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Genome analysis of crude oil degrading *Franconibacter pulveris* strain DJ34 revealed its genetic basis for hydrocarbon degradation and survival in oil contaminated environment

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ABSTRACT

Franconibacter pulveris strain DJ34, isolated from Duliajan oil fields, Assam, was characterized in terms of its taxonomic, metabolic and genomic properties. The bacterium showed utilization of diverse petroleum hydrocarbons and electron acceptors, metal resistance, and biosurfactant production. The genome (4,856,096 bp) of this strain contained different genes related to the degradation of various petroleum hydrocarbons, metal transport and resistance, dissimilatory nitrate, nitrite and sulfite reduction, chemotaxy, biosurfactant synthesis, etc. Genomic comparison with other *Franconibacter* spp. revealed higher abundance of genes for cell motility, lipid transport and metabolism, transcription and translation in DJ34 genome. Detailed COG analysis provides deeper insights into the genomic potential of this organism for degradation and survival in oil-contaminated complex habitat. This is the first report on ecophysiology and genomic inventory of *Franconibacter* sp. inhabiting crude oil rich environment, which might be useful for designing the strategy for bioremediation of oil contaminated environment.

Keywords: Crude oil, *Franconibacter*, petroleum hydrocarbons, Genome sequence, Comparative genomics