

## **Identification And Computational Analysis of Biotic Stress Tolerant Genes from *Piper nigrum* Genome**

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### **Abstract**

Black pepper (*Piper nigrum* L.) is a woody perennial spice crop that is essential for both traditional medicine and cuisine. The major disease 'Quick wilt' that severely threatens *Piper nigrum* is found to be caused by oomycete *Phytophthora capsici*, which affects the leaf, stem, spike, collar, and root. Plants use a wide range of defensive mechanisms to protect themselves against biotic and abiotic stress that includes the accumulation of stress related genes and its respective protein counterparts. Through computational analysis, six biotic stress tolerant genes that belong to TPR motif were identified from *Piper nigrum*. Using MEME, the conserved motifs of stress related genes were found. Predictions based on secondary and three-dimensional structural studies of stress related genes were also made, suggesting a potential functional connection to *Piper nigrum*. Their role in the defense responses was predicted by the GO and KEGG functional annotations. The structural details phylogenetic relationships and conserved sequence motifs of stress related genes were further identified through subsequent computational analysis.

### **Keywords**

Biotic stress, *Phytophthora capsica*, *Piper nigrum*, Quick wilt, TPR motif.