How does the reductive genome evolution proceed in intracellular symbionts?

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Genomes of intracellular symbionts provide insights into reductive genome evolution (RGE). They appear to have evolved by reducing their genomes from their ancestors. Recently genomes of two chemoautotrophic intracellular symbionts of deep-sea clams, *Calyptogena okutanii* and *C. magnifica*, are reported. To understand reductive genome evolution (RGE), we compared the *Calyptogena* symbiont genomes and focused on the distributions of deletions and repeats in the genomes. As a result, their genome architectures were highly conserved excepting one inversion. Many deletions from small (less than 100 bp) to large (1-11 kbp) sizes were detected. And deletion numbers decreased exponentially with size. Furthermore, deletions have occurred more frequently in non-coding regions than in coding regions. Because *Calyptogena* symbiont genomes lack *recA*, we propose that deletions and the single inversion occurred by RecA-independent recombination (RIR) at short-repeats with simultaneous consumption of repeats. Densities of deletions and short-repeats, as well as A+T content were higher in non-coding regions than in coding regions. Thus it is suggested that short-repeats were regenerated particularly in non-coding regions by accelerated mutations with enhanced A+T bias due to the absence of *mutY*. We further propose that extant *Calyptogena* symbiont genomes are in an actively reducing stage of RGE consisting of small and large deletions, and deletions are caused by short-repeat dependent RIR along with regeneration of short-repeats.