

The international debate on The importance of eDNA as a bioindicator for bacterial biodiversity in Baghdad river

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One of the most critical problems of the 21st century is the continuous ongoing decrease in Earth's biodiversity. Worldwide, wild flora and fauna populations are depleted owing to anthropogenic disturbances and species extinction levels exceed those of pre-human periods which have a significant impact on our planet's human health and sustainability. We focus on Tigris river in Baghdad, Iraq, the second longest river in Western Asia, a length 1,800 km², originates in Armenian Highlands in Turkey, source of water for supplies drinking water, agriculture, industry, domestic water supply and for disposal of sewage. Water samples were collected from gradient area of pollution from November 2018-July 2019. Populations and communities information by collecting DNA from environmental samples (eDNA), defining it as a "complex mixture of genomic DNA from many different organisms found in an environmental sample." This method includes the metabarcoding of the mixed DNA samples of any source, followed by the next-generation high performance sequencing (NGS), using universal polymerase chain reaction (PCR) to determine the species composition of the

sample. In Sample Preparation DNA/RNA is extracted from a sample; qualified samples proceed to library construction. The sequencing library is prepared by random fragmentation of the DNA or cDNA sample, followed by 5' and 3' adapter ligation, then PCR amplified, gel purified and Sequencing. In Generation of Raw Data the Illumina sequencer generates raw images utilizing sequencing control software for system control and base calling through integrated primary analysis software called RTA (Real Time Analysis). 12 phylum of bacteria in result of taxonomy abundance ratio with least in Chloroflexi and Synergistetes (0.01%) with abundance count (3) and highest ratio in Proteobacteria (57.27 %) with abundance count (22,068). In Result of Assembly Total bases (bp) for water sample (by FLASH) was recorded 85,413,665. With Read Count, Total number of reads, for Illumina paired-end sequencing, this value refers to the sum of read 1 and read 2 N (%), GC content (GC %), ratio of bases that have phred quality score of over 20 (Q20 %), Ratio of bases that have phred quality score of over 30 (Q30 %), 186,224, 0.0002, 51.21, 97.45, 91.97 respectively.