Genomic and epigenetic adaptation of eukaryotes: a case study from extremophilic red algae

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Life employs diverse strategies to overcome a wide range of external challenges presented by its environments, including those posed by extreme environments. Yet, the study of evolution under these harsh conditions has primarily focused on prokaryotic organisms, with little attention given to eukaryotic cases. In this case study, we investigated how extremophilic red algae use genetic and epigenetic traits to be resilient to environmental stresses. Our study revealed that horizontal gene transfer, subtelomeric gene duplication, and the reduction of non-essential genomic elements are all critical for adaptation to extreme environments. These evolutionary drivers facilitated local adaptation to the surrounding environment and were closely related to speciation among extremophilic red algae. Thus, our findings from genome analysis substantially deepen our knowledge of eukaryotic evolution in extreme environments, moving beyond the previous gene-level approaches. Moreover, we identified specific changes in chromatin that are potentially related to the genome evolution of extremophilic red algae. Given the diverse but understudied eukaryotic lineages, this study contributes to a better understanding of how chromatin influences eukaryotic evolution.