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Firmicutes–An Overview

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ABSTRACT

In the diverse bacterial flora the taxonomy has an important role to play to understand the microorganisms. Firmicutes are those gram positive microorganisms which is rod shaped (Bacilli) and few cocci too. For the further assessment 16SrRNA sequencing of firmicutes and result assessment are discussed

KEYWORDS: *Firmicutes, 16SrRNA, sequencing, and rod shaped microorganisms.*

INTRODUCTION

Taxonomic interpretations

The phylogenetic conclusions were availed for evaluating and modifying the taxonomic outline of the Firmicutes. In order to precisely ensure applicability and promote acceptance, the proposed modifications were made following a conservative procedures. The overall organization follows the type _taxon‘principle as applied in the previous volumes and analysis. Taxa defined in the outline of the preceding volumes and further assessment was only unified, dissected or transferred in the cases of the strong phylogenetic support. This approach is justified by the well-known low significance of the local tree topologies (also called ―range of the un sharpness around the nodes;) (Ahmed et al., 2014). Thus, many of the cases of the paraphyletic taxa found were maintained in the current road map if the respective (sub)-clusters rooted closely together, even if they were specifcally separated by intervening clusters representing other taxa. While the reorganization of these taxa may be warranted, it was not performed in the absence of confirmatory evidences. The names of validly published but phylogenetically misplaced the type strains are also generally

maintained. These strains are mentioned in the contexts of the respective phylogenetic groups. In case of the paraphyly, all concerned species or the higher taxa are assigned to the respective (sub)-groups (Arndt et al., 2012). New higher taxonomic ranks are only proposed if the species or the genera previously assigned to the different higher taxonomic units — are significantly unified in a monophyletic and specific branch.

THETAXONOMICBACKBONEANDARRANGEMENTOFTHEFIRMICUTES

In the current treatment, the phylum Firmicutes comprises three classes, Bacilli, Clostridia and Erysipelotrichi. However, the class -Mollicutes were removed from the phylum given the general low support by the alternative markers (Ludwig and Schleifer, 2005)and its unique phenotypic properties, in particular the lack of the rigid cell walls (see Emended description of the Firmicutes, this volume) (Barquera et al.,2007). The family Erysipelotrichaceae, which encompasses wall-forming Gram-positive organisms previously classified with the Mollicutes, was retained in the Firmicutes class as a novel class, Erysipelotrichi, and the order, Erysipelotrichales. While the bipartition of the classes Clostridia and the Bacilli is corroborated by the new analyses, some of the taxa previously assigned to the Clostridia tend to the root outside the Firmicutes and may represent separate phyla (Fig-1).

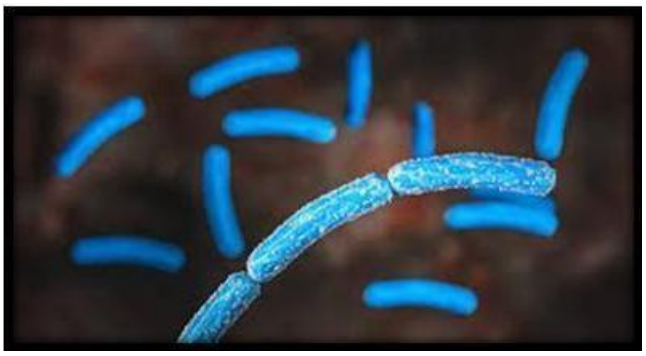

Figure: 1

These encompass taxa previously classified within the Thermoanaerobacterales and the Syntrophomonadaceae (Bokulich et al., 2013), which may contain a number of phylogenetic clades that are precisely distinct at the phylum level. However, given the absence of corroboration by the other phylogenetic markers for many of these assignments and a clear consensus on the definition of the phylum, these taxa were retained within the Firmicutes for the present. The Class Bacilli Compared to Garrity et al.(2005),only minor restructuring of the Bacilli is indicated by this new analysis and further evidences researched using the rRNA

data. The separation into two orders, Bacillales and Lactobacillales, is well supported (Caporaso et al., 2010). However, a number of the paralogous groups are found within the ―Bacilli, some of which have been specifically reclassified. The organism grouped in class firmicutes are based on the genome and proteome analysis (Dr. S. Sreeremya, 2025b). There are diverse ranges of bacterial consortium (Dr. S. Sreeremya, 2025a). Firmicutes is one category of bacterial consortium which can form a biofilm (S.Sreeremya, 2017).Gut microbiome which mainly include the firmicutestoo (S. Sreeremya et al., 2018).

THE RELATIONSHIP BETWEEN GUT FIRMICUTES AND DIETARY FIBERS

Dietary fiber, as the seventh major nutrient for the humans, is widely derived from daily foods (vegetables and also fruits, by-products of agricultural products, edible fungi, marine plant resources, medical and the food resources, etc.), and exhib-its important biological activity for the hosts (Caporaso et al., 2012). Although not broken down by human digestive enzymes, the intracellular and/orextracellular polysaccharide lyases secreted by gut microbiota (mainly Bacteroides and Firmicutes) can break them down into carbohydrates specifically oligosaccharides or mono saccharides which can be absorbed and utilized by human intestinal epithelial cells or the gut microbes (Chao et al., 2006). Some gut microbes (Roseburia, Faecalibacterium, Eubacterium, Lactobacillus spp., etc.) of the Firmicutes have a strong ability to depolymerize the dietary fibers (Chao et al., 2012). These bacteria can depolymerize many different types of the dietary fibers and produce metabolites, such as butyric acid or lactic acid that are beneficial to the human health (Conlon et al., 2015). Based on the above, we list different types of the dietary fibers [non-digestibleoligosaccharides (NDO), the non-starch polysaccharides and resistant starch] by gut Firmicutes (Table. 1).N D O [eg., fructo-oligosaccharides (FOS) ,the galacto-oligosaccharides (GOS), isomalto-oligosaccharides(IMO),the xylo-oligosaccharides (XOS)] are typically edible constituents of whole grains, the fruits, vegetables, and the other foods as well as some plant-based materials, which playa very pivotal role in regulating human health (David et al.,2014).Most NDO shave aβ-configuration and cannot be degraded by the human gastrointestinal digestive enzymes, which are highly likely to be fermented in the colon of the human digestive system (de Onis et al., 2007). Studies have shown that FOS and GOS could be completely degraded by three kinds of the Firmicutes (Lactobacillus, Roseburia, and Eubacterium), and FOS could also be degraded by the Faecalibacterium, promoting the accumulation of lactic acid or the butyrate .Non-starch polysaccharides cover a wide range, among which cellulose and the hemi cellulose are common components in plants (den Besten et al.,2013). Cellulose,

composed of the dehydrated glucose and linked by β-1,4-glycosidic bonds, is a linear polymer, which can be decomposed by the Ruminococcus spp. and some Enterococcus spp. and producea large amount of hydrogen .The Hemicellulose, composed of pentose (xylose and arabinose), hexose (glucose, mannose, and the galactose) and hexuronic acid (4-O-methyl-D-glucuronic acid, D-glucuronic acid, and the D-galacturonic acid), is a branched heteropolysaccha-ride . Studies and resarches have shown that most hemicellulose from grains could significantly modulate the composition of the gut microbiota, especially promoting the proliferation of the Bifidobacterium and Lactobacillus (DeSantis et al., 2006). The arabinogalactans encompass type 1 and type 2 structures, the latter of which are more much complex and represented by the arabinogalactan from larch (LA-AG). Are search study analyzed the gut microbiota which could degrade arabinoga-lactan, and found that they were mainly in the Roseburia. Glucomannan is mainly derived from konjac, aloe, lily, the Dendrobiumcandidum, and so on

PHYLOGENY

Morphologically and also micro biologically, Mollicutes are classified as Bacteria that were probably derived from lactobacilli, the bacilli or streptococci by regressive evolution and genome reduction, to produce the smallest and the simplest free-living and self-replicating cells (Razin et al., 1998). Their lifestyle is, in general, the parasitic. Structurally, Mollicutes are characterized by the complete lack of the cell wall and the presence of an internal cytoskeleton (Devkota et al., 2012). Based on the 16S rRNA data, the taxonomy, as well as the phylogeny and evolution, of the Mollicutes have recently been discussed. Byphylogenetic analysis, low-G+C, the Gram-positive Bacteria (Firmicutes) comprise three groups: Bacilli, Clostridia and the Mollicutes. However, based on 16S rRNA gene sequence data, only the Mollicutes are well-supported as being themonophyletic. In this study, we present the results of our analysis that availed phosphoglycerate kinase (Pgk) amino acid sequences as a molecular marker, instead of the 16S rRNA, to examine the phylogeny of Firmicutes taxa. Pgk is one of the oldest _housekeeping‘ bio enzymes; its evolutionary time has been estimated to be about years old approximately40 million years, which is about twice as long as was required for 1% mutation to occur in the cytochrome c or glyceraldehyde-3-phosphate dehydrogenase (Dinh et al.,2016). Other reviews and reports consider that Pgk is evolving at a linear rate of four to six accepted point mutations in about 100million years, i.e. about the same rate as for the cytochromec. Even for housekeeping ‘enzyme, this is a much conserved sequences. The pgk gene may be an example of core ‘household genes (Daubin et al., 2002).

The metabolic role of Pgk, especially in Mollicutes, has recently been vividly discussed. The role of Pgk is particularly consequential in Mollicutes, as these bacteria precisely lack cytochrome pigments and the citric acid cycle and are thought to synthesize most of their ATP by the substrate phosphorylation during glycolysis, mediated by the presumably essential action of the Pgk and pyruvate kinase (Do et al., 2018).

CONCLUSION

Firmicutes is understood as the phylum of bacterial consortium that constitutes a significant portion of the human gutmicrobiota, primarily encompassing genera such as Ruminococcus, Clostridium, and Lactobacillus, and is allied with the obesity-related patterns in gut microbiota composition.

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