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RECENT ADAVANCE ON MOLECULAR MECHANISMS OF ABIOTIC AND BIOTIC STRESS: MARKER ASSISTED SELECTIONS

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Abstract: -

Growth in population and climate change possess a challenge to grow crops in the environment of biotic and abiotic stress plants are simultaneously exposed to a combination of biotic and abiotic stresses that limit crop yields or reduced the crop yield under the biotic and biotic stress. Environmental stress conditions such as drought, heat, salinity, cold, or pathogen infection can have a devastating impact on plant growth and yield under field conditions. Both conventional and molecular breeding are used to reduce the stress. The conventional host-plant resistance to various biotic stresses involves quantitative traits at several loci. Markers include physiological and molecular markers for the development of the stress tolerance crop. The advents of molecular genetic technologies have advanced our understanding regarding biotic stress resistance mechanisms. In this review we update the response of plant toward biotic and biotic stress or the function of a specific gene towards improving the performance of a plant against different abiotic and biotic stresses like drought , cold, heat, salt, pests, diseases (fungal, bacterial,) and nematodes have been analysed using transgenic approach. And the method to develop stress tolerance crops through the conventional breeding as well as molecular breeding.

INTRODUCTION

Stress can be defined as an unfavorable state of crop growth and production due to environmental or biological factors, or both of them. Plant responses to a variety of stresses are highly complex, with changes at histological, physiological and cellular levels. Plants activate certain unique stress responses when stressed (Rizhsky,2004). For example, cultivable crops are grown in suboptimal environments, so plants do not fully utilize their genetic potential for growth and reproduction (Bray,2000),(Rockstrom,2000). This can be confirmed by analyzing the difference between the maximum and average yields of the crop. Differences in yield are affected by adverse environmental conditions by inducing a potentially harmful physiological change in the plant called stress (Shao,2008).

Depending on the nature of the effect, stress can be divided into non-biological and biological factors or stress. Harmful effects caused by environmental factors called abiotic stress. Environmental stresses such as heat, cold, drought, salinity and nutrient stress have a significant impact on crops, reducing the average yield of most major crops by more than 50% (Wang,2003). Under natural conditions, the combination of two or more stresses such as drought, salt, and heat, as well as the combination of drought, extreme temperature and high light intensity, are common in many agricultural regions and crops in the world. It may affect production.

Abiotic stress is the pressure caused by damage to plants caused by other organisms (Atkinson,2012). The type of biological stress imposed on plants depends on geographic conditions and climate, as well as the host plant and its ability to withstand specific stresses. The impact of climate change on the size of the habitat of pests and pathogens (Bale.2002,Luck,2011,Madgwick,2011,Nicol,2011). In addition, many abiotic stress conditions have been shown to alter plant defense mechanisms and increase susceptibility to pathogen infection (Amtmann,2008,Atkinson,2012). The habitat of pests and pathogens will be affected by climate change. For example, we know that rising temperatures will promote the spread of pathogens (Luck,2011,Madgwick,2011,Nicol,2011). Therefore, the main crops grown in our farmland in the future may face a wider range of abiotic and biological conditions, as well as the combination of these crops. There is an urgent need to pay attention to the research of plant adversity, understand the nature of adversity response, and look for plant growth methods that can withstand adversity and maintain high yields.

Abiotic stress

Abiotic stress is the negative effect of nonliving factors on living organisms in a particular environment. Abiotic stress is causing crop loss worldwide, which is the main reason that reduces the growth and reproduction of most important crop plants by more than 50% (Wang,2003). Environmental influences such as unstable rainfall and insufficient temperatures, high temperatures, salinity, alkalinity, aluminum toxicity, acidity and gravel have reduced the yields and productivity of many crops. These plants were improved by using traits and traits that give endurance to resist these stresses using traditional and modern breeding methods.

Drought stress

In nature, water is usually a limiting factor for plant growth. This also applies to residential or commercial landscaping. If there is insufficient rainfall or irrigation, the resulting water stress can be slower to grow than all other environmental stresses combined. Water stress is one of the major abiotic stresses in agriculture and one of the major abiotic stresses that limit the productivity of cultivated plants worldwide (Bohnert,1995). This is due to many factors such as rainfall, distribution, evaporation requirements and the ability of soil to store water (Wary,1994). The effects of drought are greater on sandy soils with lower water retention. In such soil, some plants can experience water stress after only a few days in the absence of water. Water stress slows down the rate of photosynthesis (Kawamitsu,2000). Plants have low stomata conductivity to save planted water in drought conditions and reduce freezing carbon dioxide, resulting in less uptake for plant growth and yield. Water stress also causes the effects of chlorophyll components and inhibits plant photosynthesis by damaging the photosynthetic equipment (Ommen,1999).

Establishing a drug-resistant plant strain through traditional methods and genetic production is also an important strategy to meet global nutritional needs for small amounts of water. Cultivation of a crop requires the identification of different genetic variants of precipitation deficiency between plant species or sexes corresponding to the introduction of this resistance in rows with expected agronomic characteristics. In genetic thinking, the process of receiving sedimentation can be divided into three parts. Avoid drying, drying, and drying. Rainwater harvesting, defined as the ability to supplement soil erosion and water scarcity. It is considered to avoid drought stresses in the root system that can drain water into shallow soil or reduce the amount of unaffected fruit air to avoid drying out. Techniques such as osmotic regulation (OA), in which plants undergo cellular turgor stress to reduce water stress, are classified as dry season.

In general drought tolerant pedigree systems and large systems, it is used for frequent training of mixed crops and polluted crops. Hybridization is an appropriate process if the goal is to transfer or transfer certain traits associated with a knockdown interference and highly compatible genotypes. On the other hand, interbreeding between the parents maintains a wide range of genetic structures and allows the production of the genotypes necessary for rain tolerance (Yunus,1982). To give ready marker for breeding community, a systematic molecular validation of notable SNPs distributed across the genome was undertaken (Ravi,2022)

Using traditional methods, breeders have made significant improvements in genetics and summer motility by breeding for seed stability. However, these training programs cannot be postponed. Another option for planting seeds in confined aquatic environments is to identify two factors that contribute to precipitation and choose those characteristics in the program. Secondary properties that contribute to resistance to lack of rain and grain include osmotic repair (OA), skin stabilization, reduced epidermal transpiration, enhanced oral conduction, and stem reserve recruitment (Bray,2000). and phenotypic choices for these powerful and effective traits. For these reasons, the promotion of rain-tolerant genetic

development using secondary donation options is limited. These limitations can be overcome by using the molecular labeling technique.

Biotechnological approaches

There are techniques that help plants withstand drought and these techniques identify and transfer the gene responsible for drought tolerance and factors that lead to drought in the crop plant. Two main methods, targeting and shooting, are used to facilitate the process of genetic engineering to obtain a transgenic plant that is drought tolerant.

- Targeted approach:- Availability of information is essential in this method as it is related to the biochemical reaction for the manufacture and synthesis of metabolites and in this method the relevant genes are used for transmission from related species. Compared to the Venetian method, this method is more accurate and has a higher probability of success (Holmstrom,1996).

Specialized plant metabolites are compounds mixed in a big range of biological functions(Marone,2022).

- Shotgun method: This method of obtaining the required genes is indirect. Random analysis of pressure-related changes in cellular processes and gene expression of two factors. Drought expresses genes. For example, the transgenic rice obtained by this method with the barley *hvaI* gene has proven to be drought tolerant. The *hvaI* gene codes for a set of three LEA proteins (late embryos) that can accumulate in vegetative organs under drought conditions (Dure,1992).
- To create the contrast, we use tissue culture to resist drought (Kavi,1986,Mohmand,1991), but there is a difficulty in choosing the desired and desired alternative, and this causes a restriction in the use of this method.

Salt tolerance

Our earth is a salty planet, most of the water contains about 30 grams of sodium chloride per liter. This saline solution affects the growth of crops or the land on which they may grow. Salt tolerance is a major problem in agriculture around the world, and it is expected to become more serious in the coming decades. To solve this problem, crops must be more salt-tolerant. In this way, crops can grow in surrounding areas that have been affected by salt. The increasing problem of salt tolerance is related to climate change, especially in lowland coastal areas. Inland salt accumulation in agricultural production due to poor drainage has become a growing problem due to the use of excessive irrigation. The water quality is poor, especially in arid and semi-arid areas.

In arid and semi-arid regions, insufficient annual rainfall in agriculture mainly depends on irrigation water. A serious problem of irrigated agriculture is the accumulation of high concentrations of dissolved salts in the soil where plant roots grow normally. The very salty soil in the root zone severely hinders the normal growth and development of plants. Salt tolerance is the main driving force limiting the growing demand for food crops. More than 20% of the cultivated land in the world is affected by salt stress. According to adaptive evolution, plants can be divided into two categories. Salt-tolerant halophytes and salt-intolerant sugar plants eventually die.

Salt-tolerant cultures are complex characteristics affected by many genetic and non-genetic factors, and improvements to them through traditional breeding have been delayed. Recent advances in biotechnology have led to the development of more effective breeding tools to replace phenotypic-based breeding systems.

High salt tolerance requires new genetic resources and more effective techniques to identify salt-tolerant genetic materials. Although new molecular tools for manipulating genetic resources are becoming available, the application of new technologies has not been fully utilized to introduce new genes for growing plants (Munns. 2005). Maintaining food production in irrigated agriculture in many parts of the world requires high salt tolerance of crops, and improving the salt tolerance of crops reduces the need for leaching, thereby reducing irrigation costs. can do. Drain the brine (Munns, 2006). Wheat is a staple food that provides about 55% of the world's carbohydrate consumption. About 95% of the wheat grown in the world is durum wheat, and most of the remaining 5% is durum wheat. In many wheat producing countries in the Indian subcontinent, such as India, Pakistan, the Middle East, Iran, Egypt, and Libya, up to 10% of wheat strips are affected by salt tolerance. The salt tolerance of wheat and many other varieties is related to its ability to eliminate sodium, so there is no high sodium concentration in the leaves, especially the leaves. Durum wheat (*Triticum turgidum*) is particularly sensitive to salt, with high sodium accumulation, low cumulative K+/Na discrimination, and less salt tolerance than bread wheat.

The salt tolerance of wheat is reflected in the growth stage, characteristics and salt content of the plant. The duration of stress, the influence of soil moisture, climate, nutrition and management practices. Several physiological characteristics, such as the selectivity of potassium, the complex orientation of Na + and Cl +, and the change in osmotic pressure caused by the accumulation of organic solutes, are all related to the salt tolerance of wheat crops. The slowdown in wheat growth due to salt tolerance is due to its combined effects on dry matter production, ion relations, water conditions, physiological disorders, biochemical interactions, and all these factors. Most types of wheat also do not respond to salt tolerance. Some varieties have been shown to be very sensitive to salt, while others show a high tolerance to salt (Bhutta, 2015).

Approaches of Salt tolerance

There are three methods of introducing salt tolerance into wheat using traditional breeding techniques of physiological phenotype and marker-assisted selection. The main salt tolerance mechanism is to reduce the salt absorbed by the roots and degrade it at the tissue and cell level, so that no toxic concentration will accumulate in the cytoplasm of the evaporated leaves (Munns, 2005). Traditional breeding greatly supports genetic techniques, such as gene mapping, cloning, functional characterization and the use of markers to select important traits. Microarray-based information and subtractive hybridization and interpretation can be used to study the involvement of genes or metabolic pathways in salt tolerance mechanisms. Advanced technologies of plant salt tolerance mechanisms have been used to identify and transform salt tolerance genes in crop plants including wheat (Shahazad, 2013).

The salt in soil water inhibits plant growth for two reasons. First, it reduces the ability of plants to absorb water, thereby slowing their growth. This is the effect of salt osmotic pressure or lack of water. Second, it can enter the sweat and eventually infect the cells of the sweat leaf, further slowing down growth. This is the effect of certain salts or excess ionic salts (Munns, 2005). Using polymerase chain reaction (PCR) to amplify DNA sequences, random DNA polymorphism analysis (RAPD) molecular marker salt tolerance technology helps to identify plant salt tolerance genes. It requires a small amount of DNA, and can easily identify markers required in many areas of plants, such as genetic maps and genetic diversity. Several biological/genetic and engineering methods can be used to solve the problem of salt tolerance. Therefore, the development of evolutionary/selective salt-tolerant and high-yielding wheat varieties is a potential alternative to solve this problem. This study provides a better understanding of the salt tolerance mechanism and genetic anatomy of wheat (Shahazad, 2013).

COLD STRESS

While the population is growing at an alarming rate, agricultural productivity is falling under the influence of various environmental influences. In particular, cold stress is one of the most important biotic stressors constraining global plant distribution and productivity (Thomashow, 1999). Every plant has an ideal temperature range for its growth and development. The ideal temperature for one crop may work for another. For example, these plants native to warm habitats can develop symptoms of infection when exposed to low temperatures (Lynch, 1990). Plants can experience temperature drops that change the physical properties of the membrane as membrane fluidity is reduced during cold stress (Orvar, 2000). The formation of ice on the outside of the cell membrane reduces the fluidity of the cell membrane, resulting in a negative water balance or a negative water potential. This negative latency means that the cells must respond by removing water from the cells to restore proper water balance. Dehydration occurs when free water from the cell is lost in ice, requiring changes in the cell membrane to maintain swelling (Steponkus, 1984). Various phenotypic responses to cold stress include low germination, stunted growth of seedlings, yellowing of leaves (chlorosis), wilting, reduced tillering, and doping. Cold stress affects the reproductive season of plants and leads to male infertility, which is believed to be a major factor in lower crop productivity (Suzuki, 2008). The main negative effect of low temperature stress is that it causes serious damage to the membrane. This damage is primarily due to severe dehydration associated with freezing during cold stress (Abbasi, 2004). In order to improve the tolerance of plants to the freezing cold, multiple techniques are used, which can be divided into branches: the effect of heat, treatment with chemicals, genetic and cellular engineering. Thermal effect includes low temperature annealing, heat conditioning, medium reinforcement, and heat stress effect. During chemotherapy, cytokinins and ABA were the most potent of all plant growth regulators (Duncan, 1991,Mitchell, 1992). Other non-hormonal growth regulators are also used to improve the cold tolerance of plants (Feng, 2003, S., Ronen, 1994). Some free radicals such as ethoxyquin, sodium benzoate, glutathione, the tyron form, ascorbate, diphenylamine, alpha-tocopherol and gallate are cold resistant by reducing the effects of cold stress or shock (Lukatkin,1997,Xu, 2000). Cellular and genetic engineering is a new direction for creating cold-resistant crops or increasing the cold tolerance of crops and is based on the great genetic diversity of its components, on the one hand, the improvement of susceptibility control and gene transfer. are the technologies in which the desired gene is obtained by harvesting the plant from a cold-tolerant plant, and on the other hand, the signs of transformation and selection (Greaves, 1996). Thus, the study of cells that survived the cooling of the callus, the culture in suspension and subsequent regeneration of the plant made it possible to obtain plants with greater genetic resistance to cooling temperatures (Dix, 1979/ Lukatkin, 1997). Plants adapt to stress by accumulating cold by activating a group of cold-responsive (COR) genes that encode a protective protein responsible for protecting the cell from cold-induced damage (Thomashow, 1999). The best cold-adaptation pathway is the concept of an ICE1-CBF-COR transcriptional sequencing in which C-repeat binding factors (CRT) (CBFs)/drought-responsive elements (DREBs) are rapidly and easily induced by cold, bound regions Inducing COR genes to activate their transcription (Chinnusamy, 2006).

BIOTIC STRESS

Abiotic stress is stress resulting from damage to plants by other organisms, such as fungi, parasites, bacteria, viruses, beneficial and harmful insects, weeds, cultivated or native plants (living or not). It affects high-yield crops (Rushton, 2005). To survive, green plants have developed extensive defense mechanisms against these substances. These defense mechanisms are primarily based on avoidance, resistance, or tolerance. Resistance is the most important defense of plants against pathogens. It is the main focus of agricultural research due to the huge economic losses caused by the severe stress of cash crops. Crop disease losses are a major problem and a major threat to agriculture and food security. To combat and resist these diseases and pests, farmers started using synthetic chemical pesticides, but after a while, scientists discovered that chemical control is not sustainable, and this is because pesticides have a very short shelf life due to pest resistance to these pesticides after a certain period, and this led to the emergence of a negative impact on biodiversity and consumers and farmers due to the excessive and excessive use of pesticides. Pathogen control is primarily achieved through the use of breeding programs for qualitative or quantitative resistance to specific pathogens or through the use of pesticides. Quantitative resistance (QR) is defined as resistance that varies continuously between various phenotypes of the host population, from barely detectable (slight decrease in pathogen growth) to very strong (insignificant pathogen growth). It is the genetic material associated with the wishes of the creator. For breeders of this type of resistance, it is not necessary to search for the original genotype in centers of diversity or wild relatives (Mcintosh, 1997). These are fortunate conditions as they are resistant to adapted varieties and are easier to breed. Genetic engineering provides multiple choices of genes resistant to challenges and is inserted into plants to provide resistance against various biological stresses.

GENETIC ENGINEERING OF PLANTS FOR RESISTANCE TO DISEASES:

Plant diseases cause an annual loss of around 12%, with an increase of 9-20% in the post-harvest period after the adoption of various agricultural practices and pesticides (Agrios, 2004). Plant disease resistance is essential for stable food production and can significantly reduce agricultural use of land, water, fuel and other inputs. Chemical controls used for some diseases are very effective, but are often nonspecific and kill both beneficial and pathogenic organisms (Manczinger, 2002). Various strategies have emerged for the molecular basis of plant-pathogen interactions and the development of pathogen resistant crop varieties (Punja, 2000).

RESISTANCE TO FUNGAL DISEASES

Fungi cause some serious plant diseases such as mold, Botrytis cinerea, rot, downy mildew, and downy mildew. All types of crops often suffer significant losses. Fungal diseases are treated with chemical germicides or heavy metals that pose numerous risks, including adverse environmental effects and increased production costs for farmers, and in some cases conventional farming is used to produce fungal-resistant varieties. After selecting and cultivating cultivated plants based on their desired characteristics, agricultural scientists now use molecular biology and genetic engineering tools to develop genetically modified plants using desired genes (Grover, 2003). The advantage of genetic engineering is that it contains genes that produce resistance proteins of all kinds to all crops in order to improve disease resistance (Van der Biezen, 2001). Defensively sensitive genes have been used to produce genetically modified plants that are resistant to fungi (Grover, 2003). Chitinase, glucanase, and other antifungal genes are used to treat plants that are resistant to fungi. Chitinase hydrolyzes components of chitin, which is the main cell wall component of many fungal pathogens such as Rhizoctonia solan. On the other hand, β-1,3-glucanase degrades glucan in the cell wall of fungi. The synthesis of chitinase and glucanase is known to occur in response to pathogenic infection. When both enzymes are present at the same time, fungal growth is more effectively suppressed (Neuhaus,1999). Antifungal genes were modified to be resistant to fungal pathogens in different crops (Jauhar , 2002/ Sahrawat, 2003). Other proteins are used to prevent fungal infections. For example, polygalacturonase inhibitor protein (PGIP) is a glycoprotein found in the cell walls of many plants that can inhibit the action of the fungal endopol salacturonase (Oelfose, 2006). Polygalacturonase inhibits fungal infections by promoting host cell wall rupture.

RESISTANCE TO BACTERIAL DISEASES

Bacterial infection is of great economic importance in many plant species, including various types of vegetables and fruit trees. Due to the lack of known antibacterial properties, the antibacterial properties of forest species are far from genetic and are not commonly used in conventional breeding programmes, making the production of antibacterial crops impossible. It uses the genes of fungi, insects, animals, and other plants to increase plant resistance to plant pathogens and protect plants from specific pathogens. This protein inhibits bacteria, peptides, and lysozyme commonly found in insects (Jaynes, 1987), plants (Broekaert, 1997), animals (Vunnam, 1997) and humans (Mitra,1994 / Nakajima, 1997) and is now responsible for plant disease resistance.

Antibacterial peptides (AMPs) contain the α-helix system, which is ubiquitous and abundant in many organisms. AMP is distinguished from vacuum cleaners by phagocytosis of frogs, insects, and mammals (Biggin, 1999/ Tossi, 200). Antimicrobial peptides play an important role in protecting plants from infectious diseases. The most notable of these peptides is their unique shape. They have some common functions such as low weight and high cysteine levels that help support the protected scaffold by forming disulfide bonds and can be customized for different structures. Different classes of peptides may act synergistically against pathogens when produced by the same tissue and help expand immunity to a wider range of bacteria (Padovan, 2010).

Antioxidant peptides such as cecropin are found in the lymphatic blood of the large silk moth (Hyalophora cecropia) (Durell, 1992/ Tripathi,2004). These peptides interact and regulate the phosphorylated membranes of Gram-negative and Gram-positive bacteria, producing numerous ion-permeable channels (Durell, 1992). A transgenic tobacco plant that expresses cyclopentex is P. Increased resistance against intravenous administration (Huang,1997). The synthetic hydrolyzing peptide analogs of the shiva-1 and sp-37 transgenic potato are Erwinia carotovora subsp. Sterilized and genetically modified potato plants (Arce,1991). Similarly, transgenic rice plants showing an elevated cecropin B gene X. showed a significant reduction in pest incidence in oryzae pv. oryzae (Coca, 2004). In addition, the expression of the SB-37 soluble peptide analogue in transgenic apple trees was E. showed increased resistance to E. Amelopora (Norelli,1998). In addition, exposure of poplar to D4E1 resulted in resistance to germplasm and Xanthomonas popul (Mentag, 2003, Montesinos, 2007).

Another viral component of Hyalophoracecropia is atatasin (Hultmark, 1983). The mechanism of the antibacterial activity of this protein is to prevent the binding of skin proteins to Gram-negative bacteria (Carlsson, 1998). In potatoes, the attack increases bacterial resistance via bacteria E. Carotobora strains in fact (Arce,1991). The atatasin gene is also expressed by transgenic pears and apples in global warming-tolerant growth (Ko, 1999/ Norelli, 1994/ Reynoird, 1999).

Lysozyme is a whole family of enzymes found in many tissues of humans, animals, plants, bacteria and phages. The lysozyme gene is used to protect against bacterial pathogens in genetically modified plants and plants (Trudel, 1995). Chicken protein lysozyme (HEWL), T4 lysozyme (T4L), T7 lysozyme (Huang,1997), and human and bovine lysozyme are cloned and shipped to improve plant resistance to bacteria or fungi. Theonine is an antibacterial plant protein that can inhibit many bacteria in the laboratory (Molina. Carmona et al., Does P,1993). discuss genetically modified barley and tobacco-derived alpha-thionine cells that promote injection resistance.

RESISTANCE TO VIRAL DISEASES

The most important plant pathogens are plant viruses, and these viruses have emerged as an important factor in reducing yields in horticultural fields and crops. Virus types vary, some viruses colonize hosts, while some viruses infect only one specific species. The presence of a mutation in the viral genome leads to the emergence of various types of viruses, while other types disappear (Jones.2009, Mangrauthia.2008). Viruses lead to infection of the target hosts. In this immune system, the dominant resistance gene (R) interacts with the pathogenic virulence gene (avr). Although it does not prevent pathogens from entering the host, there is also an underlying response, the development of recessive resistance genes, that limits the extent of invasion (Iriti.2007, Ritzenthaler.2005). Genetic engineering also offers an excellent way to protect crops from destructive viral pathogens. Genetic engineering has brought new hope to the development of plant varieties to overcome the various shortcomings associated with traditional breeding (Verma.2001, Beachy1990) colleagues propose that the expression of viral proteins as mutated genes in plants confers resistance to viruses. Transgenic crops that confer resistance to viral coat proteins include rice, potatoes, wheat, tobacco, peanuts and sugar beets. The protein coat approach to resistance engineering has been shown to be widely used on a variety of viruses, including sense, negative sense, single-stranded and double-stranded viruses. RNA virus and at least one nucleic acid virus resistant to the first transgenic plant virus published in 1986 [Powell.1955]. Transgenic plants that primarily produce viral coat proteins by introducing the tobacco mosaic virus (TMV) coat protein (CP) gene into tobacco are more resistant to TMV infection than non-transgenic plants. Papaya ringspot virus (PRSV) is present in different strains and causes huge losses in papaya production in many countries. Resistance to this virus was acquired in high-yield papaya hybrids using viral coat protein sequencing as the transgene (Gonsalves.2004). With this approach, virus resistances can be developed so that it is difficult to develop resistant varieties by better conventional means. Protein replicase is the second most commonly used mutant gene to improve resistance to a virus in cultures, a strategy known as resistance to protein-mediated homology (RPMR) (Goel.1990). RPMR is highly specific, immunogenic more resistant than capsule protein-mediated CPMR), but the molecular mechanism of RPMR is not fully potent. Other proteins, such as functional proteins and proteases, can also be used to improve virus resistance in plant serum. Viral motor proteins (MPs) allow the infection to spread between neighboring cells (cell to cell) as well as throughout the body (over long distances), and expression in transgenic motor proteins is an ideal strategy to generate viral resistance. Factory. Transgenic plants harboring mutant PMVs are resistant to many TMVs in addition to AIMV, cauliflower mosaic virus (CaMV) and other viruses (Cooper.1995). Some viruses, such as Como, Nepo and Potyvirus, use multiprotein strategies for gene expression. Polyprotein processing is a critical step in viral infection that uses polyprotein strategies to prevent cleavage of polyproteins by the expression of defective proteases (Maiti.1993, Vaedi.1993).

EXPRESSION OF PLANT DEFENCE GENES

Plants have their own defense networks against plant pathogens through various proteins and other organic molecules produced before infection or during pathogen attack. Recombinant DNA technology has allowed plants to respond to pathogens using unique dominant resistance genes not commonly found in susceptible plants (Keen.1999) or by selecting plant genes that enhance or activate the expression of existing defense mechanisms (Bent.1999, Rommens.2000). Plant resistance genes (R) were cloned for pathological systems in different plants (Bent.1996). The Bs2 resistance gene in pepper specifically recognizes strains of X. campestris pv and confers resistance to them. vesicatoria contains the corresponding bacterial virulence gene avrBs2 (Tai.1999).

INSECT RESISTANCE

Agricultural productivity is severely affected by pests and diseases, pest populations, especially leaf pathogens (rust, mold, wind, smoke) and some insects by weather events before and during the growing season. Traditional farming methods help botanists develop high-yielding plant varieties. At the same time, these methods are expensive in terms of time, resources and germplasm. In addition, assessments in critical areas are also needed. Spontaneous detection based on hotspot regions sometimes does not provide consistent results. It seems likely that a combination of farming methods is needed to increase yields (Roy.2011). Meanwhile, chemical pesticides are used to control the use of chemical pesticides, which leads to environmental degradation, adverse effects on human health and other organisms, elimination of beneficial insects, and development of insect-resistant pests (Wahab.2009). These limitations of traditional breeding and overcoming these limitations of using chemical pesticides to improve pest resistance through genetic engineering have the potential to bring significant benefits to agriculture (Ferry.2013). With the advent of recombinant DNA technology and successful plant transformation techniques, the first transgenic tomatoes, tobacco and cotton were introduced in 1987 (Umbeck.1987, Vaeck.1987). The weeping gene of Bacillus thuringiensis (Bt) has been widely used to induce insect resistance. Bacillus thuringiensis is a soil bacterium first discovered by Ishwata in Japan in 1901 and Berliner in Germany in 1911 (Baum.1999). It is a Gram-positive bacterium that produces crystallized protein bodies (SCRs) during reproduction. It also produces cytotoxins that increase the activity of exudative toxins. Kaline is toxic to insects, but not to humans and animals (BANR.2000). The weeping venom is classified according to its primary amino acid sequence, with over 500 different Cry gene sequences grouped into 67 groups (Cry1-Cry67). They are globular molecules consisting of three distinct functional domains linked by short conserved sequences. Cry toxin mainly contains two receptors such as cadherin and membrane-anchored proteins such as glycosylphosphatidylinositol (GPI) proteins involved in the action of cry toxin (Gomez.2007). Transfer the Cry protein to related crops to prevent pests. Insects or insects that eat ramie protein dissolve in the center of the digestive tract or the insects are cleaved by digestive proteases. Some of the resulting polypeptides can bind to receptors on epithelial cells in the midgut, leading to cell lysis and eventual insect death (Gahan.2010).

OTHER CANDIDATES GENES

1- Plant protease inhibitors (PI):

Protease inhibitors are classified according to their specificity. Four types have been identified: serine, cysteine, metallic protease and aspartate inhibitors. Among these inhibitors, serine and cysteine (PI) are abundant in plant storage tissues (Reeck.1997) and plant seeds and can aid in the defense system against insects.

2- Lectins:

12 Lectins are a group of non-immunogenic carbohydrate-binding proteins with at least one non-catalytic domain that reversibly binds to specific monosaccharides or oligosaccharides (Peumans.1996). Plant lectins are particularly effective in sucking Hemiptera sap (Powell.1955). Transgenic rice sprouts containing the bell lectin GNA (eye drops) are resistant to brown leafhoppers (BPH) (Nilaparvara lugens) and green leafhoppers (GLH) (Nephotettix virescens) (Yang.1998) and leaf beetle (Empoasca fabae).

3- Alpha-amylase inhibitors:

Alpha-amylases form a family of endo-amylases that catalyze the hydrolysis of α-D-(1→4) bonds in starch, glycogen and other carbohydrate components. Alpha-amylase inhibitors are attractive candidates for seed beetle control because of their strong dependence on starch for energy. Enzymes play an important role in carbohydrate metabolism in microorganisms, plants and animals. Many insects, particularly weevil-like insects, that feed on starchy seeds in the larval and/or adult stages depend on their amylases to survive. Therefore, alpha-amylase inhibitors are attractive candidates for seed beetle control because of their strong dependence on starch for energy (Crosbie.2006).

HERBICIDE RESISTANCE

Herbicides are insecticides used to eliminate unwanted weeds. In other words, herbicides are chemicals that are used to control unwanted plants. The term herbicide refers to plants that have been developed to be resistant to herbicides, either by genetically modified techniques or by selection for resistance to changes in cell or tissue culture. The first drug-resistant, bromomoxinil-resistant plant in the United States, canola-resistant glucosinolate in Canada, was first marketed in 1995. Bromoxinil-resistant plants have been removed from the market, but plants remain glyphosate-resistant such as cotton and cotton wool. Soybeans dominate the communities in which they grow (Schutte.2004).

Vegetation can be managed or managed in several ways, including prevention, crop management, crop rotation, and chemical management. For prevention, use methods to prevent weeds from invading an area, or to prevent overgrown weeds and weeds from spreading to prevent weeds from moving from field to field. Crop management includes agriculture that removes weeds from the field (Walker.1995). Crop rotation is a method of preventing changes in weed control or the frequency of weed changes in people or communities due to agricultural or environmental practices, as well as the management of chemicals, including pesticides. Although this herb is also known as an herbicide, the herbicide does not appear to harm crops and can also be toxic to humans. Therefore, to overcome this limitation, weed-free plant species can be generated using genetic engineering techniques. Evidence from plant genetics (also known as genetically modified organisms and plant biotechnology) around the world is quick and conclusive, and corn, soybeans, canola and cotton are the favorites for these plants. Glyphosate resistance is achieved in transgenic plants through the introduction of EPSPS synthase mutant cells. EPSPS synthase distinguishes between natural phosphophenol pyruvate and glyphosate (Stalker.1985).

MOLECULAR MARKERS

Molecular breeding includes marker-assisted selection, marker-assisted backcrossing, and other new breeding approaches such as repeat marker-assisted selection and genome selection. Use of molecular markers to select plants carrying the desired genomic region involved in the expression of the trait of interest, which are determined by both key genes and QTLs (Choudhary,2008). Drought resistance genes are regulated under drought stress, respond to signal transduction and stress response, and produce appropriate products that help plants withstand drought conditions (Zhou,2010).

MARKER ASSISTED SELECTION (MAS)

Beckmann and Soller used the term "diamond" for the first time (Beckmann.1986). Marker-assisted identification is a tool that helps accelerate the selection of wheat against a variety of abiotic trends. MAS is considered an effective approach to improving tolerance. It can be used with MAS if a closely related marker is detected that reliably predicts the phenotype of a trait. Index-dependent selection validated the utility of different genomic regions of crop plasma in water-deficient conditions. DNA amplified random polymorphism (RAPD), enzyme restriction fragment length polymorphism (RFLP), use of various molecular markers including single sequence repeat (SSR) and amplified fragment length polymorphism (AFLP) facilitate culture and culture. The main issues for DNA markers in MAS are closely related markers (<5 cm(cm)), the quantity and quality of DNA required for MAS, simplicity of the marker analysis process and profitability (Collard.2008). It includes a very diverse system of indicators. Once molecular markers related to performance or other morphological characteristics related to drought tolerance have been identified, these markers can be used as selection criteria for drought tolerance. The application of marker selection to drought-resistant evolutionary genotypes is in the experimental stage. In particular, recognition of RFLP tags related only to osmosis regulation retained its green color and acquired root characteristics.

MARKER ASSISTED BACKCROSS BREEDING (MABC)

Reverse crossbreeding is the most common breeding method used to incorporate one or more important genes into another breed. Marker-assisted backward hybridization is known to improve the efficiency of reverse crossover when the phenotype of the gene of interest cannot be readily determined. Therefore, posterior offspring (BCs) with marker alleles can be selected from donor parents nearby or within the desired gene with a high probability of carrying the gene. Marker-assisted reverse display (MABC) processes are performed at three levels. The first level, known as forward determination, is where the marker is used to screen for a target gene, or QTL (Hospital F.1997). Screening is used to detect recessive alleles, which is time consuming when using traditional screening methods. The second level, known as recombination selection, involves the selection of the crossed offspring that has undergone a recombination event between the adjacent marker and the locus of interest (Ribaut.1998, Salina.2003), and the third level is the maximum value of the paternal repeat genomic region. It is known as background selection, including selection of backcross offspring with. Use of high-density molecular markers from whole genomes (Frisch.1999, Hospital F.1997).

MARKER-ASSISTED GENE PYRAMIDING (MAGP)

In this process, two or more genotypes derived from two or more organ donors are grouped together into a single genotype with a unique character known as the pyramid booster gene. New MABC methods such as MARS and genetic selection have been developed to overcome the weaknesses of MAS.

MARKER-ASSISTED RECURRENT SELECTION (MARS)

When a marker is involved in population selection (A. Gazal.2016), screening and recombination with the goal of increasing the frequency of the preferred allele known as MARS. High-density genomic markers associated with multiple beneficial traits (genes/QTL) of interest were identified from a variety of sources, with selections based on genomic regions involved in the expression of complex traits, most notably in populations. The genotype is formed (Ribaut.2010). MARS allows selection of genetic makeup and episodic level in the first selection cycle for the same growth stage, improving efficiency and accelerating conventional selection (Jiang.2013). MARS is based on the presence or absence of a F2-derived phenol labeling (ie, F4 or F5), followed by F2 or F3 genotyping (to assess manufacturer efficacy), followed by the low QTL marker alleles (Eathington.2007). An applicable recombination cycle is allowed. QTLs are determined from a core population that has been developed by crossing excellent lines. In addition, lines cross with the desired and excellent alleles that are ideal for major QTLs and group those alleles into a single cluster. Phenotypical analysis of strains obtained by interbreeding and selection of superior strains for cultivar development. As a result of MARS compared to MABC, more QTLs large and small are captured to take advantage of larger genetic gains (Bent.2006). Therefore, MARS is an advanced culture procedure to collect the different QTLs that determine the abiotic and biological tolerances of crops (Crosbie.2006, Ragot.2000, Ribaut.2000).

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