The status of the genus *Pseudoroseovarius* Sun et al. 2015

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The results of phylogenetic analyses of the genera *Aliiroseovarius* Park et al. 2015 and *Pseudoroseovarius* Sun et al. 2015 and comparison of the phenotypic features of their members showed that these genera should be united. Based on nomenclatural priority of the genus *Aliiroseovarius*, it is proposed to reclassify *Pseudoroseovarius crassostreae* as a later homotypic synonym of *Aliiroseovarius crassostreae*, *Pseudoroseovarius halocynthiae* as a later homotypic synonym of *Aliiroseovarius halocynthiae*, *Pseudoroseovarius sediminilitoris* as a later homotypic synonym of *Aliiroseovarius sediminilitoris* and *Pseudoroseovarius zhejiangensis* as *Aliiroseovarius zhejiangensis* comb. nov.

One supplementary figure is available with the online Supplementary Material.

The genus *Aliiroseovarius* proposed by Park et al. (2015) includes its type species *Aliiroseovarius pelagivivens* with type strain GYSW-22\(^{T}\) isolated from seawater and the species *Aliiroseovarius crassostreae*, *A. halocynthiae* and *A. sediminilitoris*. The latter three species were transferred to this genus from the genus *Roseovarius*; their type strains (CV919-312\(^{T}\), MA1-10\(^{T}\) and M-M10\(^{T}\), respectively) and strain GYSW-22\(^{T}\) form a cluster in the phylogenetic trees that is independent of phylogenetic lineages of other *Roseovarius* species. However, the same *Roseovarius* species, *Roseovarius crassostreae*, *R. halocynthiae* and *R. sediminilitoris* transferred by Park et al. (2015) to the genus *Aliiroseovarius*, were reclassified several months later as members of another new genus, *Pseudoroseovarius*, based on their clustering with *Pseudoroseovarius zhejiangensis*, the type species of the genus, in an independent phylogenetic clade (Sun et al., 2015a, b).

Reconstruction of the maximum-likelihood (Fig. 1) and neighbour-joining (Fig. S1, available in the online Supplementary Material) phylogenetic trees based on 16S rRNA gene sequences of the type strains of *Aliiroseovarius* and *Pseudoroseovarius* species and related bacteria shows that these species form a monophyletic clade. The trees were generated as described previously (Dobritsa & Samadpour, 2016). The close phylogenetic relationships of members of this clade are highlighted by comparatively high levels of 16S rRNA gene sequence similarity (97.6–95.3 %). Comparison of the phenotypic traits of *Aliiroseovarius* and *Pseudoroseovarius* presented in their original descriptions (Park et al., 2015; Sun et al., 2015a) shows that the genera share many characteristics, including chemotaxonomic features. Members of the two genera are catalase- and oxidase-positive mesophiles, neutrophiles and chemo-organotrophs. Tolerance to NaCl in growth media is variable for members of these genera; the maximum NaCl concentrations are in the range 4–12 %, but all species require NaCl (0.5–1 %), and optimal growth occurs in the presence of 1–2 % NaCl (Boettcher et al., 2005; Kim et al., 2012; Park & Yoon, 2013; Park et al., 2015; Sun et al., 2015a). The major isoprenoid quinone is ubiquinone-10 (Q-10). The common main polar lipids are phosphatidylglycerol and phosphatidylcholine and one unidentified aminolipid. The predominant fatty acid (65.5–80.2 %) is C\(_{18,1}\)ω7c. Such phenotypic similarities should be expected because the descriptions of *Aliiroseovarius* and *Pseudoroseovarius* include the descriptions of the same former *Roseovarius* species as their members.

Therefore, the results of phylogenetic analyses demonstrating the high level of relatedness of members of the genera *Aliiroseovarius* and *Pseudoroseovarius*, including their placement in the same monophyletic clade, and the absence of phenotypic traits supporting the existence of these genera as separate taxa indicate that they should be united. Thus, it is proposed to transfer species of the genus *Pseudoroseovarius* to the genus *Aliiroseovarius*, since the latter has nomenclatural priority. *P. crassostreae*, *P. halocynthiae* and *P. sediminilitoris* should be reclassified as later homotypic synonyms of *A. crassostreae*, *A. halocynthiae* and *A. sediminilitoris*, respectively, and *P. zhejiangensis* is proposed to be reclassified as *Aliiroseovarius zhejiangensis* comb. nov.

The features differentiating *A. zhejiangensis* as a separate species from *A. crassostreae*, *A. halocynthiae* and *A. sediminilitoris* are given in the description of *P. zhejiangensis* by Sun et al. (2015a). The level of 16S rRNA gene sequence similarity between the type strain of *A. zhejiangensis* comb. nov., JB3\(^{T}\), isolated from chemical plant wastewater, and
Fig. 1. Maximum-likelihood phylogenetic tree based on 16S rRNA gene sequences, showing the positions of the type strains of *Aliiroseovarius* and *Pseudoroseovarius* species and related bacteria. The sequence of *Stappia stellulata* NBRC 15764T was used as the outgroup. GenBank accession numbers are shown in parentheses. Bootstrap values (≥50%) are given at branch points. Bar, 0.02 substitutions per nucleotide position.
*Aliiroseovarius* GYSW-22\(^{T}\) is 95.3 %, which is lower than the 97 % value considered the threshold for bacterial species demarcation (Tindall et al., 2010). Based on the data from Park et al. (2015) and Sun et al. (2015a), the phenotypic features differentiating the type strains of *A. pelagivivens* and *A. zhejiangensis* comb. nov. include the abilities to grow at 4 and 40 °C, to reduce nitrates, to hydrolyse aesculin, gelatin and Tween 40, to produce N-acetyl-β-glucosaminidase, α-glucosidase and β-glucosidase, and to assimilate L-arabinose, D-fructose, sucrose, trehalose and salicin. There is also a significant difference in the DNA G+C contents of *A. zhejiangensis JB3\(^{T}\) and *A. pelagivivens* GYSW-22\(^{T}\), 68.1 and 59.0 %, respectively.

**Emended description of the genus *Aliiroseovarius* Park et al. 2015**

*Aliiroseovarius* (A.li.i.ro.se.o.va’ri.us. L. pronoun alius other, another; N.L. masc. n. *Roseovarius* a bacterial generic name; N.L. masc. n. *Aliiroseovarius* the other *Roseovarius*).

The description is as provided by Park et al. (2015), but with correction that the DNA G+C content is 55.4–68.1 mol%.

The type species is *Aliiroseovarius pelagivivens*.

**Description of *Aliiroseovarius zhejiangensis* comb. nov.**

*Aliiroseovarius zhejiangensis* (zhe.ji.ang.en’sis. N.L. masc. adj. zhejiangensis pertaining to Zhejiang province in China, where the type strain was isolated).

Basonym: *Pseudoroseovarius zhejiangensis* Sun et al. 2015.

The description is as provided by Sun et al. (2015a).

The type strain is JB3\(^{T}\) (=MCCC 1K00457\(^{T}\)=KCTC 42443\(^{T}\)).

**References**


