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J Plant Biochem Physiol 2018, Volume 6
DOI: 10.4172/2329-9029-C1-003

6th Global Summit on Plant Science

October 29-30, 2018 | Valencia, Spain

Identification of endophytic bacterial communities in Pakistani wheat

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Wheat (*Triticum aestivum*) is among one of the major staple food, although cultivated world widely but very little is known about the association of endophytic bacteria within the roots, stem and leaves. The main objective of this study was to identify the culturable endophytic bacteria of wheat from roots, stem and leaves and analyze the diversity among different wheat varieties (Punjab 2011, Galaxy 2013-2014, Inqilab 91, Faisalabad 2008, Ujala 2015, TW1312, TW1410, TW1415, 15BT023) grown under the same field conditions. The density of endophytic populations varied from $6x10^7$ to $1.4x10^6$ CFU g^{-1} of fresh weight. Among the total 85 isolated endophytic bacteria, 37.2% were isolated from roots, 35.9% from stem and 26.9% from leaves. Based on 16S rDNA sequences, 32 different strains were isolated comprising of 3 phyla, 5 classes and 12 sub classes. Among these phyla, Firmicutes (44.7%) were most abundant, followed by Proteobacteria (30.6%) while the Actinobacteria (24.7%) were isolated less frequently. The common genera among all the varieties and wheat lines include *Bacillus, Microbacterium, Arthrobacterium, and Enterobacterium*. To access and compare the community structure, diversity indices were calculated. The abundance and level of colonization by SEM (Scanning Electron Microscope) analysis also demonstrated that the endophytes were more abundant in roots as compared to leaves. This study also indicates that the specific wheat varieties may also contribute in the distribution of bacterial endophytes. Future studies will be required to determine the potential application of these isolates in growth promotion, biological control, and enzyme production not only in wheat but also in other commercially important crops to fulfill the food demand and to overcome the rate of poverty.

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