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Understanding role of genome dynamics in host adaptation of gut commensal, *L. reuteri*

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Abstract

Lactobacillus reuteri is a gram-positive gut commensal and exhibits noteworthy adaptation to its vertebrate hosts. Host adaptation is often driven by inter-strain genome dynamics like expansion of insertion sequences that lead to acquisition and loss of gene(s) and creation of large dynamic regions. In this regard we carried in-house genome sequencing of large number of *L. reuteri* strains origination from human, chicken, pig and rodents. We further next generation sequence data in understanding invasion and expansion of an IS element in shaping genome of strains belonging to human associated lineage. Finally, we share our experience in high-throughput genomic library preparation and generating high quality sequence data of a very low GC bacterium like *L. reuteri*.

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