Effect of mutation rate and population size on genome size variation

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Résumé

Genome size variation, and particularly non-coding genome size variation, remains poorly understood in evolutionary biology, particularly in bacterial species. Notably, very different species, such as endosymbiotic bacteria or marine bacteria, have comparable genome sizes, while closely related species can diverge very fast in terms of genome size. Despite extensive research, none of the hypotheses proposed in the literature is firmly established, mainly due to the many confounding factors related to the diverse habitats and histories of species. Computational models may help overcome these difficulties and rigorously test hypotheses. In our study, we use Aevol, a platform designed to study the evolution of genome architecture, to test the influence of population size (N) and mutation rate (μ) on changes in genome size. By subjecting pre-evolved individuals to new conditions characterized by a change in either or both N and μ, we aim to elucidate their respective impact on genome size variations.

Our experiments revealed that an increase in either population size or mutation rate both lead to significant reduction in genome size, but through very different paths. Under increased mutation rate, genomes exhibited a reduction in both coding and non-coding sequences, akin to endosymbiotic bacteria genomes. By contrast, under conditions of increased population size, genomes loose only non-coding sequences while maintaining their coding size, leading to densely packed genomes akin to those observed in certain marine bacteria. Conversely, a decreased population size lead to a genome size growth through the accumulation of deleterious mutations, potentially resulting in an evolutionary catastrophe.

Interestingly, our findings suggest that while both N and μ influence the coding and non-coding genome size, the coding density of the genome appears to be determined by N $\times$ μ. Thus, a broad range of genome sizes and density can be achieved by different combinations of N and μ.

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We propose that the different impact of N and μ on genome size variation can be explained by the interplay between selection for phenotypic adaptation and selection for robustness. This offers new insights into the mechanisms of genome size variations in bacterial species. Luiselli, J., Rouzaud-Cornabas, J., Lartillot, N., & Beslon, G. (2024). Genome streamlining: effect of mutation rate and population size on genome size reduction. *bioRxiv*, 2024-03.

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