

SUMMARY AND CONCLUSION

The rumen is home to millions of micro organisms namely bacteria, protozoa, fungi and bacteriophages. These organisms live in a symbiotic relationship and play a significant role in rumen digestion. Protozoa is second most widely found organisms in the rumen with its population ranging from 10^5 - 10^6 cells/g. The present study was aimed to study the biodiversity of rumen protozoa by phylogenetic analysis.

In the study, the rumen liquor sample was collected with the help of a stomach tube. DNA was extracted using three different protocols, out of which only one worked out. This DNA was subjected for amplification by PCR using primer specific to conserved region of 18S rDNA. The fragment of size 943 bp was obtained and then proceeded for cloning by T/A strategy and then sequenced. The sequence was analysed with BLAST and has found to show similarities with sequences of uncultured rumen protozoa. This confirms the authenticity of the study.

This is just a preliminary study to standardize the DNA extraction protocol from the ruminal protozoa. The study has contributed in creating a primary database for the rumen protozoa which will, in future be used to carry out diversity and dynamics study of rumen protozoa. The details of diversity and dynamics studies will help in improving feed conversion efficiency and in turn, the production of milch animals.

APPENDIX