



Relative abundance of hydrogenotrophic microorganisms in response to diurnal variation of hydrogen partial pressure in the bovine rumen

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Type of thesis: Computational

Required competences: Microbial physiology and ecology, Multivariate statistics, Basic physical chemistry

Acquired competences: Redundancy analysis, Thermodynamics and kinetics of biochemical conversions, Understanding of the ruminal microbial metabolism, Functional analysis

Date: by mutual agreement

Description

Hydrogen is a key product of rumen fermentation in response to ingestion of fibrous feeds and has been suggested to control various metabolic pathways that utilize or produce hydrogen (Van Lingen et al., 2016). This control of the metabolism by hydrogen can be described by thermodynamics and kinetics of biochemical reactions. The proceeding of every reaction in which hydrogen is involved has implications for the abundance of microorganism that employ specific metabolic pathways (Van Lingen et al., 2017). For example, increased hydrogen partial may increase the relative abundance of reductive acetogenic bacteria (Gagen et al., 2015) and could possible affect methanogenic archaea (Wallace et al., 2015) that employ hydrogenotrophic conversions resulting in acetate and methane, respectively.

In the ruminal ecosystem, hydrogen partial pressure is commonly considered too low for substantial reductive acetogenesis, which explains why methanogenesis by archaea with a lower threshold for hydrogen is the major hydrogenotrophic pathway. However, as a result of feed intake by cattle, hydrogen partial pressure in the rumen may vary



greatly throughout the day (Van Lingen et al., 2017). Depending on the actual diurnal pattern of hydrogen partial pressure, reductive acetogenesis and a few other minor hydrogenotrophic conversions may be temporarily feasible to proceed for kinetic and thermodynamic reasons.

This project will assess the thermodynamic feasibility of methanogenic and acetogenic pathways in response to ruminal hydrogen partial pressure and relate the relative abundance of acetogenic and methanogenic microorganisms to measured values of hydrogen partial pressure. The student will quantify the thermodynamic feasibility of acetogenic and various methanogenic pathways as affected by environmental conditions in the rumen, after which hydrogenotrophic microorganisms from an in-house dataset will be identified by a function analysis. Subsequently, the student will perform a multivariate analysis (likely a redundancy analysis) to relate the relative abundance of hydrogenotrophic microorganism to measured values of hydrogen partial pressure.

References

Gagen et al., 2015. Hydrogenotrophic culture enrichment reveals rumen Lachnospiraceae and Ruminococcaceae acetogens and hydrogen-responsive Bacteroidetes from pasture-fed cattle. *FEMS Microbiology letters* 362:fmv104. doi:10.1093/femsle/fmv104

Van Lingen et al., 2016. Thermodynamic driving force of hydrogen on rumen microbial metabolism: a theoretical investigation. *PLoS ONE* 11:e0161362. doi:10.1371/journal.pone.0161362

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Wallace et al. 2015. The rumen microbial metagenome associated with high methane production in cattle. *BMC genomics* 16: 839. doi: 10.1186/s12864-015-2032-0