

The rumen plasmidome

A genetic communication hub for the rumen microbiome

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Plasmids are episomally replicating genetic elements which carry backbone genes that are important for their replication and maintenance within their host, and accessory genes that might confer an advantage to their host in its ecological niche. As such, they are often perceived as a powerful evolutionary force, which horizontally introduces new traits into bacterial cells and genomes. In our recent publication “Insight into the rumen plasmidome” we characterized the metagenomic plasmid population of the bovine rumen microbial ecological niche. The rumen is the first compartment of the digestive tract of ruminants; it functions as a pre-gastric anaerobic fermentation chamber, where plant fibers are degraded and converted into chemical compounds which are subsequently absorbed and digested by the animal.

This process holds enormous significance for mankind as it converts the energy stored in indigestible plant mass into milk and meat, which are digestible and consumed worldwide.² This process is performed by a complex microbiota which inhabits the rumen compartment and degrades and ferments the plant material, consisting mainly of indigestible sugar polymers such as cellulose and hemicelluloses.^{2,3} This complex and condensed microbiota (10^{11} microbes/ml) is composed of microorganisms from all domains of life which essentially enable the ruminant to digest its feed.^{2,4} Hence, the existence and well being of the animal is supported through a symbiotic relationship, in which the microorganisms provide the ability to digest and degrade plant material, and the

host accommodates them and provides the plant fibers they require.

The complexity of this microbial environment raises intriguing questions regarding genetic interactions and the mobility of its functions. By learning about the functions that are fixed and mobilized on plasmids, one can gain insight into the genetic interactions and physiological requirements of the hosting microorganisms.

While most research on plasmids from specific ecological niches has traditionally been restricted to bacterial isolates and their plasmids, recent metagenomic approaches have allowed the examination of plasmids from non-cultured microorganisms.⁵⁻⁹ Our metagenomic approach, which was based on an innovative procedure in which we selectively amplified and deep sequenced the plasmid population, provided a wider view of rumen plasmid traits and identities, and of the taxonomical distances that can be crossed by being carried on plasmids.

Our findings indicated that rumen plasmids carry traits which uniquely represent advantageous functions within the rumen ecological niche, making the burden of carrying the plasmid worthwhile for the microbial host. These traits include amino acid metabolism, protein metabolism, respiration and carbohydrate metabolism, which are needed within the rumen ecosystem.^{1,4} This suggests that the accessory functions carried by plasmids could reflect the most advantageous functions within a given ecological niche. By analyzing the phylogenetic associations of different genes present on the plasmid contigs, we could deduce that they are mobilized across taxonomic levels, to as high as the phylum level at relatively high

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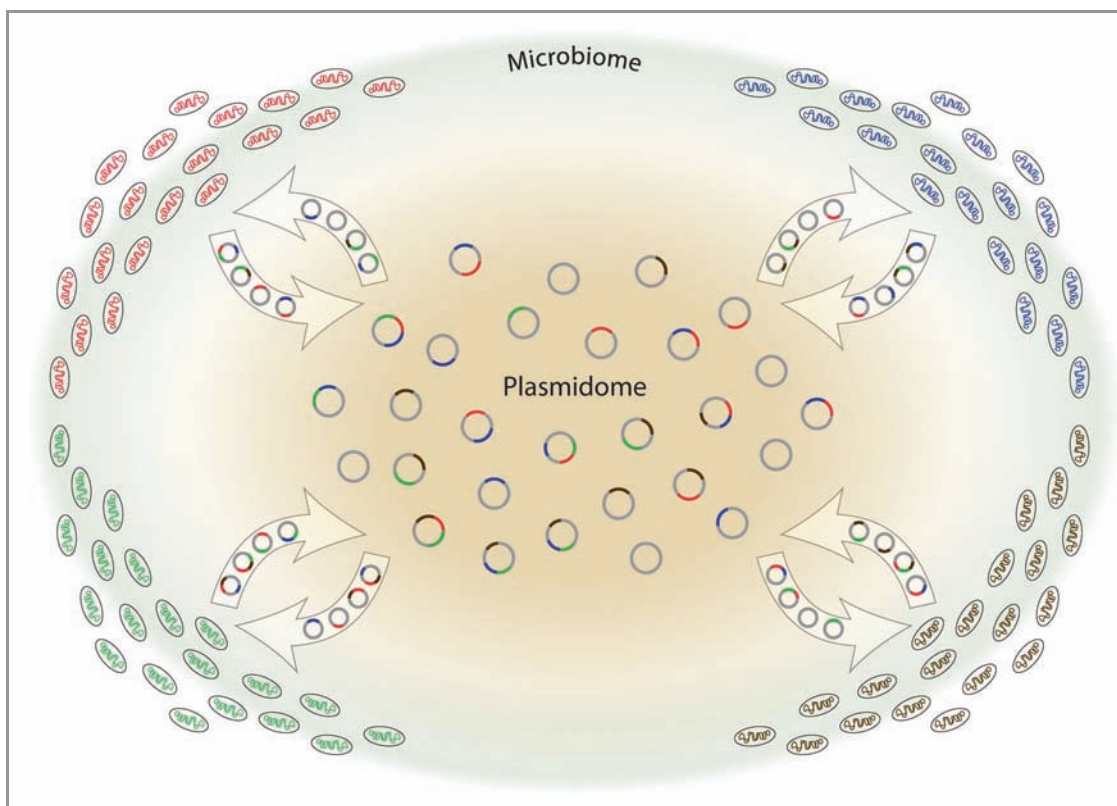


Figure 1. Genetic communication in the rumen microbiome through the rumen plasmidome. The different bacteria of various taxonomic levels composing the rumen microbiome (oval shapes with different DNA colors) and the plasmids carrying backbone genes (gray) interact for the exchange of functions that confer advantages. Bacterial genes are transferred to and fixed in the plasmids (colored fragments) residing within the bacterial hosts if they confer an advantage to their hosts in the rumen ecological niche. These advantageous genes become part of the rumen plasmidome and are mobilized to other bacteria of different and distinct taxonomical levels. The plasmids then collect more genes to be mobilized and fixed if they are relevant to the rumen ecological niche. The rumen plasmidome thus serves as a communication channel for the mobilization of genes among different bacterial taxa.

frequency: at this level, 14% of the contigs were mosaic.

Furthermore, some of the detected plasmids matched those previously isolated from rumen bacteria in different locations around the world, further emphasizing their central evolutionary role in the rumen microbial population. These findings from our exploration of the metagenomic

plasmid population within the complex microbial habitat of the rumen¹ suggest that in this habitat, the plasmids have certain hereditary characteristics—as they recur and are acquired at different locations and time points, while serving as a channel for the exchange of rumen-advantageous functions between the rumen microbes (Fig. 1).

Based on these findings, a model of cooperation between the rumen populations of plasmids and microbes can be suggested, in which plasmids carry functions that help them prosper within their microbial hosts, while different microbial species can exchange genes across large phylogenetic distances.

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