

## عنوان مقاله:

Balances after almost 40 years of use of 16S rRNA gene sequence in prokaryote systematics

## محل انتشار:

اولین کنگره بین المللی و سیزدهمین کنگره ژنتیک ایران (سال: 1393)

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## خلاصه مقاله:

The use of the 16S rRNA gene sequence has been so well accepted among taxonomists and molecular microbial ecologists that the gene of this molecule is the one with most frequent entries in public sequence repositories. Since the early beginning of this century, its use in new taxa classifications has been regarded as compulsory to reveal their genealogical position. Due to this reason, most of the entries that correspond to taxonomic papers are of acceptable to high quality in terms of length and ambiguities. However, entries corresponding to environmental sequences are often of bad quality or too short for adequate phylogenetic inferences. Moreover, during the last two decades, the deposit of environmental 16S rRNA gene entries has increased exponentially, overtaking in orders of magnitude the arithmetic increase of entries corresponding to cultured organisms. To provide to the taxonomist's community a useful tool, the LTP was created as a curated database with prealigned sequences only from type strains of validly published names, and using the universal alignment and format provided by the ARB package [1]. This tool has been useful to calculate the different category thresholds for the taxonomic hierarchy based on the deposited sequences. These thresholds show how consistently taxonomists create their units. In addition, the thresholds calculated had been used to evaluate (i) the correspondence with partial stretches of the molecule, and (ii) the putative abundances of different taxa among the environmental sequences. Finally, we propose a nomenclatural schema for sequences corresponding to uncultured organisms as well as we update the putative census of prokaryotic species in the biosphere.

## کلمات کلیدی:

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