

# Thermococcales in the Deep Sea: Adaptation to High Hydrostatic Pressure

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## Abstract

**Background:** The deep-sea hydrothermal vents, characterized by extreme pressure, temperature, and redox gradients, are hypothesized as cradles of early life (Martin et al., 2008). Thermococcales archaea—strictly anaerobic, hyperthermophilic, and often piezophilic—are key models for studying adaptation to these environments (Bertoldo and Antranikian, 2006). Traditionally classified into three genera, their taxonomy and adaptive mechanisms remain underexplored.

**Methods:** We employed a multidisciplinary approach, combining omics, culture-based physiology, biophysics, and genetics, to dissect the adaptive strategies of Thermococcales under deep-sea vent conditions.

**Results:** Sequencing of 69 new Thermococcales genomes, alongside existing data, yielded over 100 high-quality, closed chromosomes—one of the most comprehensive datasets for an archaeal order. Pangenomic and bioinformatic analyses reclassified these genomes into five distinct genera, challenging current taxonomy. Integration of pangenomic data with metabolic predictions revealed the distribution, evolutionary history, and metabolic specializations across species and ancestors. Notably, the piezophilic *Thermococcus barophilus* thrives under high hydrostatic pressure (HHP), unlike the piezosensitive *Thermococcus kodakarensis*. Comparative studies uncovered proteome structural adaptations and unique hydration dynamics under HHP (Martinez et al., 2016). In *T. barophilus*, HHP induces repression of amino acid biosynthesis genes, resulting in auxotrophy for 17 amino acids, and upregulates energy and carbohydrate metabolism (Cario et al., 2015; Vannier et al., 2015). The mechanism for amino acid acquisition under HHP remains unresolved; ongoing genetic, physiological, and omics investigations aim to clarify this.

**Conclusions:** This work redefines Thermococcales taxonomy and elucidates HHP adaptation mechanisms, including metabolic shifts and amino acid auxotrophy. Their stable enzymes and pathways offer promising biotechnological applications for industrial catalysis and bioremediation under extreme conditions. Continued omics studies will further illuminate their adaptive and applied potential.

## References

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