Correcting bias in microbiome analyses

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Video Byte

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Abstract

The ribosomal RNA (rRNA) gene approach to sequencing genetic material has revolutionized microbiome science. But it isn't perfect. The method relies on the assumption that counts of rRNA genes translate into microbial abundance. Exceptions to that rule, however, are known, such as the observation that rRNA gene counts can be higher in fast-growing microbes. Now, researchers report a new relationship between rRNA genes and cell volume that could help correct for biases inherent to microbiome studies. An analysis of previously reported data showed that the number of 16S or 18S RNA genes per cell follows an allometric power law of cell volume. Applying this relationship to a dataset for bacteria found in intertidal rocks allowed for more accurate biovolume and cell count distributions to be estimated for all taxa detected. The development of more comprehensive cell-size databases could help strengthen the bias-correcting relationship and boost the power of current microbiome analyses.