

SFB1032 Seminar Announcement

Friday, July 3rd: Seminarraum LS Gaub at 10.30am



Fiber-degrading bacteria in the gut: Of rumen and human

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A cellulolytic fiber-degrading bacterium, *Ruminococcus champanellensis*, was isolated from human faecal samples and its genome was recently sequenced. Bioinformatic analysis of the *R. champanellensis* genome revealed numerous cohesin and dockerin modules, the basic elements of the cellulosome, and manual sequencing of partially sequenced genomic segments revealed two large tandem scaffoldin-coding genes that form part of a gene cluster. Representative *R. champanellensis* dockerins were tested against putative cohesins, and the results revealed three different cohesin-dockerin binding profiles which implied two major types of cellulosome architectures: (i) an intricate cell-bound system and (ii) a simplistic cell-free system composed of a single cohesin-containing scaffoldin. The cell-bound system can adopt various enzymatic architectures, ranging from a single enzyme to a large enzymatic complex comprising up to 11 enzymes. The variety of cellulosomal components together with adaptor proteins may infer a very tight regulation of its components. The cellulosome system of the human gut bacterium *R. champanellensis* closely resembles that of the bovine rumen bacterium *Ruminococcus flavefaciens*. The two species contain orthologous gene clusters comprising fundamental components of cellulosome architecture.