

## Genomic potential of a new genospecies of oligotrophic *Agrobacterium* strain isolated from deep within Lechuguilla Cave, New Mexico

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The isolation and whole genome sequencing of *Agrobacterium* strains from various distinct environments highlights the metabolic flexibility and adaptive nature of members from this genus. *Agrobacterium* sp. LC34 was isolated from a deep subsurface (- 400 m), ultraoligotrophic site in Lechuguilla Cave, New Mexico, USA. Whole genome sequencing revealed a distant relationship to currently described and/or sequenced type species of *Agrobacterium* strains. Genome mining coupled with phylogenomic analysis identified two host-associated bacterial strains e.g. *Agrobacterium* sp. SUL3 and *Rhizobium* sp. Root65, belonging to the same genospecies (average nucleotide identity of > 97%) as strain LC34. Cave isolate strain LC34 has the smallest genome size (5.6 mb) followed by strains Root65 (5.8 mb) and SUL3 (6.0 mb). Comparative pangenome analysis of these three *Agrobacterium* strains identified 4,275 core genes (77.5 % – 81% of total predicted genes), with between 484 – 1,266 unique genes in each strain. Unique genes in each strain were further annotated using the **F**unctional **O**ntology **A**ssignments for **M**etagenomes hidden markov model (FOAM) database. Interestingly, proteins related to nucleotide metabolism and mineral and phosphate transportation appears to be enriched in the unique proteome of strain LC34, suggesting the importance of these pathways in adaptation of the stringent growth regarding low carbon availability indicative of the cave environment. Additionally, we demonstrate that the strain LC34 is capable of cell-cell signaling as evidence by its ability to accumulate *N*-dodecanoyl-L-homoserine lactone, C12-*N*-acyl-homoserine lactone, through an *in vitro* analysis, which was corroborated by the identification of a luxIR homolog in its genome. The presence of *luxIR* homolog in strain LC34 suggests that cell-cell signaling mechanisms as a potential adaptation of *Agrobacterium* strains to survive in environments that are relatively low in nutrients.