

**P039** Complete genome sequence and proteome analysis of the hyperthermophilic archaeon *Thermococcus gammatolerans*

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We have sequenced and annotated the complete 2.05 Mb genome of *T. gammatolerans*, an hyperthermophilic and highly radioresistant archaeon. Genome composition comparison between *T. gammatolerans* and *T. kodakarensis* KOD1, a close relative in the Thermococcales order, showed that although approx. 70% of genes from each genome are highly similar (~67% identity), their synteny is not conserved. Contrary to other closely related archaea, massive genome rearrangements cannot be explained by the presence of mobile elements such as IS. Moreover, we deepen the characterization of *T. gammatolerans* species and by contrast to previously published evidence, we show that this archaeon is able to grow with and without elemental sulfur in various culture media. In order to gain new insights into the radioresistance of the archaeon, we have evaluated this phenotype in various growth conditions. Finally, we analyzed by nanoLC-MS/MS the proteome of this organism from exponential and stationary growth phase cells, allowing identification of peptides from 1076 different proteins.