



**Draft genome sequences of *Lactobacillus equicursoris*
CIP 110162 τ and *Lactobacillus* sp. strain CRBIP
24.137, isolated from thoroughbred racehorse feces and
human urine, respectively**

Sylvie Cousin, Valentin Loux, Laurence Ma, Sophie Creno, Dominique
Clermont, Chantal Bizet, Christiane Bouchier

► To cite this version:

Sylvie Cousin, Valentin Loux, Laurence Ma, Sophie Creno, Dominique Clermont, et al.. Draft genome sequences of *Lactobacillus equicursoris* CIP 110162 τ and *Lactobacillus* sp. strain CRBIP 24.137, isolated from thoroughbred racehorse feces and human urine, respectively. *Genome Announcements*, 2013, 1 (4), pp.1-2. 10.1128/genomeA.00663-13 . hal-02645656

HAL Id: hal-02645656

<https://hal.inrae.fr/hal-02645656>

Submitted on 29 May 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Draft Genome Sequences of *Lactobacillus equicursoris* CIP 110162^T and *Lactobacillus* sp. Strain CRBIP 24.137, Isolated from Thoroughbred Racehorse Feces and Human Urine, Respectively

Sylvie Cousin,^a Valentin Loux,^b Laurence Ma,^c Sophie Creno,^c Dominique Clermont,^a Chantal Bizet,^a Christiane Bouchier^c

Institut Pasteur, Centre de Ressources Biologiques de l'Institut Pasteur, Département Microbiologie, Paris, France^a; Institut Pasteur, Plate-forme Génomique, Département Génomes et Génétique, Paris, France^b; INRA, UR1077 Mathématique, Informatique et Génome, Jouy-en-Josas, France^c

We report the draft genome sequences of strain *Lactobacillus equicursoris* CIP 110162^T, isolated from racehorse breed feces, and *Lactobacillus* sp. strain CRBIP 24.137, isolated from human urine; the two strains are closely related. The total lengths of the 116 and 62 scaffolds are about 2.157 and 2.358 Mb, with G+C contents of 46 and 45% and 2,279 and 2,342 coding sequences (CDSs), respectively.

Received 30 July 2013 Accepted 31 July 2013 Published 22 August 2013

Citation Cousin S, Loux V, Ma L, Creno S, Clermont D, Bizet C, Bouchier C. 2013. Draft genome sequences of *Lactobacillus equicursoris* CIP 110162^T and *Lactobacillus* sp. strain CRBIP 24.137, isolated from thoroughbred racehorse feces and human urine, respectively. *Genome Announc.* 1(4):e00663-13. doi:10.1128/genomeA.00663-13.

Copyright © 2013 Cousin et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](http://creativecommons.org/licenses/by/3.0/).

Address correspondence to Christiane Bouchier, bouchier@pasteur.fr.

Lactobacillus equicursoris strain CIP 110162^T was isolated from the feces of a healthy thoroughbred racehorse in Japan, whereas *L. equicursoris* strain 66C is a clinical isolate from a human urine sample; 66C was deposited at the collection of the Institut Pasteur under the name CRBIP 24.137. It was previously demonstrated that strain CIP 110162^T formed a subcluster in the *Lactobacillus delbrueckii* phylogenetic group and was closely related to *L. delbrueckii* but yet genetically distinct from its phylogenetic relatives (1). Sequence analysis of the 16S rRNA gene revealed that strain CRBIP 24.137 shows 99.1% similarity with the strain *L. equicursoris* CIP 110162^T. DNA–DNA relatedness between strain 66C and the closely related type strains was more than the 70% cutoff value that is recommended for species delineation (2). The average nucleotide identity between the 2 genomes is 99.8% (3). These figures confirm that the two strains belong to the same species.

Here, we report the genome sequences of *L. equicursoris* CIP 110162^T and *Lactobacillus* sp. strain CRBIP 24.137, obtained using a whole-genome strategy based on Illumina paired-end sequencing, with insert lengths of about 420 and 352 bp, respectively (Illumina HiSeq 2000), as observed on Agilent high-sensitivity DNA kit. Quality-filtered reads (71,743,098 and 68,403,694 reads, 97 and 97.7 bases mean read length, and ~3,040 and 2,790-fold coverage, respectively) were assembled using ABySS software (version 1.2.6 [4]) with different *k*-mer lengths (*k*) of 25, 30, 40, and 60. Scaffolds with maximum lengths of 122,530 and 254,168 bases were obtained with *k* values of 40 and 60, respectively.

The draft genomes for CIP 110162^T and CRBIP 24.137 consist of 2,156,576 and 2,357,741 nucleotides (nt) split into 116 and 62 scaffolds and with G+C contents of 46 and 45%, respectively. The scaffolds were annotated with the AGMIAL platform (5), an integrated bacterial genome annotation system. The prediction of coding sequences used the self-training gene detection software SHOW based on hidden Markov models (<http://genome.jouy.inra.fr/ssb/SHOW/>). tRNAs and rRNAs were detected using

tRNAscan-SE (6) and RNAmmer (7) softwares, respectively. The numbers of predicted coding sequences (CDSs) were 1,937 and 2,104, respectively; 3 rRNA operons with 1 copy each of 23S, 5S, and 16S and 55 tRNA genes were detected for strain CIP 110162^T, while 5 rRNA operons with 2 and 3 copies of 5S and 16S, respectively, and 72 tRNA genes were detected for strain CRBIP 24.137.

Nucleotide sequence accession numbers. The strains are publicly available in two European collections under no. CIP 110162^T, DSM 19284^T, CRBIP 24.137, and DSM 23909. The draft of the whole-genome sequencing project has been deposited in EMBL under the accession no. [CAMA01000001](http://www.ebi.ac.uk/EMBL/seqdata/study/study_CAMA01000001) to [CAMA01000232](http://www.ebi.ac.uk/EMBL/seqdata/study/study_CAMA01000232) and [CALZ01000001](http://www.ebi.ac.uk/EMBL/seqdata/study/study_CALZ01000001) to [CALZ01000161](http://www.ebi.ac.uk/EMBL/seqdata/study/study_CALZ01000161), respectively. The versions described in this paper are the first versions.

ACKNOWLEDGMENTS

We thank N. Joly (Biology IT Center, Institut Pasteur, Paris) for the read quality filtering software. We are grateful to the INRA MIGALE bioinformatics platform (<http://migale.jouy.inra.fr>) for providing computational resources. We thank the DSMZ for providing DNA–DNA hybridization data.

This communication is an initiative of the European Consortium of Microbial Resource Centers (EMbaRC), supported by the European Commission's Seventh Framework Programme (FP7, 2007–2013), Research Infrastructures action under the grant agreement no. FP7-228310.

REFERENCES

- Morita H, Shimazu M, Shiono H, Toh H, Nakajima F, Akita H, Takagi M, Takami H, Murakami M, Masaoka T, Tanabe S, Hattori M. 2010. *Lactobacillus equicursoris* sp. nov., isolated from the faeces of a thoroughbred racehorse. *Int. J. Syst. Evol. Microbiol.* 60:109–112.
- Goebel SE. 1994. A place for DNA–DNA reassociation and 16S rRNA sequence analysis in the present species definition in bacteriology. *Int. J. Syst. Bacteriol.* 44:846–849.
- Richter M, Rösselo-Mora R. 2009. Shifting the genomic gold standards for the prokaryotic species definition. *Proc. Natl. Acad. Sci. U. S. A.* 45:19126–19131.
- Simpson JT, Wong K, Jackman SD, Schein JE, Jones SJ, Birol I. 2009.

- ABySS: a parallel assembler for short read sequence data. *Genome Res.* 19:1117–1123.
5. Bryson K, Loux V, Bossy R, Nicolas P, Chaillou S, van de Guchte M, Penaud S, Maguin E, Hoebeke M, Bessi eres P, Gibrat JF. 2006. AGMIAL: implementing an annotation strategy for prokaryote genomes as a distributed system. *Nucleic Acids Res.* 34:3533–3545.
 6. Lowe TM, Eddy SR. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. *Nucleic Acids Res.* 25: 955–964.
 7. Lagesen K, Hallin P, R odland EA, Staerfeldt HH, Rognes T, Ussery DW. 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. *Nucleic Acids Res.* 35:3100–3108.