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Transcriptome Studies Associated with Disease Resistance in Chilli

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Chilli (*Capsicum annuum* L.) is an economically important vegetable and spice crop, but its cultivation is severely constrained by several diseases such as anthracnose, wilt, leaf curl and powdery mildew, resulting in significant yield losses (Sharma et al., 2018; Meena et al., 2020). Disease resistance in chilli is a complex trait controlled by multiple genes, and conventional symptom-based studies provide limited insight into the underlying defence mechanisms (Dangl and Jones, 2001; Dodds and Rathjen, 2010). Recent advances in sequencing technologies have enabled transcriptome analysis to study global gene expression changes during pathogen attack, helping to identify key genes and pathways associated with disease resistance in chilli (Wang et al., 2009; Mortazavi et al., 2008; Kim et al., 2017). Such studies provide a deeper understanding of plant-pathogen interactions and support the development of disease-resistant chilli varieties, contributing to sustainable crop protection.

Transcriptome responses in chilli plants during disease infection

During disease infection, chilli plants exhibit extensive changes in gene expression that determine the progression of resistance or susceptibility. Transcriptome analysis has shown that pathogen attack induces activation of defence-related genes involved in pathogen recognition, signalling and stress response, while genes associated with normal growth are often suppressed (Liu et al., 2017; Zhang et al., 2018). Differential expression of pathogenesis-related proteins and regulatory genes has been observed in infected tissues, indicating an active molecular defence response. Resistant chilli genotypes display faster and stronger transcriptional activation of defence genes compared to susceptible ones, which helps restrict pathogen multiplication and disease spread (Ashrafi et al., 2018). These transcriptome-level responses explain the internal defence mechanisms operating in chilli plants that are not evident from external disease symptoms. (Table 1).

Progression of molecular defence responses during disease development in chilli

Transcriptome-based studies have shown that pathogen invasion triggers coordinated regulation of defence-associated genes, with the intensity and duration of expression varying as the disease advances (Eulgem et al., 2004). Studies on plant immune signalling networks have demonstrated that resistance depends on fine tuned regulation and coordination of defence pathways rather than mere activation of individual genes (Tsuda and Katagiri, 2010). Sustained and well-coordinated defence responses enable resistant plants to cope with prolonged pathogen pressure, whereas poorly regulated responses often result in enhanced

disease susceptibility. These progressive molecular defence responses ultimately influence disease development in chilli plants as shown in Figure 1.

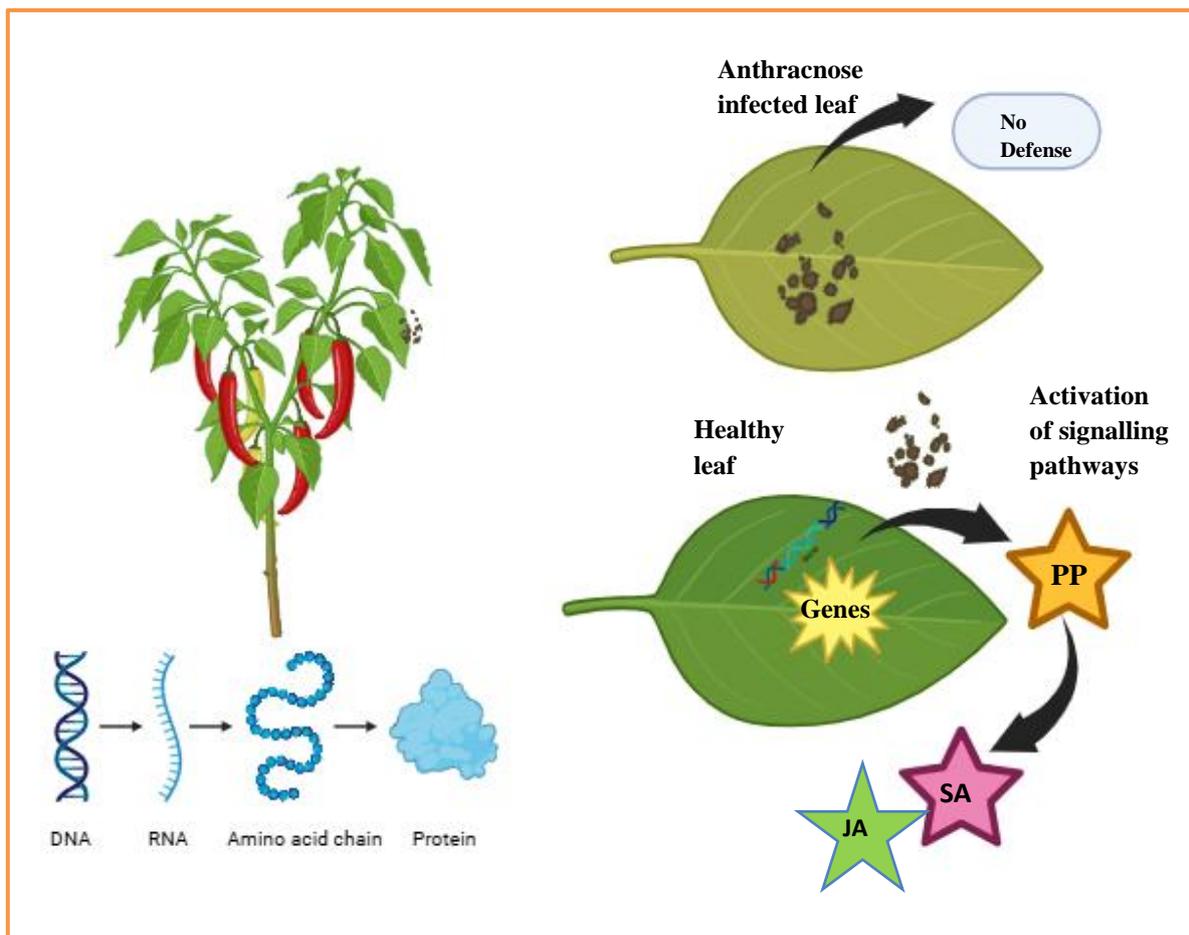


Fig 1: Defense response and activation of signalling pathways in response to diseases in chilli

JA - Jasmonic acid pathway

SA- Salicylic acid pathway

PP - Phenyl propanoid acid Pathway

Transcriptome based strategies for improving disease resistance in chilli

Transcriptome based strategies provide a strong foundation for improving disease resistance in chilli by revealing genes and molecular pathways involved in plant defence responses. Transcriptome analysis helps in identifying resistance-associated genes and stress responsive regulatory mechanisms that differentiate resistant and susceptible chilli genotypes. The genes identified through such studies can be effectively utilized for developing molecular markers, which support marker-assisted selection and accelerate breeding programmes aimed at developing disease-resistant varieties (Varshney et al., 2005; Collard and Mackill, 2008). Integration of transcriptome-derived information with conventional breeding and disease management practices reduces dependence on chemical control measures and contributes to sustainable and environmentally friendly chilli cultivation.

Table. 1 Resistance genes against major diseases in chilli

S. No.	Resistant plant	Disease	Resistant genes	Author
1	B51	<i>Colletotrichum capsici</i> .	ARR-B, bHLH, NAC, WRKY	Wang et al., 2023
2	Bhut Jolokia	<i>Colletotrichum truncatum</i>	Plant defensin 1.2, Lipoxygenase 3, Allene oxide synthase and ACC synthase 2	Mishra et al., 2017

3	<i>Capsicum annuum</i> L.)	<i>Colletotrichum acutatum</i>	CaChiIII7 chitinase	Ali et al., 2020
4	VI037601	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i>	oxidoreductase gene, WRKY and NAC	Gao et al., 2021
5	Sanxiaqing	soilborne diseases (damping off, wilting)	MYC gene (T459_04029), OXII kinase gene (T459_02659), calmodulin gene (T459_22923), and jasmonate ZIM domain-containing protein gene (T459_19535),	Zhang et al., 2021

Conclusion

Transcriptome based studies have significantly advanced our understanding of disease resistance mechanisms in chilli by elucidating complex gene expression patterns activated during pathogen infection. Unlike conventional symptom-based approaches, transcriptome analysis provides a comprehensive molecular perspective of plant defence, revealing key resistance genes, signalling pathways, and regulatory networks involved in determining resistance or susceptibility. The differential and coordinated activation of defence-related pathways such as salicylic acid, jasmonic acid, and phenylpropanoid metabolism plays a crucial role in limiting disease progression in resistant genotypes. Identification of resistance-associated genes through transcriptome profiling offers valuable resources for marker development and accelerates breeding programmes aimed at developing disease-resistant chilli varieties. When integrated with conventional plant pathology, breeding strategies, and sustainable disease management practices, transcriptome-informed approaches can substantially reduce dependence on chemical control measures. Continued advancements in high-throughput sequencing, coupled with functional validation and field-level studies, will further strengthen the application of transcriptome research in chilli improvement programmes. Overall, transcriptome-based insights hold great promise for enhancing durable disease resistance and promoting sustainable chilli production under diverse agro-ecological conditions.

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