

# Conclusion

Human beings co-evolve and co-exist with plethora of microorganisms that exhibit mutually beneficial or tolerant relationship. Human gastrointestinal tract (GIT) is an ideal abode for numerous microbes to thrive and proliferate due to its large surface area and rich stock of nutrients. Microbes residing in human GIT, collectively termed as human gut microflora, act crucially in structural and functional development of mucosal immune system. Intestinal microflora can rightfully be considered as a positive health asset with its repertoire of beneficial activities. However, abrupt changes in microbial balance of human gut result in serious intestinal disorders like inflammatory bowel diseases (IBD), irritable bowel syndrome (IBS), colorectal cancer (CRC) and gastric cancer.

A modest effort was made in this present work to realize the molecular underpinnings of microbial establishment in human gut. Comprehensive codon and amino acid usage based investigations of the gut-

associated microbes revealed various factors like genomic compositional constraint, natural selection for efficient translation, gene expression level, hydrophobicity and aromaticity of the encoded proteins to be instrumental in dictating codon and amino acid usage signatures. It was very interesting to note that the bacterial communities of human gut adopt the codon usage fashion of their host i.e., human, which might be attributed to their strategy of successful colonization in human intestinal niche. Comparative genomics and proteomics based analysis resulted in fruitful inferences regarding bacterial policies of adaptation in human gut. Bacterial members were found to possess sophisticated metabolic apparatus for efficient degradation of nutrient resources in human intestine. Another imperative finding was that the bacterial communities were found to be well-equipped with enriched stock of Carbohydrate-Active enZymes and diverse array of carbohydrate degradation pathways that human

beings lack. Such observations could be well correlated with the fact that members of human gut microflora enhance digestive abilities of human beings besides ensuring their self-existence.

Extensive scrutiny of the global set of secretory proteins i.e., secretomes, in gut microbial masses, excavated some meaningful information pertaining to acclimatization in human intestine. Secretomes were found to use inexpensive amino acids with reduced biosynthetic cost and avoid the practice of aromatic and bulky amino acids. Protein secretion has been suggested to be a 'one-way' path and the loss of secretory proteins is virtually irretrievable. Thus, bacterial masses of human gut seem to be intelligent and pragmatic in employing less costly amino acids for secretory components that are lost permanently. It was striking to notice that secretory proteins were found to evolve at par with non-secretory components in the gut-associated microbial members. It might be hypothesized in this regard that bacterial masses of human gut co-evolve and co-exist with human host right from birth and atypical evolutionary signatures of secretomes might confer an added advantage to the

microbial residents for proper stay in human gut environment.

*Helicobacter pylori* 35A is a menacing pathogen that resides in human GIT and has been associated with serious pathogenic complications like gastric ulcer and gastric cancer. Scrutiny of potential therapeutic targets in pathogenic *H. pylori* 35A produced a comprehensive set of unique (absent in human) essential proteins that might act as promising targets to thwart the survival of the agent of infection. Subsequent screening and molecular docking investigations revealed that drug Nitrofurantoin and phytochemical D-Limonene might act as potential lead molecules for successful drug development against *H. pylori* associated infections.

Facts and facets of intricate bacterial adaptation that came out of this present endeavor might prove utility in unraveling the tangles of bacterial behavior in human intestinal environment. However, with the surge of metagenomic data and with the rapid advancement of bioinformatics based tools, techniques and platforms this is just the beginning of the exciting journey pertaining to research associated with human gut microflora.