When 16s rRNA outperforms WMGS metagenomics

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The biggest drawback of 16S rRNA gene sequencing is that the reads originate from a single short region and the resulting reads lack sufficient specificity for reliable species-level identification. Whole metagenomic sequencing (WMGS) is seen as a solution to this problem that should provide the highest degree of specificity. We argue that WMGS for metataxonomics can be inefficient since most parts of a typical microbial genome are non-specific and provide no value for species identification. Consequently, the sequencing budget is spent on useless parts of genomes and the process's sensitivity is significantly reduced. This is a problem, especially in the low-abundant samples contaminated by eukaryotic DNA. Unlike WMGS, where, in theory, all organisms could be classified down to the species level, in 16S rRNA the set of identifiable species depends on a chosen primer combination.