

Screening and Evaluation of Plant Growth Promoting Rhizobacteria of Wheat/Faba Bean for Increasing Productivity and Yield

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Abstract : Background and Aims: Legume/cereal intercropping is used worldwide for enhancement in biomass and yield of cereal crops. However, because of intercropping, the belowground biological and chemical interactions and their effect on physiological parameters and yield of crops are limited. Methods: Wheat faba bean (WF) intercropping was designed to understand the underlying changes in the soil's chemical environment, soil microbial communities, and effect on growth and yield parameters. Experimental plots were established as having no root partition (NRP), semi-root partition (SRP), complete root partition (CRP), and their sole cropping (CK). Low molecular weight organic acids (LMWOAs) were determined by GC-MS, and high throughput sequencing of the 16S rRNA gene was carried out to screen microbial structure and composition in different root partitions of the WF intercropping system. Results: We show that intercropping induced a shift in the relative abundance of some genera of plant growth promoting rhizobacteria (PGPR) such as Allorhizobium, Neorhizobium, Pararhizobium, and Rhizobium species and resulted in better growth and yield performance of wheat. Moreover, as the plant's distance of wheat from faba beans decreased, the diversity of microbes increased, and a positive effect was observed on physiological traits and crop yield. Furthermore, an abundance and positive correlations of palmitic acid, arachidic acid, stearic acid, and 9-Octadecenoic with PGPR were recorded in the root zone of WF intercropping, which can play an important role in this facilitative mechanism of enhancing growth and yield of cereals. Conclusion: The two treatments clearly affected soil microbial and chemical composition, which can be reflected in growth and yield enhancement.

Keywords : intercropping, microbial community, LMWOAs, PGPR, soil chemical environment

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