Widespread Hexachlorocyclohexane (HCH) contamination was documented around the premises of the lindane production unit and at one of the major dumpsites used by the unit. Extensive use of HCH as pesticides along with other organochlorine led to the evolution of bacterial strains capable of either tolerating or degrading these recalcitrant compounds. As a result of such high contamination of HCH so observed on alteration of microbial community at these dumpsites. So far microbial diversity at the HCH dumpsite and the impact of HCH on the microbial community structure has been studied only through the use of culture dependent approaches and these studies have revealed the presence of several microbial genera including *Sphingomonas*, *Sphingobium*, *Novosphingobium*, *Sphingopyxis* and *Pseudomonas* predominantly at these locations. Now a days culture independent approach (metagenomics) holds a great promise to explore the microphylla and to assess the functional role played by them at the HCH dumpsites. This can eventually lead to the development of a robust technology for the bioremediation of HCH specifically at the dumpsite. The development of *in-situ* bioremediation strategies at the HCH dumpsite requires a better understanding of microbial community structure and function. In order to achieve this, the approaches that were applied include bacterial Tag-Encoded FLX Amplicon (TEFAP) Pyrosequencing, Illumina and shotgun metagenomepyrosequencing. A relatively high abundance of bacterial (*Chromohalobacter*, *Marinimicrobium*, *Idiomarina*, *Salinosphaera*, *Halomonas*, *Sphingopyxis*, *Novosphingobium*, *Sphingomonas* and *Pseudomonas*), archaeal (*Halobacterium*, *Haloarcula* and *Halorhabdus*) and fungal (*Fusarium*) genera were clearly observed at the HCH dumpsite. The site located one km away from the dumpsite that was suspected to be under impact of human animal waste, showed a comparatively high proportions of *Sarcosphaera* and *Peziza* while the further distant site i.e. the one located five km away from dumpsite showed relatively high proportion of *Trichocladium* and *Oidium*. The genera *Cladilinea*, *Streptomyces* and *Gemmatimonas* were most commonly found at the site five km away, having the lowest HCH contamination.

The phylum distribution showed that the impact of HCH could not alter the higher rank distributions. This may be reason for equal phylum distribution observed at all three sites. The species richness as expected was found to be parallel mirrored by the
rarefaction curves. Dumpsite and the site one km away correlate positively than the correlation observed in the other two sites (one km and five km). By comparing Illumina and Pyro-454 data the microbial diversity so documented was observed to be identical. But due to small read length provided by Illumina platform the data could not be used for SSU typing based approach. 16S rRNA variable region distribution was found to present in all the genera. The genera like *Streptococcus, Blautia, Leptobacillus, Thiothrix, Alistipes, Enterococcus* and *Corynebacterium* were enriched by SSU rRNA approach in comparison to Amplicon based (TEFAP) method. Here it can be explained that the genera which could not show their occurred by the TEFAP approach but later on their presence was seen in rRNA typing, it may be speculated to be as a result of PCR biasness. Thus natural attenuation, a process in which microbial community contributing to the pollutant degradation is already in operation, needs to be monitored in detail by several other parameters like salinity, organic wastes and time. Regarding for rapid degradation of HCH isomers at the dumpsite, the metagenomic data suggests that it may indeed be possible to effectively biostimulate the indigenous bacterial community by application of specific nutrients that would target the productivity of specific taxa. The result clearly indicates that with increase in HCH contamination there is a relative increase in cellular process such as membrane transport, motility/chemotaxis, phage, prophage, transposase, plasmids, and genes associated with membrane transport. This supports the hypothesis that with increasing HCH contamination there is an increase in microbial acquisition at the dumpsite. The data thus suggest a strong HCH degradation potential and lateral transfer of catabolic genes (*lin*) within the indigenous microbial community at the HCH dumpsite.