm2) 'Yang 96 (487)' (Pm21), 'Yang 93-111' (Pm4a) 'Yang 96 (487)' (Pm21). The ensuing F2 populations have been planted and screened on the seedling stage. A overall of seventy five F2 flowers from cross 'Yang 93-111' 'Yang 94-143' have been obtained. RFLP with the probes BCD1871 and Whs 350 identified fifty-three plants carrying Pm2. Furthermore, RFLP evaluation with probe BCD 1231, confirmed that 39 of those fifty-three plants also carried Pm4a [13].

Mutation breeding

Some disease-resistant varieties had been evolved by mutation breeding the use of physical or chemical mutagens. The wheat range *Sinvalocho gama* in opposition to *Puccinia graminis* f. sp. *tritici*, the oats range Alamo-x in opposition to *Puccinia coronata*, the rice varieties Fulgenate and RD 6 in opposition to *Pyricularia oryzae*, and the bean varieties Universal and Unima in opposition to *Colletotrichum lindemuthianum* have been evolved with the aid of using mutation breeding [14]. Two mutants, I3-forty eight and I3-54, acquired by irradiation with fast neutrons from wheat cv. Hobbit 'sib 'were determined to be significantly greater resistant than Hobbit 'sib' to *Erysiphe graminis* f. sp. *tritici*. Constitutive expression of a thaumatin-like protein gene becomes detected in each I3-48 and I3-54, however not in Hobbit 'sib' [15].

Durable resistance

Durable resistance is resistance that stays powerful in a cultivar this is broadly grown for an extended time frame in surroundings favorable to the disease. Durable resistance can't be recognized at once after or on the time of release of a variety, because it must be grown for an extended time. Durable resistance can't be recognized below greenhouse situations or in experimental station farms due to the fact the crop must be grown in large areas. Durable resistance can probably be recognized primarily based totally on relative overall performance of different cultivars throughout this period. Durable resistance can be a race-nonspecific or horizontal resistance, partial resistance, area resistance, or quantitative resistance. Even a single foremost gene can contribute to long lasting disease resistance. A quantity of Australian wheat varieties carrying the stem rust resistance gene Sr26 derived from Thinopyrum elongatum have remained immune to stem rust on the grounds that 1967, regardless of being grown over a massive area [3]. Sometimes, even partial resistance might also additionally damage down quickly. A wheat cultivar Joss Cambier owning partial resistance to stripe rust (Puccinia striiformis) released within side the United Kingdom in 1969 have become especially susceptible in 1971 because of a new race of P. striiformis.

Multiline mixtures

To avoid speedy breakdown of disease resistance within side the field, multiline cultivars had been developed. Two forms of multilines are used. "Clean crop" multilines are the ones wherein every range accords a wide spectrum of resistance. "Dirty crop" multilines are the ones wherein a susceptible range is purposefully brought within side the multiline aggregate. The susceptible range will lessen the choice stress at the pathogen and retard the advent of latest races. Host combos may also limitation the unfold of a disorder appreciably relative to the suggest disorder stage of the components. Reduction as much as eighty percentage in powdery mildew infection in comparison with the suggest disease stage of the factor grown as natural stands changed into stated in barley. Reduction in disease occurrence can be because of the lower within side the spatial density of susceptible plants. This lower limits the quantity of susceptible tissue in a given area. It additionally reduces the opportunity of survival of spores that depart every parent lesion. Spore density declines exponentially alongside a gradient from the source. Varietal aggregate may also lessen the disease occurrence because of the barrier impact furnished with the aid of using resistant plants that fill the space among susceptible lines. Reduced disease occurrence will also be because of the resistance induced by incompatible pathogenic spores. Induced resistance is usually extra than induced susceptibility. Induced resistance in varietal mixtures could be great. In the varietal aggregate, slower model of the pathogen is not unusual place in comparison to unmarried range cultivation.

Conclusion

Staring from the start of human civilization diseases covers an extended adventure from early man to the modern civilized guy. With the development of lifestyles paperwork and with the change of surroundings numerous diseases have passed off in endemic to epidemic form. Some of the maximum wellknown examples are past due blight of potato, powdery mildew of grapes, Bengal famine, coffee rust and recently a brand new rust has been recognized in Uganda i.e. Ug99 in wheat. These diseases specially passed off in view that formerly focus became given on traditional method, which incorporates mass selection wherein varieties are decided on the idea in their phenotypic performance. Apart from that with the time, different techniques like pedigree, backcross, recurrent selection, interspecific breeding came into existence. But with the development of latest technologies and with the invention of molecular markers it paved a brand new pathway for coming across the disease resistant developments connected to the molecular markers. Thus via the existing take a look at we are able to say that we should not only focus to a selected method for release of disease resistant range as with the time diverse advanced races of pathogens are evolving. So, we need to appearance each corner and corner of the breeding fields and have to take a look at the mechanism in their virulence and then to think for a new goal which fulfill our preference of controlling them effectively.

Conflict of interest

Authors have strong views about the article being submitted for publication and our organization strives to maintain the highest standards of integrity, and it is vital that the authors are confident of our commitment.

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