

# The *Brucella* genomic origami: How bacteria without plasmids or external recombination evolve and adapt to their intracellular niche

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## Abstract

A comprehensive understanding of *Brucella* genomic evolution requires the integration of multiple analytical scales, each offering distinct resolutions to capture fine-level mutations and broad structural modifications. Most evolutionary and pathophysiological studies have focused on single-nucleotide polymorphisms and gene-level mutations to elucidate the biogenesis and dynamics of *Brucella* organisms. In contrast, large-scale genomic rearrangements have received comparatively less attention. This presentation explores the evolution of *Brucella* genomic architectures, emphasizing the secondary modifications of the chromosomes and chromids, which have profoundly impacted gene expression and bacterial evolution. Examines how internal genomic rearrangement mechanisms and the spatial organization of multiple replicons in bacteria that gave up plasmids and for eons have avoided external recombination have adapted and evolved. Comparative analyses of phylogenetically related *Brucella* strains with distinct genomic rearrangements will illustrate these evolutionary and adaptive mechanisms. As a case study, the loss of motility in *Brucella* will be examined as a strategic adaptation linked to the restructuring of replicons and specialization within specific ecological niches.

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