

Assessing Transcriptional Isoform Switching Between Intestinal Crypts and Villi

Dennis A. Aldea and Michael P. Verzi
Rutgers, The State University of New Jersey

Transcription from DNA to mRNA is a complex process in eukaryotes. Whether by alternative promoters, alternative mRNA splicing, or post-translational modifications, genetic information may be modified as it passes from a gene to a protein. These modifications enable isoform switching—the transcription of multiple mRNA variants, called isoforms, from a single gene. Here, we investigate differences between isoforms present in intestinal crypt and villi cells. Crypt and villi compose the intestinal epithelium—a tightly-folded layer of cells lining the intestines and separating their contents from the rest of the body. Villi are the folds of the intestinal epithelium; crypts are the pockets between villi. Villi are composed of differentiated epithelial cells, whereas crypts are composed of undifferentiated intestinal stem cells. We hypothesize that differences between mRNA isoforms present in crypt and villi cells partly result from isoform switching—alternative transcription of the same genes resulting in different mRNA isoforms. Although some differences in gene expression between crypt and villi cells have been identified, the extent of isoform switching between the two cell types has not been examined. We will assess isoform switching between crypt and villi cells by analyzing RNA-seq data collected from both cell types in mice (*Mus musculus*). We will be assessing isoform switching using AIDE (Li et al., 2019) and IsoformSwitchAnalyzeR (Vitting-Seerup & Sandelin, 2019) for our investigation. Supported by R01DK112365 and R25ES020721.

Does mRNA isoform switching contribute to crypt-villus identity?

