Immune-modulating gut symbionts are not “*Candidatus* Arthromitus”

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To the Editor: It is becoming increasingly evident that the microbial community of the intestine is critical for refining the immune system of its host. Nothing illustrates this better than the segmented filamentous bacteria (SFB). These vertebrate gut symbionts are tightly anchored to epithelial cells of the ileal mucosa and possess the unique ability to specifically modulate the host immune response, which has consequences that extend beyond the gut wall. SFB trigger a diverse array of immune functions, inducing innate immune responses,^{1–3} increasing and activating cytotoxic intraepithelial lymphocyte populations,⁴ and coordinating T-cell responses, including the specific induction of CD4⁺ T-helper 17 cells.^{2,3} They appear to act as a double-edged sword for the mammalian immune system—on one side mediating protective immunity by potently inducing IgA-secreting cells⁵ but on the other side promoting autoimmune disorders by triggering rheumatoid arthritis⁶ and multiple sclerosis⁷ in experimental mouse models. This makes SFB one of the very few examples of gut commensals that can stimulate the postnatal maturation of the immune system.

Although the study of gut bacteria has traditionally occurred within the realm of microbiology, immunological studies

Figure 1 Phase contrast micrographs of an *Arthromitus* filament from the termite gut (a) and a segmented filamentous bacterium (SFB) from the murine ileum (b). Phylogenetic tree showing the distinct positions of “*Candidatus* Arthromitus” from arthropods and the SFB (“*Candidatus* Savagella”) from mammals (c) (modified from ref. 10).

have formed the vanguard in the quest to understand the SFB. This is why we wish to draw attention to proposed changes to the classification of this immunologically significant group. When Snel *et al.*⁸ showed that SFB form a distinct lineage of uncultivated bacteria within the bacterial family *Clostridiaceae*, they assigned them to the genus *Arthromitus*—a group of equally conspicuous bacterial filaments from arthropod guts that had been described by the American scientist Joseph Leidy over 160 years ago.⁹ However, assuming relatedness based on morphology alone was a mistake. Using molecular phylogenetic analysis of 16S rRNA gene sequences, we have recently shown that Leidy’s *Arthromitus* in fact belongs to a different bacterial family, the *Lachnospiraceae*¹⁰—despite their striking similarity to mammalian SFB (Figure 1).

Given the immunological importance of mammalian SFB, it is imperative that these two bacterial groups be distinguished from

each other. Biological functions attributed to Leidy’s *Arthromitus* will not necessarily apply to mammalian SFB and vice versa. In view of their distinct phylogenetic positions, the same name can no longer be used for both groups. Given the historical priority of Leidy’s *Arthromitus*, and the apparent absence of SFB-like 16S rRNA gene sequences from arthropod guts, we proposed to rename SFB to “*Candidatus* Savagella”¹⁰—in honor of the American gut microbiologist Dwayne C. Savage, who was the first to describe this bacterial group in the ileum of rodents.¹¹

DISCLOSURE

The authors declared no conflict of interest.

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