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Proper Nomenclature for the Human Granulocytic Ehrlichiosis Agent

To the Editor: In their recent article, "Antigenic variations in vector-borne pathogens," Barbour and Restrepo discuss the outer membrane protein components of *Anaplasma marginale* and related bacteria (1). Citing a reference by Zhi et al. (2), they state that *Ehrlichia granulocytophila* is the agent of human granulocytic ehrlichiosis (HGE).

The use of new names and combinations not widely recognized for genera and species lends increasing confusion to a group of bacteria already in taxonomic disarray. Several other species names have been suggested for the HGE agent since the initial description of the clinical illness caused by this agent and the in vitro technique used to isolate the agent in blood samples (3,4). Both *E. phagocytophila* and *E. equi* are genetically nearly identical to the HGE agent, and the three are probably conspecific. Thus, most scientists in the field today would support use of the name *Ehrlichia phagocytophila* to describe these bacteria.

Recent phylogenetic analyses show that *E. phagocytophila* strains align into a clade that includes *Anaplasma marginale*, the historical precedent in this grouping. Such phylogenetic analyses, which are also supported by comparative antigenic and biological studies, have resulted in a proposal for reclassification of several *Ehrlichia* spp., including *E. phagocytophila*, into the genus *Anaplasma* (5). Until a cogent reclassification based on objective criteria is firmly accepted, the creation and use of new scientific name combinations for a single bacterium yield clinical and laboratory confusion and should be avoided.

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Single Nucleotide Polymorphisms in *Mycobacterium tuberculosis* Structural Genes

To the Editor: A recent article by Fraser et al. (1) discussed the frequency of single nucleotide polymorphisms (SNPs) in two genomes of *Mycobacterium tuberculosis*, strains H37Rv (2) and CDC1551 (unpublished). The article contains an inaccurate representation of our published *M. tuberculosis* data on SNP frequency. The authors state that "detailed comparison of strains H37Rv and CDC1551 indicates a higher frequency of polymorphism, approximately 1 in 3,000 bp, with approximately half the polymorphism [sic] occurring in the intergenic regions. In other words, 50% of the polymorphisms are in 10% of the genome. While this rate is higher than that suggested (3), it still represents a lower nucleotide diversity than found in limited comparisons from other pathogens."

On the basis of comparative sequence analysis of eight *M. tuberculosis* structural gene loci (open reading frames [orf]), we initially published an estimated average number of synonymous substitutions per synonymous site (K_s value) that indicated that this pathogen had, on average, approximately 1 synonymous difference per 10,000 synonymous sites (4). This finding was unexpected given the relatively large population size of *M. tuberculosis* and paleopathologic