

Genomic and phenomic analysis of a marine bacterium, *Photobacterium marinum* J15

ABSTRACT

Photobacterium species are widely distributed in the marine environment. The overall metabolism of this genus remains largely unknown. In order to improve our knowledge on this bacterium, the relationship between the genome and phenome of the *Photobacterium* isolate was analyzed. The cream colored, Gram-negative, rod-shaped and motile bacterial strain, J15, was isolated from marine water of Tanjung Pelepas, Johor, Malaysia. The 5,684,538 bp genome of strain J15 comprised 3 contigs (2 chromosomes and 1 plasmid) with G + C content of 46.39 % and contained 4924 protein-coding genes including 180 tRNAs and 40 rRNAs. The phenotypic microarray (PM) as analyzed using BIOLOG showed the utilization of; i) 93 of the 190 carbon sources tested, where 61 compounds were used efficiently; ii) 41 of the 95 nitrogen sources tested, where 22 compounds were used efficiently; and iii) 3 of the 94 phosphorous and sulphur sources tested. Furthermore, high tolerance to osmotic stress, basic pH and toxic compounds as well as resistance to antibiotics of strain J15 were determined by BIOLOG PM. The ANI and kSNP analyses revealed that strain J15 to be the same species with *Photobacterium marinum* AK15 with ANI value of 96.93 % and bootstrapping value of 100 in kSNP. Based on the ANI and kSNP analyses, strain J15 was identified as *P. marinum* J15.

Keyword: *Photobacterium marinum* J15; Genome-scale metabolic network reconstruction; BIOLOG phenotypic microarray