

LETTER TO THE EDITOR

Radical changes to chlamydial taxonomy are not necessary just yet

We, the undersigned, strongly object to the proposed reclassification of the order *Chlamydiales* (Everett *et al.*, 1999). It should not be accepted at this stage. That *Chlamydia psittaci* and *Chlamydia trachomatis* each comprised a heterogeneous group of organisms lumped into two species was recognized when those species were first designated. However, these organisms were placed into a single genus based on DNA homology, and a set of convenient, relatively easily assayed biological properties. The need for further *speciation* in the future was recognized, but workers in the field delayed reclassification waiting for identification of taxonomically significant biological properties. This was the basis for classifying *Chlamydia pneumoniae* as a separate species. One of our major concerns is that this new classification scheme, based almost exclusively on minor sequence differences in 16S and 23S rRNA genes, has no new biological markers for genus or species differentiation. Some of the new species include too few isolates to be confident that these small differences will be maintained as more isolates are evaluated. There is increasing agreement among microbial taxonomists that while 16S rRNA is useful for evolutionary studies, it is not always the best choice for speciation. Genus-specific genes would be better.

Even if there is a case for more chlamydial species, the same cannot be said for the division into two genera. Everett *et al.* (1999) arbitrarily define that a sequence should be >95% identical to be included in the respective genus. Given that maximum differences between *C. trachomatis*, *C. psittaci* and *C. pneumoniae* strains are between 5 and 6% (i.e. >94% identity), their proposal to establish separation at the genus level is unwarranted. Recent 16S rRNA evaluation by Tanner *et al.* (1999), found that the *C. trachomatis*, *C. psittaci*, *Chlamydia pecorum* and *C. pneumoniae* strains represent a taxonomically and phylogenetically coherent grouping into one genus. Thus there is not sufficient sequence difference that compels a division of the genus. This begs the question, do we need a new genus right now? The answer is, it is completely unnecessary! The new genus designation ignores the unique, highly conserved biology shared by these organisms that is recognized when they are in a single genus. The single genus *Chlamydia* worked. It has

taken years to educate public health workers, funding agencies and the public about these organisms called *Chlamydia*. *Chlamydia* is now a well-recognized name. To change the name would create confusion (even among scientific colleagues).

We don't dispute the sequence data, but question its use as the sole criterion to create a new genus. The proposal does not address how one is to identify isolates of *Chlamydiales* beyond identifying gene sequences. There are no commonly determined biological differences between the organisms within both proposed genera. Unfortunately, several biological markers described by Everett *et al.* (1999) such as glycogen production and motility are incorrect. Why then create an excessive nomenclature, based solely on sequence differences, that does not serve a practical purpose, particularly in the medical field? It will only produce chaos and would not result in nomenclature stability.

References

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