

Immune System Associated Genes of Microbial Populations in Camel Feces Analyzed Using Metagenomic Approach

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An analysis of the camel faecal microbial community revealed certain genes associated with Immune system. A high throughput sequencing of total DNA extracted from fecal material was done to characterize general community composition and examine the repertoire of microbial genes. The KO (KEGG Orthology) database available in MG-RAST was utilized for finding the microbial genes associated with immune system present in camel feces. 17 % percent of the sequence hits of organisms systems as per KO database are assigned to immune system. The functional genes present in camel faeces are assigned to Complement and coagulation cascades [PATH:ko04610]; NOD-like receptor signaling pathway [PATH:ko04621]; Hematopoietic cell lineage [PATH:ko04640]; T cell receptor signaling pathway [PATH:ko04660] and Intestinal immune network for IgA production [PATH:ko04672]. About 50 per cent functional genes of GRAP2, GADS; GRB2-related adaptor protein 2 are involved in TCR signalling pathway followed by TFPI; tissue factor pathway inhibitor genes (33 %) and A2M; alpha-2-macroglobulin (12%) involved in Complement and coagulation cascades. The remaining immune system functional genes comprise < 5%. Activation of T lymphocytes is a key event for an efficient response of the immune system. It requires the involvement of the T-cell receptor (TCR) as well as costimulatory molecules such as CD28. The main consequences of complement activation are the opsonization of pathogens, the recruitment of inflammatory and immunocompetent cells, and the direct killing of pathogens. The kallikrein-kinin system is an endogenous metabolic cascade. Majority of microbial community genes involved in immune system are playing a functional role TCR signalling followed by complement and coagulation cascade.