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Genomic analysis revealing the mechanisms of hydrostatic pressure adaptation of piezophilic bacterium *Pseudodesulfovibrio indicus* J2

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Deep-sea environments, including hadal zone, are characterized by high hydrostatic pressure. Piezophilic bacteria *Pseudodesulfovibrio* from the deep sea are able to cope with high pressure, but little is known about the molecular mechanisms.

Pseudodesulfovibrio indicus J2 was isolated from deep Indian Ocean at a depth of 3173 m. It is meso-piezophilic growing optimally at 10 MPa (ranging 0–30 MPa). The genome sequence was determined to gain further understanding of its piezophilic lifestyle. The genome consists of a single circular chromosome of 3,966,573-bp with a G+C content of 63.5%. It contains 3,461 predicted genes, of which many are likely associated with high pressure adaptation. The main mode of energy generation in *P. indicus* is sulfate reduction, and genes required for sulfate reduction are found. It also contains 24 *c*-type cytochrome genes, which encode *c*-type cytochromes as components of its diverse respiratory systems, enhancing its adaptation to high pressure. All of the genes required for biosynthesis of fatty acids are present. The genome also have a 3-oxoacyl-ACP synthase II gene (05800, *fabF*) involving in the production of monounsaturated fatty acids, which are responsive to hydrostatic pressure in piezophiles. Glutamate/glutamine metabolism is also important in the adaptation of piezophiles to hydrostatic pressure. Genes encoding ABC transporter glutamine-binding protein GlnH (AWY79_13805 and AWY79_13600), and gene AWY79_11040 encoding a glutamine methyltransferase, are found in the genome, which may enhance its high hydrostatic pressure adaptation.

The complete genome sequence of the deep-sea bacterium *P. indicus* J2 reflects a capacity for coping with hydrostatic pressure. Further combined studies will be required to help us draw a more accurate picture of the molecular basis in deep-sea piezophiles and increase our understanding of their ecological role in the deep ocean.