

14<sup>th</sup> International Conference on **Microbial Interactions & Microbial Ecology**  
 &  
 11<sup>th</sup> Edition of International Conference on **Advances in Microbiology and Public Health**  
 August 19-20, 2019 Vienna, Austria

## Whole-genome sequencing of a novel *Chryseobacterium* strain isolated from poultry feather waste

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**Introduction:** Prokaryotic delineation has come a long way with the erstwhile methods based mainly on physiology and chemotaxonomy. Due to the limitations of these methods, genotypic methods (16S rRNA, whole-genome sequencing, DNA-DNA hybridization, average nucleotide identity and average amino acid Identity) were included to take into account the overall genome relatedness of microorganisms. The term ‘polyphasic taxonomy’ which was introduced in 1970 has now been used for prokaryotic delineation which includes phenotypic, chemotaxonomic and genotypic parameters. The use of whole-genome sequencing has recently been recommended to be used for all prokaryotic delineations.

**Aim:** The aim of this study was to use whole-genome sequencing in an attempt to describe and name a new species of *Chryseobacterium* isolated from chicken feather waste.

**Materials & Methods:** Genomic DNA of *Chryseobacterium* sp. 1\_F178<sup>T</sup> was extracted with a NucleoSpin® microbial DNA extraction kit (macherey-nagel) with the DNA quality checked with a Nanodrop ND-1000 (v3.3.0) spectrophotometer. The Nextera® XT DNA Library prep kit was used to sequence the gDNA according to manufacturer’s instructions. An Illumina MiSeq sequencer was used to sequence the genome and the assembly was performed with PATRIC database, with SPAdes 3.10.0 as the assembly method.

**Results:** The sequenced genomes were uploaded to RAST (Rapid Annotation with Subsystems Technology) database for annotation. Genome related data including gene number, genome size, G+C content, coverage, N50 value, number of contigs, full 16S rRNA sequence etc., were obtained through RAST. The whole-genome shotgun project was deposited in DDBJ/ENA/GenBank. A Venn diagram illustrating the number of shared and unique CDS among strain 1\_F178<sup>T</sup> and its reference strains was constructed. The two closest relatives of strain 1\_F178<sup>T</sup> as determined by 16S rRNA phylogenetic studies were *C. jejuense* and *C. nakagawai*. They both had 16S rRNA sequence similarity values (99.10 & 98.75%) above the threshold value (98.5%). Their DDH (31.4 & 32.7), ANI (86.4 & 86.6) and AAI (89.3 & 89.6) values were all less than the threshold value for species delineation. Strain 1\_F178<sup>T</sup> had 2982 genes in common with its closest relatives.

**Conclusions:** The 16S rRNA, DDH, ANI and AAI values were not within the threshold range for species delineation hence confirming strain 1\_F178<sup>T</sup> as a novel species of *Chryseobacterium*.

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