

Mechanisms of tolerance in tardigrades



We take a genome-to-function approach: we first identify tardigrade-unique genes through genomic, transcriptomic and proteomic analyses, then elucidate their molecular mechanisms.

Genome Sequencing of *Ramazzottius varieornatus*: A Treasure Trove of Unique Genes

×

In collaboration with the National Institute of Genetics, we sequenced the genome of *Ramazzottius varieornatus* (YOKOZUNA-1 strain), a tardigrade species known for its exceptionally high tolerance to rapid desiccation and extreme environments. The genome size is compact at 55 Mb—approximately 1/3 the size of a fruit fly's and less than 1/50 of the human genome. It contains an estimated 15,000 to 20,000 genes. While over half are shared with other animals, there is a notable expansion of stress-response genes involved in antioxidant defense and DNA repair. Horizontal gene transfer (HGT) accounted for less than 2% of the genome, which is not as high as previously speculated for tardigrades.

Approximately 40% of the total genes are taxonomically restricted to tardigrades. Protein-based analyses have revealed that many key tolerance proteins (described below) are encoded by these unique genes, suggesting they play a pivotal role in the organism's extreme resilience. ([Hashimoto et al., Nat Commun, 2016](#))

Dsup: A Protein that Shields DNA from Radiation

+

CAHS Proteins: Stress-Responsive Fibrillization to Protect Cells

+

Establishment of Genome Editing in Tardigrades: Unlocking the Molecular Logic of Tolerance

+

Distribution of Tardigrade-Specific Tolerance Genes

+