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New Genomic Approaches Reveal the Process of Genome Reduction in Prochlorococcus

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Abstract
Small bacterial genomes are believed to be evolutionarily derived from larger genomes through massive loss of genes and are usually associated with symbiotic or pathogenic lifestyles. It is therefore intriguing that a similar phenomenon of genome reduction has been reported within a group of free-living phototrophic marine cyanobacteria *Prochlorococcus*. Here I have investigated the roles of natural selection and mutation rate in the process of Prochlorococcus genome size reduction. Using a data set of complete cyanobacterial genomes including 12 *Prochlorococcus* and a sister group of 5 marine *Synechococcus*, I first reconstructed the steps leading to *Prochlorococcus* genome reduction in a phylogenetic context. The result reveals that small genome sizes within *Prochlorococcus* were largely determined by massive gene loss shortly after the split of *Prochlorococcus* and *Synechococcus* (a process we refer to as early genome reduction). A maximum likelihood approach was then used to

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estimate changes in both selection effect and mutation rate in the evolutionary history of *Prochlorococcus*. I also examined the effect of selection and functional importance of a subset of ancestor-derived genes those are lost in *Prochlorococcus* but are still retained in the genomes of its sister *Synechococcus* group. It appears that purifying selection was strongest when a large number of small effect genes were deleted from nearly all functional categories. And during this period, mutation rate also accelerated. Based on these results, I propose that shortly after *Prochlorococcus* diverged from its common ancestor with marine *Synechococcus*, its population size increased quickly and thus the efficacy of selection became very high. Due to limited nutrients and relatively constant environment, selection favored a streamlined genome for maximum economies in material and energy, causing subsequent reduction in genome size and possibly also contributing to the observed higher mutation rate.

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