

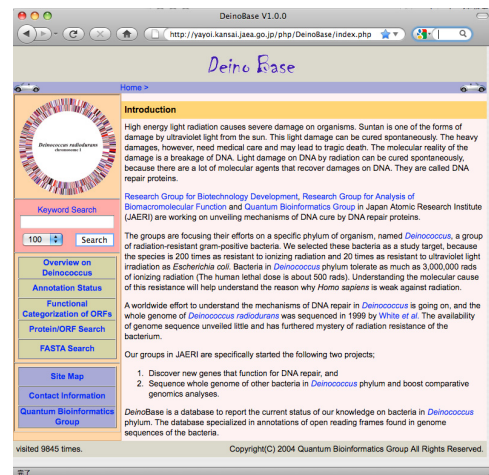
Building a Database for *Deinococcus* and *Thermus* Comparative Genomic Analyses

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It has been a while since genome sequences of both *Deinococcus radiodurans* and *Thermus thermophilus* have been sequenced. The fundamental questions that should be addressed based on these sequences were the mechanisms of radiation/desiccation and heat resistance. *D. radiodurans* is known for its abnormally high resistance against gamma ray irradiation and *T. thermophilus* is for its heat resistance. Both bacteria are classified into the same genus and are closely related, but the peculiar phenotypes are not shared, namely *D. radiodurans* is mesophilic and *T. thermophilus* is susceptible to radiation. Clues to these special characteristics of the bacteria should reside in genome sequences. For the last couple of years, we have focused on identifying genes responsible for radiation resistance in *D. radiodurans* with techniques of molecular, structural and computational biology, but we still have not had a complete picture of the resistance mechanisms.



In the last several years, omics data including transcriptomic and structuromics data of *Deinococcus* and *Thermus* species have been accumulated and a lot of efforts are now taken to integrate these data to facilitate understanding of the phenotypes. In this year, we start building integrated genome databases for *Deinococcus* and *Thermus* genus and try enabling clarification of similarity and differences of these species in genomic level, which may lead to elucidation of radiation/desiccation and heat resistance of the bacteria. We try integrating all the known omics data and predictive data based on our computational biology tools. We expect that the combination of the experimental and predictive data may bring new insights. The current status of the database will be shown in the presentation.