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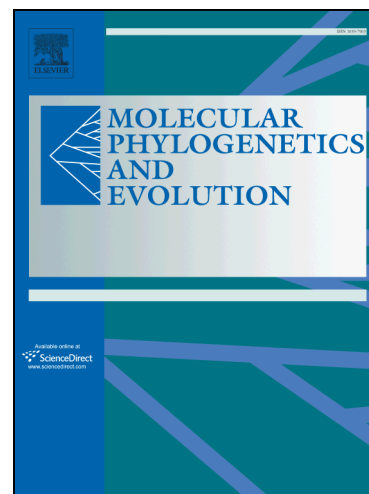
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The Conserved Phylogeny of Blood Microbiome

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Abstract

The proliferation and intensification of diseases have forced every researcher to take actions for a robust understanding of the organisms. This demands deep knowledge about the cells and tissues in an organ and its entire surroundings, more precisely the microbiome community which involves viruses, bacteria, archaea, among others. They play an important role in the function of our body, and act both as a deterrent as well as shelter for diseases. Therefore, it is pertinent to study the relation within the microbiome in a human body. In this work, we analyze the sequence data provided through the Human Microbiome Project to explore evolutionary relations within blood microbiome. The objective is to analyze the common proteins present in the different microbes in the blood and find their phylogeny. The analysis of the phylogenetic relation between these species provides important insights about the conservedness of phylogeny of blood microbiome. Interestingly, the co-existence of five of those common proteins is observed in human too.

1 Introduction

The human microbiome, which consists of viruses, bacteria, archaea, etc., play an important role in maintaining human health. Microbes may or may not be harmful to us, and they are sometimes essential for maintaining health also. For instance, they produce some vitamins that are not provided by the genes to break down our food for extracting the essential nutrients. It also instructs the immune system, if necessary, to recognize the dangerous invaders, and even produce helpful anti-inflammatory compounds that fight off other disease-causing microbes. Variations in microbes can be dangerous but at the same time it can be used to fight against diseases. Moreover, it has been estimated that the microbes are ten times of the cells in a human body

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