

ENDOPHYTIC BACTERIAL DIVERSITY IN ROOT NODULES OF NATIVE LEGUMES FROM INDIAN THAR DESERT

Nisha Tak¹, Hukam S Gehlot^{1,3}, Julie K Ardley³, Mahender S Rathore¹, Anil K Tripathi², N.S. Shekhawat¹, RaviTiwari³, Wayne Reeve³, Janet I Sprent⁴ & John Howieson³

¹Department of Botany, J.N.Vyas University, Jodhpur-342033, India

²School of Biotechnology, Banaras Hindu University, Varanasi, India

³Centre for Rhizobium Studies, Murdoch University, Murdoch, 6150, Western Australia

⁴Division of Plant Sciences, College of Life Sciences, University of Dundee, U.K

Arid and semi arid regions of the Indian Thar Desert possess several nodulating native legumes important to the local inhabitants for food, fodder, shelter and medicines. These legumes are useful in dry land cultivation and soil improvement for rain-fed crops in arid and semi arid areas. The present study was aimed to characterize the genetic diversity of thirty one root nodule bacterial endophytes strains from *Tephrosia purpurea* and *Tephrosia villosa* growing in Jodhpur and surrounding districts of Rajasthan (India). These two plants are widely distributed in degraded and waste land in the arid and semi arid regions of many states of India. Twenty one isolates from *Tephrosia purpurea* (TP) and ten isolates from *Tephrosia villosa* (TV) were analysed by ARDRA. Based on ARDRA all the thirty one isolates from *T. purpurea* and *T. villosa* were placed into three and two groups respectively. The 16s rRNA gene sequencing was performed. The 16s rRNA gene sequencing results revealed that the various isolates belonged to phylogenetically distant groups such as *Rhizobium*, *Sinorhizobium*, *Bradyrhizobium*, *Ochrobactrum* and *Methylobacterium* from alpha-proteobacteria and *Pseudomonas* from gamma-proteobacteria. Interestingly one of the isolates of *Tephrosia purpurea* (TP1) that was able to nodulate the host and accumulated pink pigment when grown on YEM and TY media. The 16s r RNA gene sequence of TP1 shows high similarity to SR2, a strain isolated from roots of an Indian desert grass (*Lasiurus indicus*) and to the *Methylobacterium* WSM 3686 and WSM 3674, that are novel and as yet not fully characterised symbionts of *Lotononis angolensis*. Both TP1 as well as WSM 3686 and WSM 3674 slowly start accumulating pink pigment with in a week on YEM and TY media. More genomic studies are needed to characterize the new pigmented nodulating rhizobia associated with *Tephrosia purpurea* and *Lotononis angolensis*. The occurrence of *Pseudomonas*, *Ochrobactrum* and other bacterial co inhabitants in the root nodules suggest multiple entries of nonsymbionts into the root nodules of native legumes growing in arid regions. Based on 16s r RNA gene sequences of *Tephrosia villosa* isolates suggest that TV1 and TV3 are *Sinorhizobium teranga*, TV4 is *Bradyrhizobium yuanmingense* and TV11 is *Bradyrhizobium japonicum*. The results of the present investigation will be discussed in relation to similarities in pigmented nodulating rhizobia of *T. purpurea* and *L. angolensis* that are growing in geographically distant continents.

Acknowledgement: Authors acknowledge the financial support from DST-FIST-II, UGC-DSA III Govt. of India and Centre for Rhizobium Studies, Murdoch University, Division of Research and Development, Murdoch University, Crawford Fund ATSE