

## **Genomic Analysis of a Marine Hyperthermophilic Archaeon *Thermococcus* sp. NA1**

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An extremely thermophilic archaeal strain, NA1 was isolated and classified to be a member of genus *Thermococcus* by 16S rRNA gene sequences. It has been known that the members of *Thermococcus* are ubiquitously present in thermal ecosystems, especially in marine environments. The NA1 strain was able to grow anaerobically at a hyperthermophilic range (70-90 °C) by reducing sulfur. We have carried out the whole genome shotgun sequencing of the *Thermococcus* sp. NA1 to search for thermostable enzymes and to understand the physiological characteristics of hyperthermophilic archae. The genome was composed of a single circular chromosome of which size and G+C content to be 1,846,670 bp and 51.85%, respectively. These values were very similar to those of typical *Thermococcus* species. The ORF prediction revealed that the NA1 genome contains annotatable 1,983 ORFs. Several genes encoding hyperthermophilic enzymes were cloned, expressed and characterized. And the comparative genomics is under way by comparison with the nearest neighbor, *T. kodakaraensis* KOD1 whole genome sequence was determined recently.