rifampicin resistant mutant of the *B. fibrisolvens* type strain 2221 at remarkably high frequencies (up to 10^{-1} per recipient) in anaerobic filter matings. The recipient strain shows an auto-aggregation phenotype but it is not yet established whether this contributes to the high transfer rates observed.

Tc^R *B. fibrisolvens* were found to carry chromosomal sequences giving detectable hybridisation to *tet*(M) or *tet*(O) probes. Chromosomal DNA from Tc^R transconjugants did not however hybridise strongly to *tet*(M) or *tet*(O) probes although a new, weakly hybridising band was detected, suggesting that a second tetracycline resistance determinant was being transferred. Comparison of total genomic DNA from transconjugants and the recipient by pulsed-field gel electrophoresis was consistent with the acquisition of a mobile chromosomal element [1]. The mobile element is about 50kb in size and has a preferred insertion site in the *Butyrivibrio* genome. The element did not hybridise with probes carrying the *int/xis* gene of Tn*916*, or with the integrase gene of Tn*5252*, and may represent a novel type of transferable element in Gram-positive bacteria. This is the first example of a chromosomal element from an obligately anaerobic rumen species.

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Restriction-modification systems in ruminal bacteria: occurrence and some evolutionary implications. P Pristas, P Javorsky (*Institute of Animal Physiology, Slovak Academy of Sciences, Soltesovej 4-6, 040 01 Kosice, Slovakia)*

Type II restriction modification systems involve a DNA methyltransferase and an endonuclease of the same recognition sequence specificity. It is generally accepted that these systems act primarily to protect bacteria from foreign DNA, particularly from infection by bacteriophages. The study of the biology of restriction-modification systems has revealed some general features and it has been shown that the composition of the bacterial chromosome and the restriction-modification systems present within cells are evolutionarily linked [1]. Restriction endonucleases have been found in bacteria from all taxonomic and ecological groups. Ruminal bacteria have been shown to be a promising source of these enzymes. Up to now ten restriction endonucleases have been isolated from bacteria of this ecological group. Our studies on variability of endonucleolytic activity in *S. ruminantium* have demonstrated a high frequency and diversity of restriction endonucleases in this species, and at least ten different specificities have been characterized [2]. In addition the observed frequency of restriction endonucleases, which were present in more than one-third of strains tested, is higher than observed in bacteria from other ecological groups. A high frequency of restriction endonucleases in *S. ruminantium* can also be inferred from the analysis of DNA. Using the method of Karlin *et al.* [1], it was shown that average counts of perfect 4- and 6-base pairs palindromes observed within *S. ruminantium* DNA are lower than in other bacteria, and even lower than those observed among phage DNAs. The observed low frequency of short palindromes is therefore in good agreement with the high frequency of restriction endonucleases observed in this genus. Similarly other ruminal bacteria

show lower counts of palindromes than would be predicted from a random distribution. We suppose that the consistently low frequencies of 4-bp and 6-bp palindromes observed within the DNA of ruminal bacteria is probably a result of the variety and multiplicity of restriction systems found in bacteria from this ecological group. Possibly, there is a correlation between bacterial population density and the frequency of restriction endonucleases.

Bacterial counts in the rumen are higher than in any other environment. Together with the high bacterial counts, there are also unusually high concentrations of bacteriophages. If the protection of cells from bacteriophage infection is a primary role of restriction-modification systems, these systems should be more frequent in the rumen than in environments with lower populations of bacteriophages. In such a strongly competitive ecosystem as the rumen of herbivorous animals the possession of restriction activity can provide a selective advantage for survival of both the individual bacterial clone and the species as a whole.

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Variability of endonucleolytic activity within natural population of *Selenomonas ruminantium.* P Pristas, I Vanat, N Kostrabova, P Javorsky (*Institute of Animal Physiology, Slovak Academy of Sciences, Soltesovej 4-6, 040 01 Kosice, Slovakia)*

The rumen is one of the most complex microbial ecosystems in nature. It is inhabited by a diverse community of bacteria, protozoa and fungi. Diversity in *S. ruminantium* strains isolated from the rumen was reported based on enzyme electrophoresis [1], as well as by DNA fingerprinting and DNA-DNA hybridization [2]. Usually, diversity was reported among bacterial isolates from different, sometimes extremely distant, sources. There is a comparative lack of data about variability within local populations.

On the basis of our previous study on the characterization of restriction activities in *S. ruminantium* [3] we analyzed a population of this species in the rumen of fallow-deer. Our analysis indicated high diversity of endonucleolytic activities within the population of *S. ruminantium.* At least 12 different restriction enzyme cleavage profiles, indicating the presence of nucleases with differing specificity, have been observed. Site-specific endonucleases were detected in 17 out of 45 strains tested; in other strains varying levels of non-specific activity were detected. Endonucleolytic activities seemed to be subspecies specific, since types of activity observed in subsp. *lactilytica* were not observed in subsp. *ruminantium* and vice versa. Plasmid DNAs ranging in size from 0.9 to more than 25 kbp were detected in 60% of strains analyzed. Little or no correlation was observed between endonuclease activity and plasmid content. The presence of endonucleases of differing specificity, as well as differences in the plasmid profiles of isolates possessing identical specific activity indicated that the population of *S. ruminantium* within the rumen of a single animal consisted of at least ten different clones.

Our results indicate a high diversity of endonucleolytic activities in *S. ruminantium* as well as high genetic variability