Physiological Characterization of Novel Bacteria isolated from the guts of Cephalotes ants

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Ants, insects from the family Formicidae, play an integral role in terrestrial ecosystems. They aerate soil, disperse seeds, and serve as a food source for other organisms. Yet, surprisingly, little is known about their behavior, feeding habits, and source of nutrition. Bacterial symbionts are known to play a key role in the diversification and ecological adaptation of numerous organisms, including ants. Previous studies have shown that “turtle ants” from the tribe Cephalotini possess an abundance of symbiotic bacteria in their gut [1], and that members from the phyla Verrucomicrobia, Bacteroidetes, and Proteobacteria are consistently detected in the gut despite variations in diet, population, and geographical location [2]. Thus, it is clear that isolating, identifying, and understanding the physiological characteristics of these core bacteria will help to elucidate the mechanisms by which bacterial symbionts interact with Cephalotes and thereby drive their ecological adaptation and evolution.

Previously, we successfully isolated two novel bacteria belonging to Verrucomicrobia and three novel bacteria belonging to Proteobacteria from ant guts. Here, we identified and characterized the Verrucomicrobia isolates CV41 and CAG34, cultivated from Cephalotes varians and Cephalotes rowheri, respectively. CV41 and CAG34 are gram-negative and coccoid. Growth was possible under an atmosphere consisting of 0.5-20% O$_2$ and up to 5% CO$_2$ for CV41 and CAG34, though CV41 could not grow in the absence of CO$_2$. Optimum growth was observed between pH 6.9-7.3, 0.5-1.5% NaCl (w/v), and at temperatures near 37 °C for CV41. Similarly, CAG34 grew optimally between pH 6.9-7.7, 0.5-1.5% NaCl, and at temperatures near 37 °C. CV41 and CAG34 primarily used identical sugar and short-chain fatty acid compounds for growth. Notably, CV41 could additionally use glycogen, D-galactose, gentiobiose, and adonitol. From comparisons of their 16S rRNA gene sequences, CV41 and CAG34 are 98% similar based on 1522 base pairs. Both isolates shared a 93% similarity with their closest cultivated neighbor Opitutus terrae PB90-1, suggesting that CV41 and CAG34 form a novel genus.

This summer research experience not only benefitted me by expanding my knowledge and laboratory skills in microbiology, but also gave me additional experience with working independently and collaboratively. I enjoyed designing and scheduling experiments, thinking through results and research papers, and troubleshooting problems. Above all, this research experience was central to helping me solidify my plans to pursue graduate school, and ultimately, a research-based career.

References