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Variability in the relative human DNA content during metagenomic analysis of gut microbiota

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Abstract

© 2015, Pleiades Publishing, Ltd. The comparative study of seven different methods for extraction of total DNA from human feces has been carried out. All these methods are recommended in protocols for metagenomic analysis of human gut microbiota. The relative abundance of human DNA in such samples registered by shotgun sequencing on a SOLiD 4 genetic analyzer has been investigated. It was shown that either initial amount of feces or a method applied for total DNA extraction insignificantly influenced the final relative human DNA proportion, which did not exceed 1% in healthy people. Invariance of this parameter allows to consider the increased proportion of human DNA in metagenomic samples as a potential marker of inflammatory bowel diseases.

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Keywords

DNA extraction from feces, metagenomic analysis, shotgun sequencing