



GAVIN CONFERENCES

International Conference on Advances in Biotechnology

July 10-12, 2017 Dubai, UAE

Assessing genetic diversity in Tunisian phytoresources and relationship with geographic origin

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In the Mediterranean context and especially taking into account the social reality and the environmental conditions of Tunisia, the effectiveness of research studies are focused on biotechnologies and environment protection. In fact, the molecular markers were used to analyze and estimate the genetic diversity among a collection of forage species as *Medicago Sulla*, *Hedysarum* and *Lathyrus*. These spontaneously widespread species in Tunisia are renowned as salt tolerant species and has a great potential for fodder and/or pastoral development. Molecular technology, agro-morphological characterisation and environmental evaluation are exploited on research studies in order to establish approaches able to protect environment and conservation of well adapted local bio-resources. This work aims to estimate genetic diversity and structure and to identify relationships with geographical origin of local phytoresources. Simple sequences repeats (SSRs), Amplified fragments length polymorphisms (AFLP) and Sequence related amplified polymorphisms (SRAP) markers were used to analyze and estimate the genetic diversity among accessions. Analysis of genetic diversity involved pheno-morphological characterization and molecular relationships could be exploited in breeding programs to improve the damaged arid and semi-arid Mediterranean areas.