Strains of *Yersinia wautersii* should continue to be classified as the ‘Korean Group’ of the *Yersinia pseudotuberculosis* complex and not as a separate species

A recent publication by Savin *et al.* proposes the novel species *Yersinia wautersii* sp. nov. originating from *Yersinia pseudotuberculosis sensu stricto* (Savin *et al.*, 2014a, b). This new taxon comprises strains known as the ‘Korean group’, previously revealed by multi locus sequence typing of the *Y. pseudotuberculosis* complex (Laukkanen-Ninios *et al.*, 2011). In making their proposal, Savin *et al.* (2014a) followed the rules of the *Bacteriological Code* that are required for a novel species to have standing in nomenclature: (1) they stated that they were proposing a novel species and used the term ‘sp. nov.’, (2) they designated strain 12-219N1T as the type strain, (3) they provided a description of the novel species, (4) they provided the logic and scientific evidence for their proposal, and (5) after publishing the paper describing the novel species in a journal outside the *International Journal of Systematic and Evolutionary Microbiology* (*IJSEM*) then validated the name by having it published in Validation List 158 in *IJSEM* (Savin *et al.*, 2014b). The fifth step completed the validation process for the name of the proposed novel species and gave it standing in nomenclature under the rules of the *Bacteriological Code*. The above facts mean that *Y. wautersii* is a ‘species with a validly published name’ under the rules of the *Bacteriological Code*. However, we disagree with the logic of Savin *et al.* that the type strain and its related strains should be classified as representatives of a separate species on the following basis: all results presented show that the ‘Korean group’ is a well-defined subpopulation of the *Y. pseudotuberculosis* complex. The authors explained that their findings on genotype and phenotype features of these strains corroborate the work of Laukkanen-Ninios *et al.* (2011) who proposed that the ‘Korean group’ is in the process of speciation. The authors moreover stated correctly that the ‘Korean group’ does not represent a species distinct from *Y. pseudotuberculosis*. Nevertheless, Savin *et al.* then proceeded to explain why the ‘Korean group’ strains do represent a new species by using *Burkholderia mallei* and *Burkholderia pseudomallei* as a comparative example. This comparison is not appropriate since the classical standard definitions for species were not applied to these two species. *B. mallei* evolved from *B. pseudomallei* by gene loss and is considered to be a clone of the latter (Godoy *et al.*, 2003; Holden *et al.*, 2004). *B. mallei* is the causative agent of glanders, a re-emerging zoonotic disease of horses, observed for centuries in the Western hemisphere with a high impact in the horse industry. It is highly adapted to its primary host, the horse, which is also its single reservoir. By contrast, *B. pseudomallei* causes a disease in humans known as melioidosis, which was first recognized in Burma in 1912 (Whitmore & Krishnaswami, 1912). This bacterium is a soil saprophyte of tropical and subtropical wetlands which occasionally causes disease in man or animal. Melioidosis accounts for 20% of community-acquired septicemias in northeastern Thailand but, contrary to glanders, it is not considered a disease of economic importance in animals.

Nomenclature can take into account the outstanding medical importance or traditional denomination of causative agents based on syndromes. This is the case for *B. mallei* and *B. pseudomallei* as well as for *Y. pseudotuberculosis* and *Yersinia pestis*, the latter being only a clone of *Y. pseudotuberculosis* with imminent pathogenicity for humans and a life cycle very different from that of the former. The correct name of *Y. pestis* should therefore be *Y. pseudotuberculosis* subsp. *pestis* as pointed out by Berrovier *et al.* (1980). This somewhat pragmatic approach to nomenclature has also been applied to other pathogenic bacteria species, such as those of the genus *Brucella*. However, Savin *et al.* have failed to prove that the pathogenicity or the life cycle of the ‘Korean group’ is so divergent that the generation of a novel species can be justified.

In summary, we argue that the previous classification used for this group of organisms is the better one – that the ‘Korean Group’ of *Y. pseudotuberculosis* should continue to be classified as a named subgroup in the species *Y. pseudotuberculosis*, not as the separate species *Y. wautersii* as proposed by Savin *et al.* (2014a). However, we agree that this and other matters of classification will be decided by the scientific community as reflected by usage, particularly in the literature.

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