The roseobacter group comprise up to 25 % of the total bacterial community in the surface waters of the ocean, and its members possess a great deal of physiological and genetic diversity. Taxonomic assignments within the roseobacter group have been primarily based on 16S rRNA gene sequences. However, recent studies have demonstrated that this gene lacks the resolution for accurately assigning organisms within the roseobacter group. To address this problem, whole-genome sequence data was used to construct a taxonomy that accurately depicts evolutionary relationships. The result of these analyses was the taxonomic reassignment of 34 species and the proposal of six novel genera.

Dimethylsulfoniopropionate (DMSP) is abundant in marine surface waters and can reach micromolar concentrations, and *Ruegeria pomeroyi*, a member of the roseobacter group, is capable of metabolizing it. Previous studies have shown that the methyl carbon and sulfur of DMSP are incorporated into methionine, and this led to the hypothesis that the direct capture of methanethiol was the major pathway for methionine biosynthesis from DMSP. To test this hypothesis, a highly efficient method for synthesizing di(methyl-^{13}C)sulfonio-^{34}S-propionate ([^{13}C][^{34}S]DMSP) was developed. The [^{13}C][^{34}S]DMSP was subsequently fed to *R. pomeroyi* in chemostat and the resulting isotopic labeling of methionine was examined. These experiments indicated that only one-third of methionine was synthesized via the direct capture of methanethiol while the remainder was synthesized by the random reassembly of the sulfur and methyl atoms. The findings also indicated that DMSP was the major source of sulfur even when present at concentrations <1 μM.