Jordan University of Science and Technology

Exploring the microbial diversity in Jordanian hot springs by comparative metagenomic analysis

Authors: Hussein EI, Jacob JH, Shakhatreh MAK, Abd Al- Razaq MA, Juhmani AF, Cornelison CT.

Abstract: Abstract A culture-independent approach was utilized in this study to reveal the microbial diversity in Jordanian hot springs represented by Ma'in and Afra hot springs. Water samples from Ma'in and Afra hot springs were collected in June 2015. The in situ temperature of water samples range was 38-59?C and the pH range was 7.4-8.4. The metagenome was extracted and analyzed using the next generation technology (bTEFAP?). A total of 314,310 sequences were parsed and 288,452 were then clustered. The sequences were predominated by bacteria (>84%) and the relative abundance of archaea in each sample was <1%. Eukaryotic microorganisms were detected but with varying abundances (0.6%-15%). Because most of the detected sequences were found to belong to the domain of bacteria (196,936 sequences out 288,452), the bacterial sequences were utilized for further microbial analyses. With respect to alpha and beta diversity, samples were rarefied to 30,000 sequences and bootstrapped at 10,000 sequences. The Shannon-Wiener Index curve plot reaches a plateau at approximately 3,000 sequences indicating that sequencing depth was sufficient to capture the full scope of microbial diversity. By examining the relative abundance of phyla detected in each sample, it appears that the biota of both Jordanian hot springs sampled are compositionally similar, with over 50% of the microbial community of each sample being comprised of the phylum Proteobacteria. The second most abundant phylum was the phylum Bacteroidetes which represents more than 13% in each sample. The phylum Firmicutes was also detected with a significant abundance. However, lower abundance of Deinococcus, Verrucomicrobia, Planctomycetes, and Chloroflexi was detected. A principal coordinate analysis plot was generated based upon the weighted UniFrac distance matrix. By utilizing Monte Carlo simulations, we were able to determine that there were no significant differences in the microbial diversity between each sample .