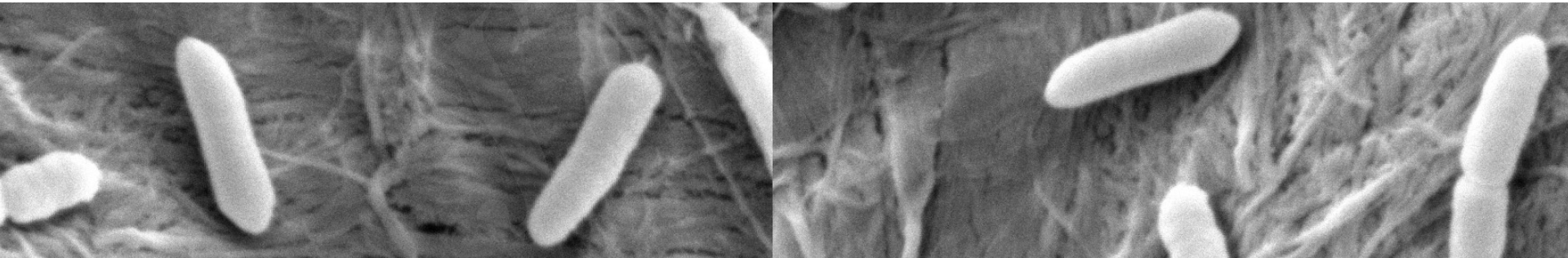


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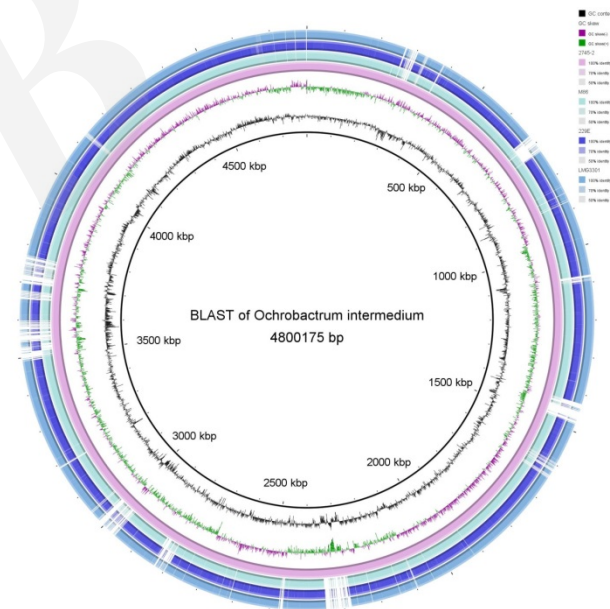
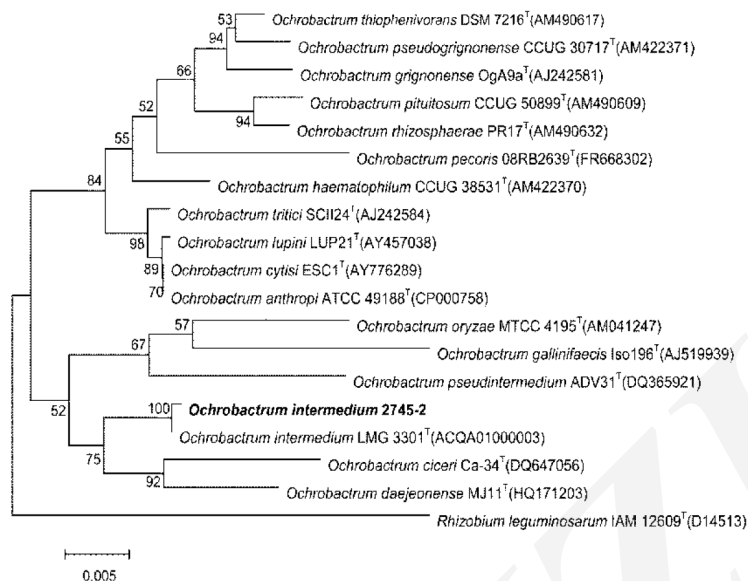
# Isolation and characterization of a crude oil degrading bacteria from formation water: comparative genomic analysis of environmental *Ochrobactrum intermedium* isolate versus clinical strains



**Key words:** *Ochrobactrum intermedium*, Oil degradation, Comparative genome, Pathogen

# Research Summary

The study was focused on the bacterium *Ochrobactrum intermedium* 2745-2  
**Phylogenetic characteristics & Genome properties & Comparative genomic analysis**



Attribute	Value
Size (bp)	4,800,175
G+C content (bp)	2,766,132
Coding region (bp)	4,145,190
Total genes	4,797
RNA genes	60
Protein-coding genes	4,737
Genes assigned to COGs	4,285

# *Innovation points*

Crude oil degradation related proteins are coded in the genome of strain 2745-2

P450

2-polyprenylphenol hydroxylase

N-acyl-L-homoserine lactone synthase

phosphomannomutase

alkaline phosphatase

dTDP-glucose 4, 6-dehydratase

alcohol dehydrogenase

glycosyl transferase

acyl transferase

rhamnosyltransferase

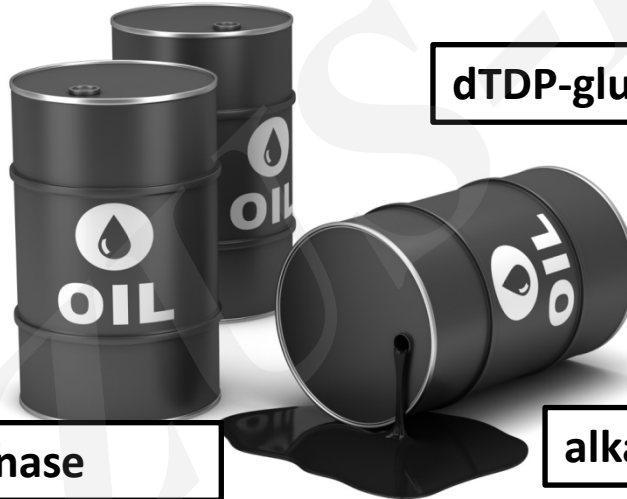
2-haloalkanoic acid dehalogenase

alkane 1-monooxygenase

glucose-1-phosphate thymidyltransferase

dTDP-4-dehydrorhamnose 3,5-epimerase

dTDP-4-Dehydrorhamnose reductase



# Innovation points

## Pathogen potential of strain 2745-2

Region	Region length	Completeness	CDS	Specific keyword
1	51kb	intact	47	terminase,portal,plate,tail
2	10.3kb	incomplete	16	tail
3	35.3kb	questionable	32	integrase,terminase,portal,head,capsid
4	40.1kb	questionable	54	terminase,portal,head,capsid,tail
5	15.5kb	incomplete	20	terminase,capsid,head,tail

