Identification of commensal microbiota bound by host immunoglobulins

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Video Byte

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Abstract

Mucosal sites such as the gastrointestinal tract are home to dense communities of commensal bacteria. At these barrier sites, plasma cells secrete a specialized type of antibody – immunoglobulin isotype A (IgA). A new method called IgA-Seq is often used to identify which bacterial taxa are bound to IgA, improving our understanding of host-microbe interactions. Unfortunately, IgA-Seq data often suffers from high variability between experiments and unresolved biases in equations used for analysis. In a new article, researchers describe the design strategy for an optimized IgA-Seq protocol. Using standardized positive and negative controls, they defined the optimal reagents and FACS parameters for IgA-Seq . Analysis with simulated IgA-Seq data showed that existing scoring methods are influenced by pre-sort relative abundance. These effects could be addressed using a novel scoring approach based on posterior probabilities. The utility of this new IgA-Seq protocol and probability-based scoring were demonstrated using both new and published data from in vivo disease models. Combining an optimized protocol with new scoring methods will enable the accurate identification and quantification of IgA-targeted commensal gut microbiota with potential applications for a wide range of sample types and other Ig isotypes.