A novel *Halomonas* species isolated from a deep-sea sediment sample of the New Britain Trench exhibits high anti-oxidative stress capability

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A piezotolerant, H_2O_2-tolerant, slightly halophilic bacterium (strain NBT06E8^T) was isolated from a deep-sea sediment sample collected from the New Britain Trench at depth of 8900 m. The strain was aerobic, motile, Gram-stain-negative, rod-shaped, oxidase-positive and catalase positive. Although 16S rRNA gene sequence analysis showed that strain NBT06E8^T is closely related to *Halomonas aquamarina* DSM 30161^T (99.5%), *Halomonas meridiana* DSM 5425^T (99.43%), and *Halomonas axialensis* Althf1^T (99.35%), combined phylogenomic and phenotypic analysis revealed that strain NBT06E8^T represents a novel species of the genus *Halomonas*. Growth of the strain was observed at 4-45 °C (optimum 30 °C), at pH 5-11 (optimum 8-9) and in 0.5-21% (w/v) NaCl (optimum 3-7 %). The optimum pressure for growth was 0.1-30 MPa (megapascal) with tolerance up to 60 MPa. Under optimum growth conditions, the strain could tolerant 15 mM H_2O_2. Whole-genome sequencing analysis of this strain revealed that it contains 39 genes affiliated with anti-oxidative stress, including *oxyR* (transcriptional regulator), *kat* (catalase), *sod* (superoxide peroxidase), *ahpCF* (alkyl hydroperoxide reductase), *ohr* (organic hydroperoxide resistance protein), *ccp* (cytochrome *c* peroxidase), *prx* (peroxiredoxin), *trx* (thioredoxin), *grx* (glutaredoxin) *tpx* (thiol peroxidase), *gor* (glutathione reductase) and so on. In addition, strain NBT06E8^T also owns 11 DNA repair proteins which may promptly repair DNA damages caused by oxidative stress. These genes are important contributors to oxidative stress resistance by maintaining the intracellular redox balance and macromolecules stability. This study indicated that strain NBT06E8^T possesses multidirectional mechanisms of oxidative stress sensing, regulation, and defense. New findings on oxidative stress mechanisms of this strain will broaden our knowledge of stress adaptation mechanisms of deep-sea bacteria and potentiate the biotechnological application of *Halomonas* species in the future.