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LOOKING IN ENVIRONEMNT FOR NEW ENZYMES AS A TOOLS FOR BIOCATALYSIS AND BIOREMEDIATION

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Abstract

Bacteria during evolution created enormous biodiversity enabling them to spread around the whole planet. Up to date, due to lack of technologies, bacterial biodiversity has not been deeply explored. Lately developed methodology comprising metagenomics and second generation sequencing opened opportunity to analyze biodiversity as well as whole genomes of bacterial communities thriving in different (sometimes extremely contaminated) environments. We have build library of one hundred metagenomic DNA isolated from different environments mainly soil highly contaminated with xenobiotics eg. pesticides. Biodiversity analysis based on 16S rRNA genes showed correlation between bacterial community composition and level as well as character of chemical pollution. Up to date four samples of metagenomic DNA have been analyzed by deep sequencing to determine their potential as a source of new enzymes suitable for biodegradation or biocatalysis. Gene assembly and bioinformatic analysis gave almost 2 mln contigs longer than 150bp, with largest contig 332 kb. Anotation of identified ORF's on KEGG and SEED databases exhibit that 11% of their number might be involved in xenobiotic degradation processes.

Despite lower O.T.U number and species richness observed in metagenoms from soils contaminated with chloroorganic pesticides, those samples exhibit 5 times more different genes involved in metabolism of aromatic (xenobiotic) compounds.

To explore this plethora of potential enzymes we are developing strategy for highthroughput protein expression and purification. This will allow us perform functional analysis of new enzymes identified in metagenoms, and fish catabolysts of high practical importance for bioremediation and biotransformation.