OP301

Isolation, Identification and 16S rDna Analysis of *Micromonospora* Bacteria from Van Lake Basin

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Aim of the study: Micromonospora bacteria were isolated from soil and sediment samples of Van Lake Basin. Phylogenetic analysis of species based on 16S rDNA, phylogenetic positions were determined.

Material and Methods: Dilution plate method was used for isolation. As a result of isolation 141 Micromonospora bacteria were purified. Moisture and pH values of sediment and soil samples were determined. according to the color group the purified isolates were divided into 11 color groups. 141 isolates for numerical taxonomy were tested for 83 characters. Phylogenetic trees were constructed according to 16S rDNA analysis.

Results: As a result of the tests applied for numerical taxonomy, a total of 7 major and 15 minor clusters were formed based on 78% similarity rate. In addition, screening electron microscopy (SEM) of isolates are reveal the spore-chain morphology and identified. Maximum Likelihood and Bayesian algorithms were used to determine the genetic distance between species. The species that we thought were micromonospora species clustered in one branch and morphologically in micromonospora were clustered in a different branch.

Acknowledgements: I would like to express my gratitude to Yüzüncü Yıl University, Scientific Research Projects Department for the support given to this project with the 2014-FBE-D092 project.

Keywords: *Micromonospora*, Van Lake Basin, 16s rDNA.