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# A Comprehensive Review of Molecular Mechanisms for Biotic and Abiotic Stress Adaptation in Roses

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**Annotation:** The agricultural sector worldwide faces an unparalleled challenge due to the growth of the population and the increasing impact of climate change. Global food production needs to increase by an estimated 60–110% by 2050 for food security, given a world population of about 9-10 billion. [1] This increasing demand is even aggravated by the rise in abiotic stress such as drought, salinity and extremes of temperature, which remain to be serious constraints to agricultural productivity and result in significant loss of arable land [2].

## Introduction:

In this global range, the rose presentation (Rosa spp.), commonly known as the "King of Flowers", is one of special cultural, aesthetic and economic value. The global trade of roses is estimated to be more than USD 28 billion, and the flowers are grown worldwide under field conditions (cut flowers), potted flowers in pots, planters, tubs, boxes, etc., landscape species and bulbs [3]. The economic importance of rose Despite its economic importance, the production of roses is particularly susceptible to environmental changes, and its disability is becoming compromised by climate-induced stress conditions [4].

Rose plants are exposed to a diverse range of abiotic and biotic stresses, which all influence growth, photosynthesis and flower quality. The main abiotic stress factors are drought, saline soil, low temperature and heat stress that interfere with basic metabolic processes like photosynthesis, nutrient acquisition by the roots or homeostasis at cellular levels. [5] At the same time, roses are extremely sensitive to biotic stresses caused by several economically important pathogens such as black spot (Marssonina rosae), grey mould (Botrytis cinerea) and powdery mildew (Podosphaera pannosa), as well as insect pests like aphids and thrips that aggravate yield losses and compromise plant health [6].

Because of climate-changing scenarios in which the frequency and severity of these stressors are predicted to increase, sustainable rugosa rose cultivars need to be developed and can be used to maintain productivity and ornamental quality under stress [7]. Accordingly, the major purpose of this review is to elucidate recent progress in the molecular mechanisms of stress resistance in roses. We specifically aimed to discuss the multi-layer regulatory networks responsible for stress responses in terms of transcriptional regulation, post-translational modification processes, phytohormone signalling and epigenetic control.[8] In addition, we emphasise how new molecular and biotechnological tools are being used to translate basic findings into breeding approaches, day after day, to develop stress-tolerant varieties.[9] It is very important to further understand the environmental and biological limitations that limit the growth of roses to provide a science-based guidance for future breeding programs and sustainable development of rose production systems [10]

**Aim of the Study**

This review aims to systematically gather and critically appraise the available information with regard to the molecular mechanisms underpinning those of R. to respond to biotic and abiotic challenges. Specifically, the review seeks to:

- Recapitulates significant biotic stresses of principal concern to roses (e.g. fungal, bacterial and viral pathogens and insect pests) and the major host defence pathways engaged.
- Explain the response of roses to abiotic stresses (drought, salinity, heat, cold stresses, and heavy metals) and related stress-signalling networks.
- Emphasise hormone signalling pathways (SA, JA, ET, ABA) and crosstalk in stress tolerance coordination.
- Evaluate transcription factor families (WRKY, NAC, bZIP, MYB, AP2/ERF) and stress-responsive genes governing adaptation.
- Describe the role of ROS balance, antioxidant systems, and osmoprotectants as key elements for stress alleviation.
- Examine the recent developments in omics (genomics, transcriptomics, proteomics and metabolomics) which reveal stress related pathways existing in roses.
- Identify and suggest future avenues for breeding and biotechnology, such as marker-assisted selection (MAS), genome editing (CRISPR/Cas) and a transgenic approach to develop stress-resilient rose varieties.

## 2. Literature Review

### 2.1 Biotic and Abiotic Stress in Roses

Roses (Rosa spp.) are among the most economically important ornamental plants worldwide; however, their growth, productivity, and ornamental quality are severely affected by a wide range of biotic and abiotic stresses. These stresses disrupt physiological processes, alter gene expression, and ultimately limit plant performance and market value.[11]

#### 2.1.1 Biotic Stress in Roses and Defence Mechanisms

Biotic stress in roses is due to living organisms such as pathogens and insect pests. Important biotic stresses of roses are fungus diseases (such as powdery mildew; genus Podosphaera or Sphaerotheca pannosa, black spot; Diplocarpon rosae, downy mildew; Peronospora sparsa), bacterial diseases (crown gall disease caused by Agrobacterium species microrganisms) and viral infections such as rose mosaic virus.[12]. Moreover, insect pests such as aphids, thrips, spider mites and beetles induce direct tissue damage as well as favour pathogen entrance.[13].

At the molecular level, biotic stress elicits a convoluted system of defence mechanisms including pattern recognition receptors (PRRs), pathogen-associated molecular pattern (PAMP)-triggered immunity (PTI) and effector-triggered immunity (ETI). The hormone signaling pathways that control these immune responses are salicylic acid (SA) for biotrophic pathogen resistance, and jasmonic acid (JA)/ethylene (ET) for resistance to necrotrophic pathogens and herbivores. The induction of defence-associated genes (e.g. pathogenesis-related, PR proteins) and the buildup of antimicrobial substances are important for control of pathogen spread.[14].

- **Major biotic stresses**

Common rose diseases include:

- ✓ **Powdery mildew** (*Podosphaera pannosa*)
- ✓ **Black spot** (*Diplocarpon rosae*)
- ✓ **Downy mildew** (*Peronospora sparsa*)
- ✓ **Botrytis blight** (*Botrytis cinerea*)
- ✓ **Crown gall** (*Agrobacterium tumefaciens*)
- ✓ Viral complexes (e.g., rose mosaic-related viruses)

Major pests include aphids, thrips, spider mites, and beetles.[11]

- **Stress perception: PTI and ETI**

Plant immunity begins with:

- ✓ **Pattern-Triggered Immunity (PTI):** recognition of PAMPs by **pattern-recognition receptors (PRRs)** → MAPK activation, ROS burst, callose deposition.
- ✓ **Effector-Triggered Immunity (ETI):** recognition of pathogen effectors by **R genes (NLR proteins)** → stronger defence, often linked to hypersensitive response (HR).[7]

- **Hormonal regulation of biotic stress responses**

- ✓ **Salicylic acid (SA):** typically dominates responses to **biotrophic pathogens**; induces PR genes.
- ✓ **Jasmonic acid (JA) & Ethylene (ET):** often regulate defence against **necrotrophy** and **insect herbivores**.
- ✓ Hormone **crosstalk** shapes the specificity and intensity of defence.[15]

- **Defence outputs**

- ✓ Induction of **pathogenesis-related (PR) proteins** (chitinases, glucanases)
- ✓ Strengthening of cell walls (lignification, callose)
- ✓ Production of antimicrobial compounds (phenolics, flavonoids)
- ✓ Activation of systemic resistance pathways [16].

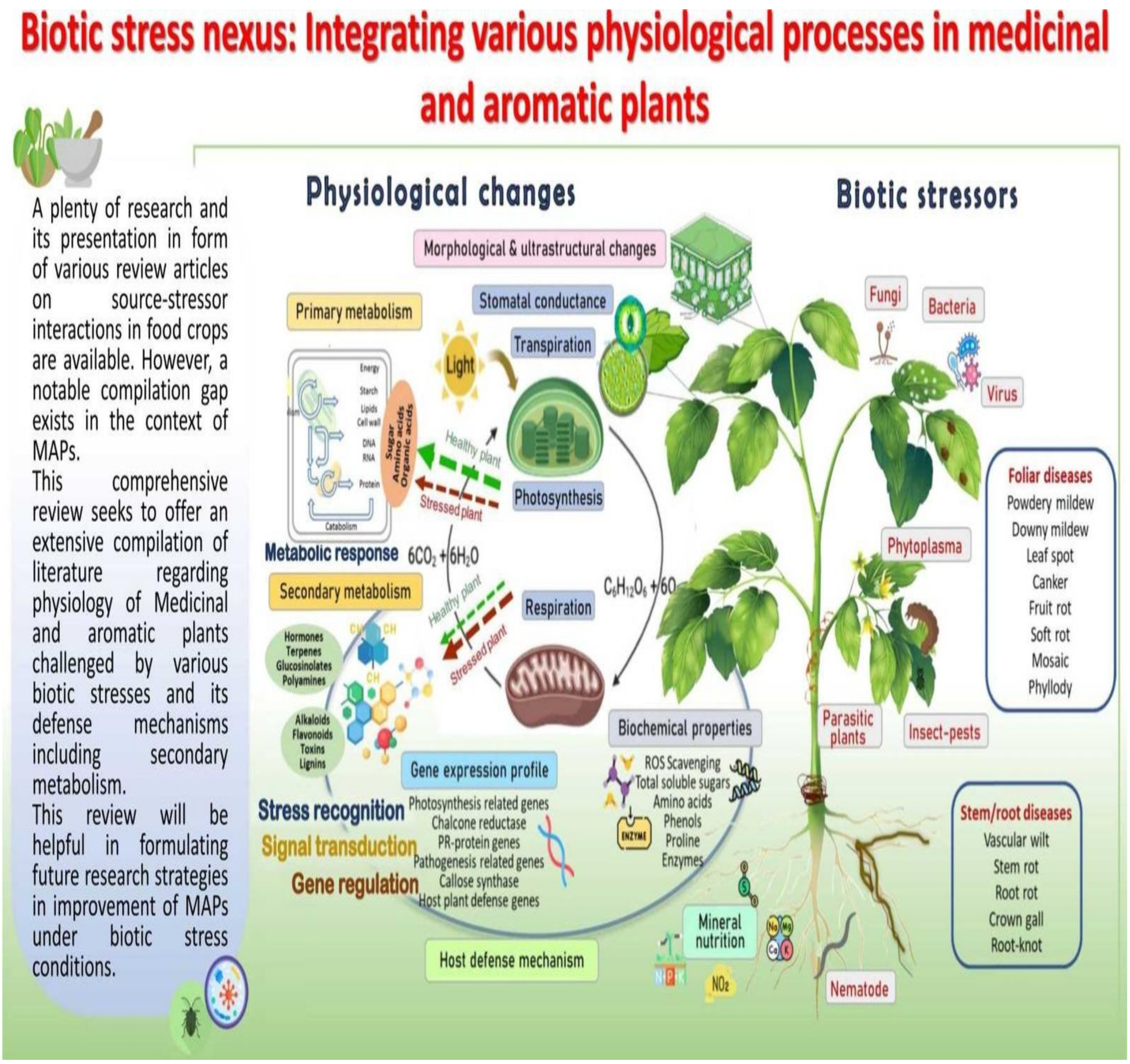


**Figure 1: Biotic Stress in Roses [4]**

### 2.1.2 Abiotic Stress in Roses and Tolerance Mechanisms

Abiotic stress includes adverse environmental conditions that negatively affect the growth and development of roses. Prominent abiotic stress types are drought, salinity, temperature (high-low), heavy metals and oxidative stress. Such stresses interfere with the water relations, photosynthesis, membrane stabilization and uptake of nutrients. [17]. Roses have developed various physiological and molecular defensive mechanisms that are involved in the response to abiotic stress, including osmotic adjustment, stomatal closure, and activation of antioxidant defence systems. At the molecular level, abiotic stress upregulates the expression of stress-responsive genes, which are triggered by major transcription factor families such as DREB, NAC, MYB and bZIP and WRKY. Plant hormones, such as abscisic acid (ABA), are central to the drought and salt stress responses through control of stomatal closure and stress gene expression.[18].

- **Major abiotic stresses**
- ✓ Drought/water deficit
- ✓ Salinity
- ✓ Heat stress
- ✓ Cold/freezing stress

- ✓ Heavy metal toxicity

These stresses affect photosynthesis, membrane stability, enzyme function, and water/nutrient balance.[19]

- ➢ **ABA signalling and stomatal regulation**

Abiotic stress commonly triggers **ABA accumulation**, activating:

- ✓ stomatal closure (reducing transpiration)
- ✓ expression of stress-protective genes
- ✓ stress-responsive protein kinases (e.g., SnRK2-like pathways) [20]

- ➢ **Osmotic adjustment and compatible solutes**

Roses accumulate:

- ✓ **proline**
- ✓ soluble sugars (trehalose, sucrose)
- ✓ glycine betaine (in some species) to protect proteins, membranes, and cellular hydration.[21]

- ➢ **ROS homeostasis and antioxidant defense**

Stress increases ROS ($H_2O_2$, $O_2^-$), requiring:

- ✓ enzymatic antioxidants: **SOD, CAT, APX, GPX**
- ✓ non-enzymatic antioxidants: ascorbate, glutathione, phenolics

Balancing ROS is essential, since ROS also act as signalling molecules.

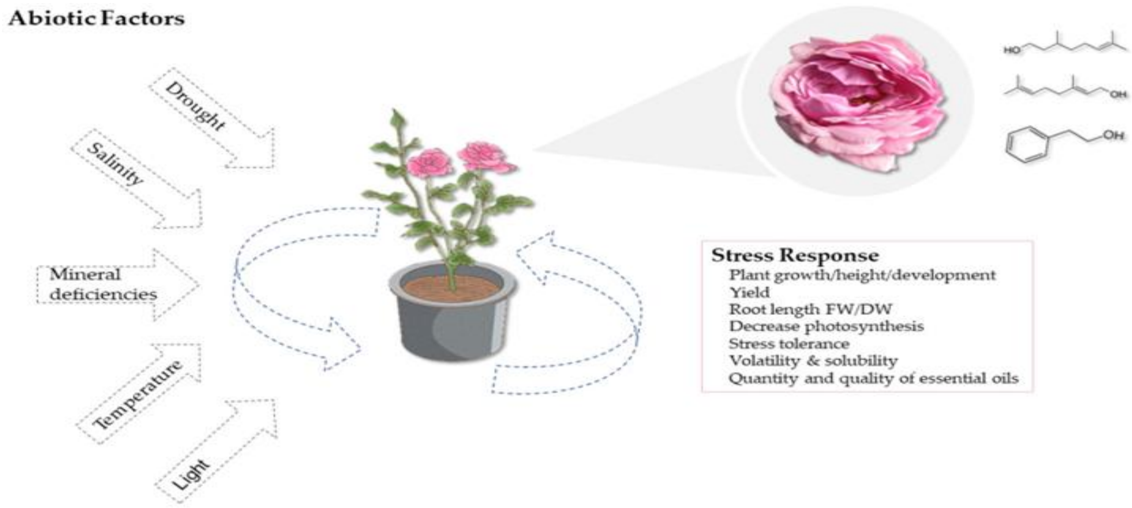


**Figure 2: Abiotic Stress in Roses [8]**

### 2.1.3 Interaction Between Biotic and Abiotic Stress

In nature, roses are frequently subjected to several stresses at the same time, and such stresses interact synergistically or antagonistically. Impairment of plant immunity and increased susceptibility to pathogens can occur due to abiotic stress, while deregulation of plant metabolism and reduced tolerance in harsh environments may be the consequence of biotic stress. [22]. Signal crosstalk (SA, JA, ET and ABA) is a mechanism that synchronizes SA responses to both stress signals and primes plants for optimal resource allocation necessary for survival.[23].

Improved knowledge about the molecular mechanisms associated with biotic and abiotic stress in roses is critical for developing climate-resilient cultivars by using conventional breeding as well as biotechnological strategies that lead to sustainable rose cultivation under shifting environmental conditions.[24].

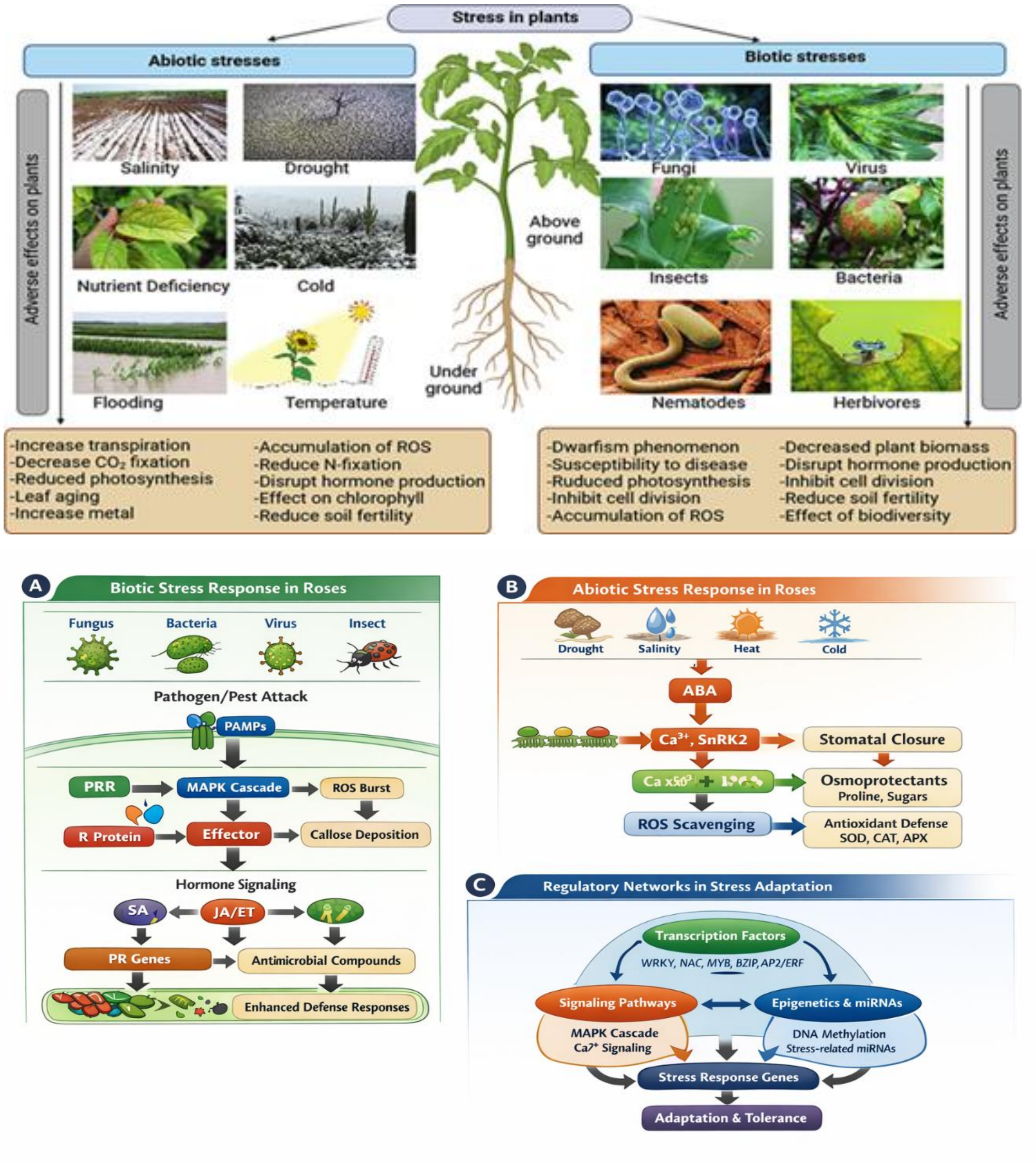


**Figure 2: Effect of abiotic and biotic stress on plants (from the authors' study).**

## 2.2. Omics and Modern Biotechnology in Rose Stress Research

### 2.2.1 Omics approaches

Omics technologies (genomics, transcriptomics, proteomics and metabolomics) together with modern biotechnology are evolving new landscapes in stress-related rose research by enabling the identification of genes, proteins and metabolites that contribute to enhanced abiotic stress resistance such as drought, salinity and high temperature. Such ‘omics' methodologies provide valuable insights for molecular breeding, grafting, and genetic engineering of stress-resistant rose genotypes due to the discovery of regulatory pathways along with phenylpropanoid biosynthesis.[25]

- Multi-Omics Integration: The scientists reveal that, when exposed to high salinity, roses respond in predictable and unique ways based on the combined effects of transcriptome, proteome and metabolome data, identifying specific metabolic pathways (e.g., starch and sucrose metabolism, phenylpropanoid biosynthesis) that are altered under stress.[26]

- Gene Identification & Function: Omics tools can contribute to the identification of novel genes, transcription factors and clusters involved in stress adaptation and clarify mechanisms such as ROS scavenging.
- Rose-Specific Findings: The rose studies of Rosa chinensis and other species have identified specific conserved transcripts and rapidly evolving genes associated with DNA damage repair, as well as responses to environmental cues.
- Breeding applications, the identification of molecular markers useful for the breeding of new genotypes displaying improved ornamental and faster/better adaptation to climate-induced stresses, is supported by these technologies.[27]

### 2.2.2 Breeding and genome editing

- ✓ Marker-assisted selection (MAS) for resistance loci
- ✓ Genomic selection for polygenic stress tolerance
- ✓ CRISPR/Cas for targeted improvement of susceptibility genes or key regulators

Omics technologies (genomics, transcriptomics, proteomics, metabolomics) combined with modern biotechnology are revolutionising rose stress research by identifying genes, proteins, and metabolites that enhance resistance to abiotic stresses like drought, salinity, and heat. These approaches facilitate molecular breeding, grafting, and the development of stress-tolerant rose varieties by uncovering regulatory pathways such as phenylpropanoid biosynthesis.**[28]**

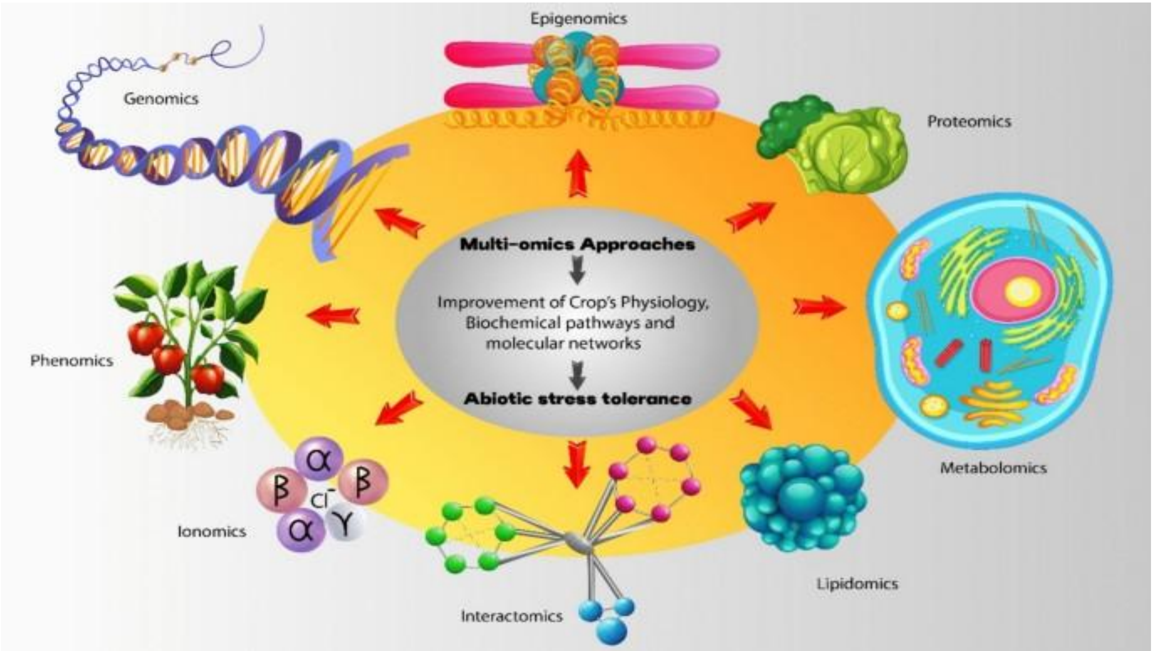


**Figure 3: Role of Genomics, Transcriptomics, Proteomics, Metabolomics, and Phenomics in Improving Crop Performance under Abiotic Stress**

### 2.3 The Exposure to Environmental and Biotic Stressors in Rose Farming

A clear picture of the stressors roses face and their physiological responses is a prerequisite for devising successful strategies to increase resistance. Roses are similar to other plants with a fairly sophisticated set of response mechanisms for dealing with adverse conditions. Nevertheless, the growing severity of these challenges requires a more detailed understanding of physiological trade-offs and defence inductions that take place at the whole-plant level.[18]

### 2.3.1 Abiotic Stressors and Their Physiological Impact

Abiotic stress condition is one of the leading environmental factors that limit plant growth, which has a devastating impact on metabolic integrity by inhibiting critical physiological and molecular systems. The most limiting abiotic factors for the cultivation of roses are:

- Drought and Salinity: They're among the leading threats to global agriculture. Approximately 45% of the arable lands are affected by drought, and salinity has led to a significant decrease in crop productivity, causing as much as 10 50% loss. Abiotic stresses are major constraints to plant growth and development that affect metabolic homeostasis at both physiological and molecular levels. The most limiting abiotic factors in the cultivation of rose are:
- Drought and Salinity: This is one of the gravest threats to global agriculture. Dry lands are affected by the salt concentration present. These stressors in roses they disturb ion homeostasis, photosynthetic efficiency and consequently the growth, yield, as well as overall ornamental value of plants.
- Low / High Temperature: Temperatures outside the optimal range may disturb the metabolic integrity of roses. Cold stress and heat stress both disturb normal cell homeostasis, interrupting nutrient uptake and causing extensive damage from leaf function to flower development.
- Heavy Metal Contaminated Soil: With the extension of industrial activities, such as mining and fertilisers/pesticides applications, heavy metal contaminations have also dramatically increased. Some pollutants including chromium (Cr), cadmium (Cd) and lead (Pb), adversely affect several fundamental developmental processes in plants, such as seed germination, photosynthesis, transpiration, and consequently plant growth, reducing their quality. [29,13]

### 2.3 Biotic Threats to Rose Health and Quality

In natural and artificial environments, roses suffer a variety of biotic stresses due to pathogens and pests. These pests are a threat to plant health and longevity, reducing their aesthetic and financial worth. There are several common biotic threats to the rose, including black spot, powdery mildew, and grey mould. In addition to diseases, insect pests, including aphids and thrips in particular, are highly detrimental to the production of cut and potted roses that inflict direct tissue damage as well as vector viral disease.[30]

### 2.4. Integrated Plant Responses to Stress

In the face of either biotic or abiotic stress, feedback mechanisms are activated in roses, and many physiological responses are generated. These adaptations include the elicitation of defence responses and the controlled decrease of growth-related programs to save resources. This dual response represents the quintessential example of the growth-defence trade-off, in which organisms strategically shift a limited energy budget away from processes associated with growth towards processes promoting their survival.[31]

Upregulation of Defence Mechanism In response to the immediate damage caused by stressors, roses upregulate a variety of defence mechanisms. The activation of Reactive Oxygen Species (ROS) as signalling molecules to induce defence pathways is significantly enhanced. This is followed by a significant induction of antioxidant enzymatic activity in order to neutralise the excessive ROS and avoid oxidative harm. In addition, hormone signal transduction pathways, especially the salicylic acid (SA), jasmonic acid (JA) and abscisic acid (ABA), are largely disturbed to mediate systemic defence response.[32]

Suppression of Physiological Processes. In the effort to reprioritise scarce resources for survival, an organism simultaneously suppresses several essential physiological processes. In general, stress causes stomata to close in order to save water, lowering both photosynthesis and transpiration. The disequilibrium of ions and the uptake of mineral nutrients are generally impeded in plants.

This resource redistribution leads to the reduced root-to-shoot ratio and plant growth/yield, representing a strategic change in plants from growth to survival.[33]

The discussion of stress-related physiological responses in roses paves the way for further examination of the underlying molecular mechanisms that are targeted by pathogens during attempts to counteract host plant defence

**2.4 Molecular Insights into Rose Defence Against Biotic Stress**

Knowledge of the molecular mechanisms' roses use to resist pathogens and pests is crucial in order to design durably resistant cultivars. These defence strategies are not as passive, but rather involve complex hormonal signalling networks, the induction of specific transcription factors and wholesale rewiring of transcription patterns to an extent to fight various classes of invaders.[34].

**2.5 Black Spot Disease (Caused by Marssonina rosae and Alternaria alternata)**

Black spot disease, which is caused by the fungi Marssonina rosae and Alternaria alternata, is one of the deadliest diseases to roses. Molecular level of this response includes intricate regulation and signalling pathway with involvement of hormones, transcription factors, oxidative stress defence mechanisms and whitefly's own genes.[35] An early induction of salicylic acid (SA) followed by a suppression of SA-mediated defence signalling in susceptible cultivars compromises the plant and favours subsequent penetration by the secondary pathogen A. alternata. It is suppressed by this decrease in the SA signaling reducing at the same time JA and promoting pathogen sporulation. The SA and JA pathways are balanced by transcription factors (TFs) such as RcWRKY40 and RcWRKY37, which regulate these responses.[36] Crucially, resistant rose genotypes were shown to have a better capability to homeostasis of ROS. These plants are characterised by the higher activities of antioxidant enzymes and ROS-scavenging-genes expression (MnSOD, Cu/ZnSOD, APX1, APX3, CAT1, POD12, POD31, POD46 and POD73), following the infection. This quick cleansing of ROS correlates inversely with the severity of disease, and is indeed an essential part of resistance.[37].

**2.6 Grey Mould (Caused by Botrytis cinerea)**

Grey mould, the defence disease caused by the necrotrophic fungus B. cinerea, is a devastating rotting and necrosis disease. As with other pathogens, roses use tissue-specific defence responses to counter this pathogen by strengthening a particular barrier according to the location of penetration.[38]

- Epidermal Tissue: Defences: The epidermis is the first line of defence. Resistance is correlated with the enhancement of cuticular wax, and genes (such as CUT1, KCS1 and KCS20) known to be involved in cuticular wax biosynthesis.
- Vascular Tissues Defences: After the pathogen has penetrated the epidermis, vascular tissues become an important front. Here, defence is controlled by MAPK-triggered WRKY transcription factors (RcWRKY22, RcWRKY24, RcWRKY33) which in turn promote pathogenesis-related (PR) gene expression and ROS homeostasis. Simultaneously, JA-responsive pathways such as degradation of the repressor RcJAZ1 and release of MYB transcription factors (RcMYB84, RcMYB123) lead to activation of downstream defence genes.[14].
- SA Pathway Activation: The transcription factor RcTGA1 is a key player in activating the SA pathway in vascular tissues, enhancing the expression of PR genes, and establishing robust vascular immunity against the spreading of the fungus.

**2.7 Powdery Mildew and Insect Herbivory**

Roses have also developed distinct molecular strategies to defend against biotrophic fungi like powdery mildew and piercing-sucking insects such as aphids.[11]

- **Powdery Mildew (Podosphaera pannosa):** Resistance to this devastating disease involves multiple layers of defence, and the exogenous application of salicylic acid (SA) has been shown to reduce infection by enhancing the plant's ability to recognise pathogen-associated molecular patterns (PAMPs). This triggers Pattern-Triggered Immunity (PTI), a foundational layer of plant defence. Specific gene families, such as TCP transcription factors and mildew resistance locus o (MLO) genes, are also integral to the resistance mechanism. MLO genes act as susceptibility factors; therefore, silencing them enhances powdery mildew resistance.[29].

- **Insect Herbivory (Aphids):** Aphid attacks trigger rapid signalling cascades within the plant. These responses begin with intracellular calcium fluxes and phosphorylation events that initiate defense signaling. This leads to the upregulation of genes involved in JA biosynthesis, such as RcLOX12, a key enzyme in the pathway. The activation of these signals culminates in the synthesis of defensive secondary metabolites, which can deter feeding or prove toxic to the insects.

Interestingly, many of the underlying molecular components, particularly transcription factors like WRKYs and MYBs, are not only central to biotic defence but also play pivotal roles in the adaptation to abiotic stress.[33].

- **Transcriptional Regulation:** The Core Machinery of Abiotic Stress Adaptation

At the heart of a plant's ability to adapt to abiotic environmental challenges lies a sophisticated network of transcriptional regulation. Transcription factors (TFs) function as master molecular switches, orchestrating large-scale changes in gene expression. In roses, a coordinated network of multiple TF families allows the plant to fine-tune its response to specific stresses such as drought, salinity, and temperature extremes. While this section discusses these TF families individually for clarity, it is crucial to recognise that they do not function in isolation. Instead, they operate as an interconnected orchestra, integrating diverse signals to produce a response that is both rapid and proportional to the threat. This concept of an integrated regulatory network will be explored in greater detail in the subsequent section.[27].

### 2.8 Engineering the Next Generation of Resilient Roses

The detailed molecular knowledge of stress adaptation pathways in roses provides a powerful toolkit for accelerating the development of stress-tolerant cultivars. By moving beyond traditional, time-consuming breeding methods, modern biotechnology and precision breeding offer targeted and efficient strategies for enhancing rose resilience while preserving their high ornamental value.[17].

**Figure 4: Symptoms of powdery mildew on cereal leaf.**

### 2.8.1 Genetic Mapping and Marker-Assisted Selection (MAS)

Grey mould, the defence disease caused by the necrotrophic fungus B. cinerea, is a devastating rotting and necrosis disease. As with other pathogens, roses use tissue-specific defence responses to counter this pathogen by strengthening a particular barrier according to the location of penetration.

- Epidermal Tissue defences: The epidermis is the first line of defence. Resistance is correlated with the enhancement of cuticular wax, and genes (such as CUT1, KCS1 and KCS20) known to be involved in cuticular wax biosynthesis.
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- SA Pathway Activation: The transcription factor RcTGA1 is a key player in activating the SA pathway in vascular tissues, enhancing the expression of PR genes, and establishing robust vascular immunity against the spreading of the fungus.

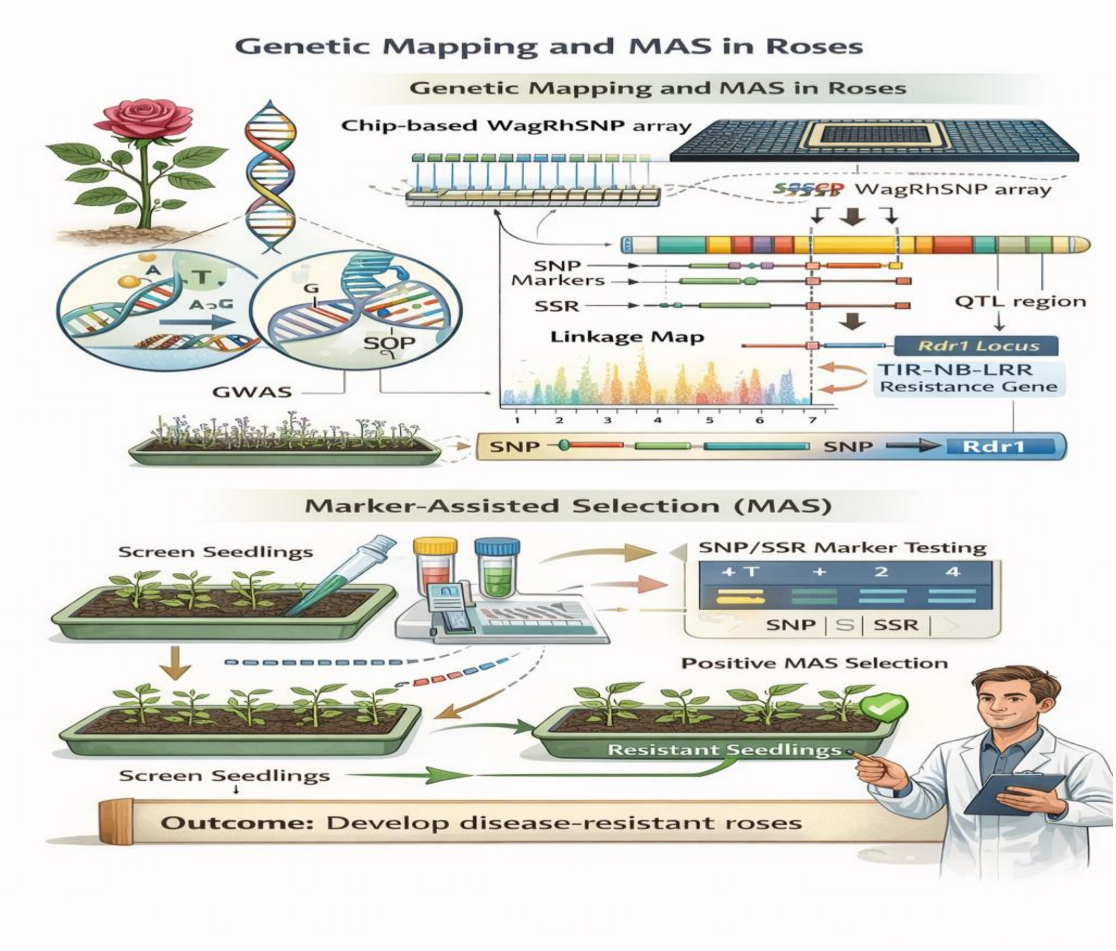


**Figure 5. Application of GWAS and molecular markers for stress-resilient rose breeding.[21]**

### 2.8.2 Functional Genomics and Precision Gene Editing

Although genetic mapping strategies are successful in revealing potential genes related to stress tolerance, functional genomics tools are required to confirm whether these genes have specific roles. In addition, contemporary techniques for genome editing have enabled the targeted modifications of validated genes to make it easier to develop stress-tolerant variants in plants.[34]

### ➢ Virus-Induced Gene Silencing (VIGS)

Virus-induced gene silencing (VIGS) is a powerful technique for the functional characterisation of candidate genes and does not require stable transgenic plant generation. This method uses genetically modified viruses to temporarily inhibit the expression of a target gene, allowing scientists to then study what happens when the gene is turned off or "silenced" in a cell. For instance, enhanced susceptibility to factors such as drought or pathogen infection after silencing of the gene in question constitutes a compelling indication for the contribution of the targeted gene to stress tolerance. VIGS is of particular interest in roses, for which stable transgenesis is still technically difficult, and it constitutes thus a cost-effective high-throughput platform enabling preliminary validation of genes before selection in breeding programs or genome editing.[35].

### ➢ CRISPR/Cas9 Genome Editing

CRISPR/Cas9 genome editing technology has revolutionised the field of plant molecular biology1 by facilitating targeted and specific modifications to genomic loci2. This RNA-guided nuclease creates double-stranded breaks in specific DNA sequences, which are subsequently repaired by cellular DNA repair pathways to produce small insertion or deletion mutations capable of abrogating gene function. CRISPR/Cas9 represents a promising technology for directly modifying traits associated with stress tolerance in rose breeding. [36].The creation of new rose cultivars with high tolerance to drought, salinity and extreme temperatures can be achieved through the manipulation of genes involved in osmotic adjustment proteins, ROS scavenging enzymes or hormonal signalling pathways. Thus, CRISPR/Cas9 could greatly speed up the creation of climate-resilient rose cultivars is a very valuable tool for future ornamental plant breeding.[37].

## 2.9 Conclusion and Future Perspectives

Resistance mechanisms to the complex and combined challenges of biotic and abiotic stresses in roses are an extremely complex biological process regulated through multiple and integrated molecular networks. [38]As summarized in this study, stress resilience in roses is orchestrated by a complex network composed of transcription factors, dynamic phytohormone signalling cascades, rapid posttranslational modifications and stable epigenetic regulation. Advances in plant molecular biology have recently made it possible to identify important regulatory genes and signalling pathways involved in rose drought, saline, cold/hot stress resistance and disease resistance, which present potential molecular targets for breeding of rose stress-tolerant cultivars.[39].

However, despite these landmark successes, there remain several challenges that hinder the appropriate translation of molecular findings to practical breeding applications. One of these is the functional confirmation of the genes-of-interest obtained from high-throughput genomic and transcriptomic studies. Moreover, the use of advanced genetic engineering techniques in roses is limited by the low efficiencies that stable transformation systems present for most species of Rosa, affecting gene functional analysis as well as targeted genome modifications. [40]. In addition, there is a wide distance between work done in well-controlled laboratory scales and that performed in natural or agronomical fields. This stresses the need for in-depth field-based validation, well-defined stress-screening methodology, and multi-environment testing to ensure reliability and relevance of stress tolerance traits.[41].

The sustainability for long-term rose improvement is based on interconnected cycling and integration between gene discovery, functional genomics, and applied breeding tools. This framework is spearheaded by genome-wide association studies and QTL mapping on a broad scale to find new genes and allelic variants that predict stress tolerance amongst different rose germplasm. Subsequently, these candidate genes can be functionally tested at high-speed using reverse genetics tools such as VIGS and CRISPR/Cas9-mediated genome editing. [42].Function analysis of these specific genes will be directly utilised in practical apple breeding through MAS

(Marker-Assisted Selection) in conventional breeding or precision genome editing to regulate gene expression and finally rearrange target traits into elite lines. Taken together, this combination of approaches builds a robust pipeline for breeding climate-resilient rose cultivars that maintain floricultural value over time and have increased stability against the increasing threats of global climate change.[43].

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