What is the RGBC?

The Ruminant Genome Biology Consortium has been formed to capture the learning’s of communities who have already developed genomic tools for their own ruminant (Bovine, Ovine and Caprine) species. The idea is to share those learnings across species which do not yet have the scientific and financial infrastructure arising from organized agriculture in the developed world with those of new ruminant species. It is anticipated that in time more ruminant species will be sequenced, enabling a concerted effort to identify genomic features associated with adaptation to different environments and signatures of selection sweeps in both wild and domesticated ruminants. Immediate functions of the consortium can include assisting the Genome 10k project (Genome 10K Community of Scientists, 2009) choose appropriate ruminant species for sequencing.

Ruminants co-evolved with grasslands to occupy approximately 40% of the land surface of this planet. Their co-evolution with grasslands, ease of domestication and close association with development of human civilisations places them in a unique position of providing food, fibre, labour and comfort to most current human societies. The ruminants of major economic importance (bovine, ovine, caprine) have (or are currently having) their genome sequenced. Information about the process of domestication, selection for specific traits is sought with the idea that these may further enhance their productivity for human ends. However, little is known of the genome rearrangements that have facilitated these utilitarian activities, and enabled ruminants to occupy diverse environmental niches. Because ruminants do not directly compete with humans for food (humans are not able to digest grasses and low quality feeds for which ruminants have adapted) they complement rather than compete with man in a world where energy consumption on food production is potentially limiting.