

## Rhizosphere associated antagonistic bacteria as potential candidates for the development of biopesticides

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Rice is an imperative food crop of Pakistan, which is prone to bacterial leaf blight (BLB) caused by *Xanthomonas oryzae* pv. *Oryzae* (Xoo). The disease is destructive in most of the Basmati rice growing areas of Pakistan. The significant damage caused by this disease need the development of strategies to control it with eco-friendly means. Plant growth promoting rhizobacteria (PGPR) are the group of beneficial bacteria that can play a vital role directly or indirectly by decreasing or preventing some of the harmful effects of phytopathogens. For the development of biopesticides for the biocontrol of BLB, antagonistic bacteria have been isolated, characterized and then evaluated in the field. In addition to disease suppression, the selected bacteria significantly increased yield under field conditions. The production of siderophores, hydrogen cyanide and proteases were found to be partly responsible mechanisms for the suppression of causal pathogen. Colonization of antagonistic bacteria was studied under sterile as well as in field conditions using immunofluorescence marker employed in combination with confocal laser scanning microscopy. Development and application of multi-strain formulation for control of BLB was studied in combination with binding agents under Net-House conditions. Mixed inoculum of antagonistic bacteria suppressed the disease incidence more effectively when used as an aerial spray in combination with binding agents. The present studies highlight the significance of using bacterial antagonists with multiple plant growth promoting traits for the biocontrol of plant pathogens like Xoo. These features are being exploited for the development of biopesticides for rice against BLB causing pathogen.

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## A comparative study of gene co-expression network of three economically important crops under drought stress

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The rapid accumulation of microarray data from multiple species provides a new parallel scope to study the evolution of biological systems. Here we present a systematic comparison of gene-co-expression networks between three economically important major crops, namely wheat, rice and maize under water stress to elucidate common mechanisms that are conserved between aforementioned crops, as well as those that are crop specific. We inferred drought responsive co-expression networks from publically available expression arrays to reveal the interactions of drought-responsive genes underlying complex molecular mechanisms among the three species. The largest co-expression network was created for wheat (3321 nodes, 819 066 edges) followed by rice (2471 nodes, 600 155 edges) and maize (1779 nodes, 212 353 edges). A comparison of the co-expression networks of these three species showed that, under drought stress, rice had more signalling genes and comparatively fewer carbon-metabolizing genes than wheat and maize did. Osmoregulation could be a secondary mechanism for drought tolerance in rice because it had the lowest number of osmoregulating genes in its co-expression network among the three species. Of the 17 important drought-specific transcription factor (TF) families in the network, MYB was the most numerous in all, followed, by bHLH, ERF, C2H2, NAC, and bZIP with little variation in connectivity across the three species. The interaction of these genes offered fresh insights in studying the function of drought-responsive genes across species and in identifying the target pathways for improving drought tolerance.

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