

Identification of acacia gum fermenting bacteria from pooled human feces using anaerobic enrichment culture

ABSTRACT

Commercial acacia gum (AG) used in this study is a premium-grade freeflowing powder. It is a gummy exudate composed of arabinogalactan branched polysaccharide, a biopolymer of arabinose and galactose. Also known as food additive, acacia gum (E414), which is presently marketed as a functional dietary fiber to improve overall human gut health. The health effects may be related to the luminal pH regulation from the short-chain fatty acids (SCFA) production. Studies suggested that amylolytic and butyrogenic pathways are the major factors determining the SCFA outcome of AG in the lower gut. However, the primary bacteria involved in the fermentation have not been studied. This study aimed to investigate the putative primary degraders of acacia gum in the gut ecosystem. Isolation and identification of gum-fermenting bacteria were performed through enrichment culture fermentation. The experiment was conducted in an anaerobic chamber for 144 h in three stages. The study was conducted in triplicate using an anaerobic chamber system. This culture system allows specific responses to support only bacteria that are responsible for gum fermentation among the gut microbiota. Five bacterial strains were isolated and found to be gum-fermenting bacteria. Based on the 16s RNA sequence, the isolates matched to butyrateproducing *Escherichia fergusonii*, ATCC 35469.