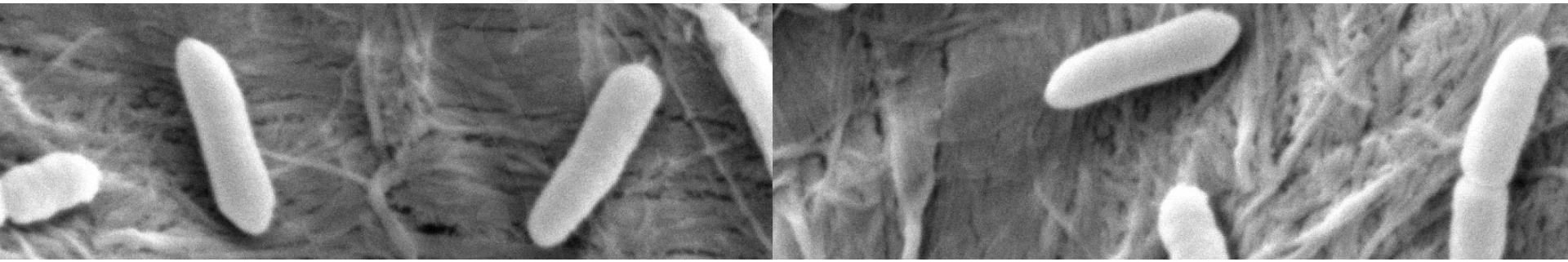
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Isolation and characterization of a crude oil degrading bacteria from formation water: comparative genomic analysis of environmental *Ochrobactrum intermedium* isolate versus clinical strains

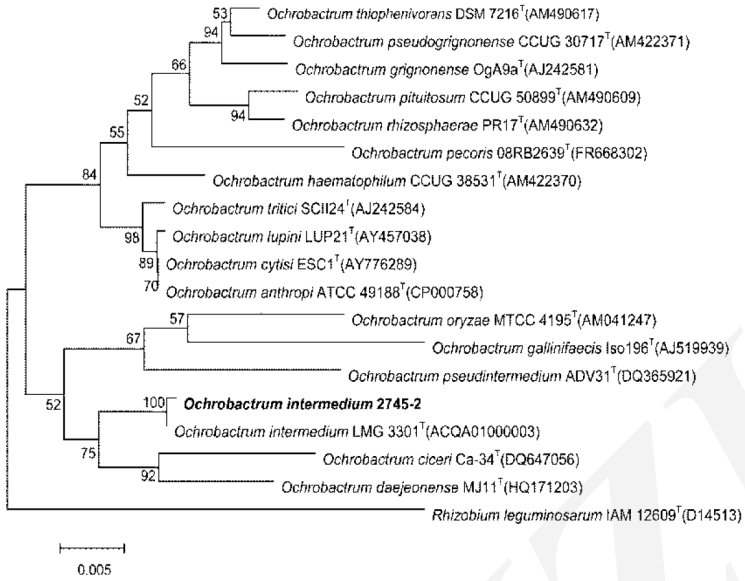


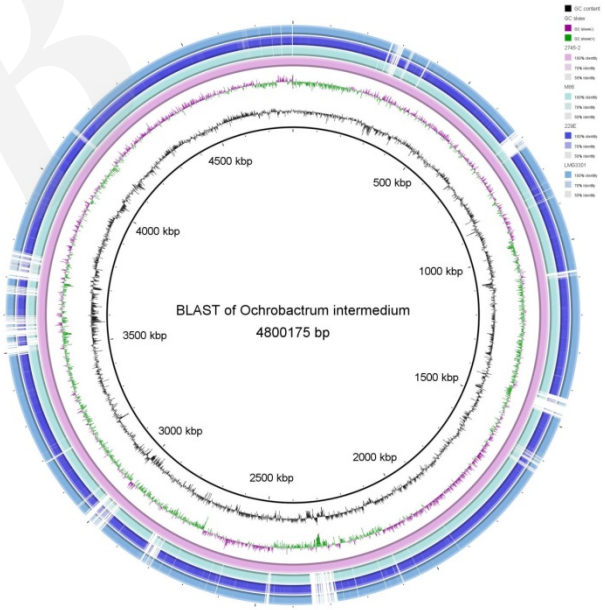
Key words: *Ochrobactrum intermedium*, Oil degradation, Comparative genome, Pathogen

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 thymidylyltransferase
- 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

