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## Why are homopolymeric tracts so frequent in endosymbiont genomes?

Kinjo, Yukihiro<sup>1</sup>, Tokuda, Gaku<sup>2</sup>, Hongoh, Yuichi<sup>3</sup>, Ohkuma, Moriya<sup>1</sup>

<sup>1</sup>Japan Collection of Microorganisms, RIKEN BioResource Center, <sup>2</sup>Tropical Biosphere Research Center, University of the Ryukyus, <sup>3</sup>Tokyo Institute of Technology

Accuracy of an information transfer in the central dogma depends on the sequences characteristics of template DNA. Especially, a long mononucleotide repeat (homopolymeric tract: HPT) is known as one of the most error prone sequences, and generally causes deleterious effects on life activities. Thus an HPT tends to be selectively eliminated from open reading frames (ORFs). However, obligate intracellular symbionts (endosymbionts) have atypical, highly frequent HPTs within ORFs in their genome. This situation has long been considered as genetic responses to the relaxed selection due to their lifestyle change to an intracellular environment. However, the frequencies of HPTs could be extraordinarily too high to explain by the relaxed selection. In this study, we demonstrated that the frequency of HPTs in an endosymbiont genome was far exceeded by that expected by neutral evolution and that it showed a distinctive trend in endosymbionts. In addition, mutation rates within the HPTs in the genomes were more conserved than expected by chance. Furthermore, we found unequal distribution of the HPTs among functional categories of genes in the genomes. These results suggest the possibility that transcriptional/translational errors occurred within HPTs could shape differences of gene expression efficiency among functional categories, and might have evolved positively as a functional mechanism in endosymbiont genomes.

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