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High-quality draft genome sequence of a new phytase-producing microorganism *Pantoea* sp. 3.5.1

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Abstract

© 2015 Suleimanova et al. Strain 3.5.1 was isolated from soils of the Republic of Tatarstan, Russia, on the basis of presence of a high phytate-degrading activity. Strains with such activities attract special interest because of its potential use as feed additives and natural manures. Strain 3.5.1 harbors a 99 % 16S rRNA nucleotide sequence similarity to different *Pantoea* species (*P. vagans*, *P. ananatis*, *P. agglomerans*, *P. anthophila* and *Pantoea* sp.) and exhibits unique biochemical properties that do not allow strain identification up to species. Moreover, the strain 3.5.1 shows a low ANI and MALDI-TOF Mass Spectrometry scores. Thus, it is likely that the strain 3.5.1 represents a new *Pantoea* species. Here, we present the genome sequence of *Pantoea* sp. strain 3.5.1. The 4,964,649 bp draft genome consists of 23 contigs with 4,556 protein-coding and 143 RNA genes. Genome sequencing and annotation revealed two phytase genes and putative regulatory genes controlling its activity.

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Keywords

454, Genome, Ion Torrent, *Pantoea*, Phytase, Strain 3.5.1