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GENOME ANNOUNCEMENT

Genome Sequence of *Paenibacillus alvei* DSM 29, a Secondary Invader during European Foulbrood Outbreaks

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***Paenibacillus alvei* is known as a secondary invader during European foulbrood of honeybees. Here, we announce the 6.83-Mb draft genome sequence of *P. alvei* type strain DSM 29. Putative genes encoding an antimicrobial peptide, a binary toxin, a mosquitocidal toxin, alveolysin, and different polyketides and nonribosomal peptides were identified.**

Paenibacillus alvei is an aerobic, Gram-positive, and endospore-forming bacterium, which shows swarming activity on solidified culture media (5). *P. alvei*, *Brevibacillus laterosporus*, *Enterococcus faecalis*, and *Achromobacter eurydice* occur as secondary invaders of honeybees during outbreaks of European foulbrood (3). In addition, *P. alvei* is described as a causative agent of human infections (8).

The genome sequence of *P. alvei* DSM 29, which was isolated from foulbrood-diseased honeybees, was determined by using the 454 GS-FLX system and Titanium XL chemistry (Roche 454 Life Science, Mannheim, Germany). The initial assembly of one paired-end and three shotgun pyrosequencing runs yielded 266 contigs and 18-fold coverage. Closing of gaps was performed by PCR and Sanger sequencing of the resulting products. The draft genome (6.83 Mb) consists of 25 contigs, comprising one chromosome and at least four plasmids (pPAV14, pPAV16, pPAV109, and pPAV141). The genome (45.9 mol% G+C content) contains approximately 6,605 predicted protein-encoding genes.

Analysis of the *P. alvei* genome sequence revealed that this organism bears the potential to produce a variety of polyketides and nonribosomal peptides. At least six putative gene clusters encoding nonribosomal peptide synthetases, three single nonribosomal peptide synthetase-encoding genes, and five putative hybrid clusters harboring polyketide synthases and nonribosomal peptide synthetases were identified.

We found 10 different putative genes coding for chitin-degrading enzymes. Chitin stabilizes the cuticles of the epidermis and trachea as well as the peritrophic matrix in insects (7). Hyaluronate lyases are known virulence factors, as they are able to degrade the connective tissue of eukaryotes (6). We identified one putative hyaluronate lyase (PAV_3c01910), which, together with chitin-degrading enzymes, might contribute to the invasive capacity of the pathogen.

The genome of *P. alvei* harbors putative genes for one antimicrobial peptide (PAV_2c01250 to PAV_2c01270) and different toxins such as one binary toxin (PAV_1c12540, PAV_1c12550), one putative mosquitocidal toxin (PAV_2c04820), and alveolysin (PAV_7c02420). The latter is a thiol-activated membranolytic toxin (4). In addition, other genes are related to a toxin-antitoxin system (PAV_109p01200), hemolysin III-like proteins, and an insecticidal toxin complex. The insecticidal toxin complex produces orally active toxins, which are located on the surface of the toxin-producing pathogen (2). Three components (A to C) are required to exhibit full toxicity. The complete operon coding for the insecticidal toxin complex of *P. alvei* shows high similarity to the *tca* operon of *Bacillus thuringiensis* IBL 200 (1). However, the gene region of *P. alvei* shows some differences in gene organization compared to that of *B. thuringiensis*. In *P. alvei*, the genes encoding component A are duplicated (PAV_1c12470 and PAV_1c12480, PAV_1c12500 and PAV1c_12510) and component B is encoded by two separate open reading frames (PAV_1c12450 and PAV_1c12460).

Nucleotide sequence accession number. The genome sequence of *P. alvei* DSM 29 has been deposited in GenBank under accession number AMBZ00000000.

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