

Identification of bioaerosols from environmental samples in the AIST, Tsukuba, Japan

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The bioaerosols are the climate particles, fogs or residue of μm extend, related with metabolically dynamic or dormant suitable particles. They contain living being's incorporated microorganisms, for example, infections, microscopic organisms, and organisms plant material just as dust. Cutting edge Sequencing (NGS) is a novel technique for DNA sequencing that rapidly and productively read the hidden arrangement of a living being by methods for greatly equal sequencing. The point of this investigation is distinguishing life forms which contained in natural examples by utilizing NGS. This examination checked the natural example (bioaerosols) from November 2013 to January 2015 for 50 days utilizing air tests were gathered at AIST, Tsukuba, Japan. Tests were bio-broke down utilizing a cutting edge sequencing strategy. In this examination, we utilized two NGS stage, GS FLX+ (Roche 454 sequencing) and Illumina Miseq. The

example was recognized plants, eukaryotes and microbes. The example was partitioned into two subgroup subgroups as per the size of its bioaerosols, huge subgroup contains bioaerosols whose width is greater than $3.3\mu\text{m}$, and little subgroup contains those littler than $3.3\mu\text{m}$. The most bountiful microorganisms in a few examples were of the Actinobacteria (class), Alphaproteobacteria, Bacilli and Clostridia. For the creature location utilizing inward interpreted spacer 1, in particular uncultured parasites were identified in the greater part of the hits, with a high number of Cladosporium sp. in the examples. For the plant recognizable proof, the ITS1 data just coordinated contagious species. Notwithstanding, focusing of the rbcL district uncovered different plant data, for example, *Medicago papillosa*. All in all, hints of microscopic organisms, parasites, and plants could be identified in the bioaerosols, however not of creatures utilizing those groundworks.