

Novel enzyme discovery from the rumen microbiome

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Abstract

Lignocellulose is a major component of the woody portion of plants. The polymers it houses, like xylan and cellulose, could be used as biofuels or in other plant-based materials. The breakdown of lignocellulose requires specialized carbohydrate-active enzymes (CAZymes), but targeted discovery of novel CAZymes is difficult due, in part, to their structural diversity. In a recent paper, researchers have proposed a new method to speed up this process. They combined phenotype-based selective pressure with functional profiling to screen unknown enzymes. Feeding cattle a forage-based diet applies selective pressure on their rumen microbiota for microbes with specialized fiber-degrading enzymes. Three glycoside hydrolase families had increased abundance in feed-efficient cattle compared to their inefficient counterparts on this diet. Screening some members of those families against a database of uncharacterized enzymes led to the identification of putative xylanases and endoglucanases. The xylanolytic activity of the most abundant xylanase was confirmed with computer simulations and laboratory assays. This study demonstrated the utility of this combined approach to discover other potentially useful enzymes for the biotechnology industry and identified several novel lignocellulolytic enzymes. This approach could be applied to any easily manipulated microbiota of interest.