



Complete and Draft Genome Sequences of Nine *Lactobacillus sakei* Strains Selected from the Three Known Phylogenetic Lineages and Their Main Clonal Complexes

Valentin Loux,^b Gwendoline Coeuret,^a Monique Zagorec,^{a*} Marie-Christine Champomier Vergès,^a Stéphane Chaillou^a

^aMICALIS institute, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France

^bMalAGE, Mathématiques et Informatique Appliquées du Génome à l'Environnement, INRA, Université Paris-Saclay, Jouy-en-Josas, France

ABSTRACT We present here the complete and draft genome sequences of nine *Lactobacillus sakei* strains, selected from the entire range of clonal complexes from the three known lineages of the species. The strains were chosen to provide a wide view of pangenomic and plasmidic diversity for this important food-borne species.

Lactobacillus sakei is a highly prevalent species found in meat and seafood products. It is used as a model organism for studying food fermentation, biopreservation, and spoilage. These different outcomes might depend on the food matrix and storage conditions but can also be strain dependent, as the species is known to exhibit high intraspecies diversity (1, 2).

Therefore, sequencing of the *L. sakei* genome was carried out to obtain at least two complete genome sequences from strains belonging to each of the three lineages previously shown by multilocus sequence typing (2). The remaining strains were sequenced as drafts. Furthermore, two complete large plasmids were fully sequenced to increase our knowledge of the plasmidic repertoire of the species, including the 70-kb plasmid pJ23A1 of the parent strain, *L. sakei* 23K (3).

The whole-genome sequencing of these strains was carried out by Eurofins MWG Operon Laboratories (Ebersberg, Germany) using either a mix of Sanger and pyrosequencing GS-FLX+ for complete genomes or Illumina MiSeq 2 × 150-bp paired-end libraries for draft genomes. Reads were assembled *de novo* by Velvet software (4). All contigs were aligned against the relevant 23K strain complete genome using progressiveMauve (5), and annotation was performed with a combination of MicroScope (6) and AGMIAL (7) platforms.

Accession number(s). Sequence data have been deposited in DDBJ/ENA/GenBank under the accession numbers cited in Table 1.

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Address correspondence to Stéphane Chaillou, stephane.chaillou@inra.fr.

* Present address: Monique Zagorec, SECALIM, INRA, Oniris, Université Bretagne Loire, Nantes, France.

TABLE 1 Overview of the complete and draft genome assemblies from nine *L. sakei* strains

| Phylogeny | Status | Original strain name (synonym[s]) | Collection name | Source, yr | Genetic element | No. of contigs | Size (bp) | Coverage (x) | No. of CDSs ^c | BioProject no. | GenBank accession no. |
|------------------------|----------|-----------------------------------|-----------------|----------------------|----------------------------|----------------|-----------|--------------|--------------------------|----------------|---------------------------|
| Lineage 1 ^a | | | | | | | | | | | |
| CC1A | Complete | J64 (64, JOUY-64) | CNCM I-4394 | Dry sausage, 1982 | Chromosome | 1 | 2,050,232 | 49 | 2,102 | PRJEB22335 | LT960781 |
| | | | | | Plasmid 2 (pJ64A2) | 1 | 46,347 | 65 | 55 | | LT960782 |
| | | | | | Plasmid 3 (pJ64F) | 1 | 1,526 | 127 | 2 | | LT960783 |
| CC1A | Complete | MFPB16A1401 | CIP 110933 | Beef carpaccio, 2009 | Chromosome | 1 | 1,994,583 | 51 | 1,960 | PRJEB22338 | LT960788 |
| | | | | | Plasmid pMFPB16A1401A1 | 1 | 47,094 | 63 | 53 | | LT960789 |
| Lineage 2 | | | | | | | | | | | |
| CC2A | Complete | 23K ^d | | Dry sausage, 1990 | Plasmid pJ23A1 | 1 | 70,516 | 51 | 92 | PRJEB22564 | LT907984 |
| CC2B | Complete | MFPB19A1501 (MFPB19) | CNCM I-4396 | Beef carpaccio, 2009 | Chromosome | 1 | 2,045,293 | 65 | 1,977 | PRJEB22337 | LT960784 |
| | | | | | Plasmid 2 (pMFPB19A1501A1) | 1 | 57,338 | 67 | 67 | | LT960785 |
| | | | | | Plasmid 3 (pMFPB19A1501A1) | 1 | 11,996 | 154 | 16 | | LT960786 |
| | | | | | Plasmid 4 (pMFPB19A1501B) | 1 | 11,156 | 252 | 9 | | LT960787 |
| CC2B | Draft | J156 (156, JOUY-156) | CIP 110931 | Dry sausage, 1990 | Chromosome | 53 | 1,799,177 | 58 | 1,817 | PRJEB22332 | OBHL01000001–OBHL01000053 |
| | | | | | Plasmid pJ156A1 | 1 | 48,944 | 86 | 55 | | OBHL01000054 |
| | | | | | Plasmid pJ156B | 1 | 12,002 | 299 | 15 | | OBHL01000055 |
| | | | | | Plasmid pJ156C | 1 | 10,871 | 237 | 9 | | OBHL01000056 |
| | | | | | Plasmid pJ156D | 1 | 6,593 | 343 | 7 | | OBHL01000057 |
| | | | | | Plasmid pJ156E | 1 | 2,855 | 501 | 4 | | OBHL01000058 |
| CC2C | Draft | J160x1 (160x1) | CIP 110932 | Horse meat, 1981 | Chromosome | 32 | 1,842,916 | 61 | 1,857 | PRJEB22333 | OBHK01000001–OBHK01000032 |
| | | | | | Plasmid pJ160A1 | 1 | 51,764 | 504 | 62 | | OBHK01000033 |
| | | | | | Plasmid pJ160E | 1 | 2,211 | 441 | 4 | | OBHK01000034 |
| Lineage 3 | | | | | | | | | | | |
| CC3A | Complete | FLEC01 | CNCM I-4395 | Human feces, 2008 | Chromosome | 1 | 1,902,372 | 46 | 1,919 | PRJEB22336 | LT960777 |
| | | | | | Plasmid 2 (pFLEC01A2) | 1 | 31,701 | 55 | 36 | | LT960778 |
| | | | | | Plasmid 3 (pFLEC01B) | 1 | 12,663 | 345 | 16 | | LT960779 |
| | | | | | Plasmid 4 (pFLEC01C) | 1 | 11,068 | 377 | 10 | | LT960780 |
| CC3A | Draft | J112 (112, JOUY-112) | CIP 110930 | Dry sausage, 1990 | Chromosome | 38 | 1,893,060 | 85 | 1,913 | PRJEB22330 | OBHN01000001–OBHN01000038 |
| | | | | | Plasmid pJ112A1 | 1 | 52,100 | 85 | 62 | | OBHN01000039 |
| | | | | | Plasmid pJ112B | 1 | 11,994 | 129 | 14 | | OBHN01000040 |
| | | | | | Plasmid pJ112C | 1 | 10,871 | 452 | 9 | | OBHN01000041 |
| | | | | | Plasmid pJ112D | 1 | 6,593 | 588 | 7 | | OBHN01000042 |
| CC3B | Complete | J54 (54, JOUY-54) | CNCM I-4393 | Dry sausage, 1990 | Chromosome | 1 | 1,964,671 | 76 | 1,982 | PRJEB22334 | LT960790 |
| | | | | | Plasmid 2 (pJ54A1) | 1 | 33,463 | 86 | 36 | | LT960791 |
| | | | | | Plasmid 3 (pJ54C) | 1 | 13,205 | 241 | 15 | | LT960792 |
| CC3B | Complete | T332 (332) ^e | | Pork meat, 1987 | Plasmid p332A2 | 1 | 72,950 | 43 | 89 | PRJEB22565 | LT907987 |
| Admixed ^b | Draft | J18 (18, JOUY-18) | CIP 110934 | Dry sausage, 1990 | Chromosome | 27 | 1,824,746 | 56 | 1,826 | PRJEB22331 | OBHJ01000001–OBHJ01000027 |

^aAccording to Chaillou et al. (2).

^bMultilocus sequence typing previously revealed that strain J18 is a mixture of the three lineages due to numerous recombination events (2).

^cCDS, coding sequence.

^dPlasmid pJ23A1 originated from the strain *L. sakei* 23, the chromosome of which has already been sequenced (3).

^ePlasmid p332A2 was sequenced from strain 332, the chromosome of which has been sequenced.

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