



Lacticaseibacillus parahuelsenbergensis and L. styriensis, isolated from grass and corn silage

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INTRODUCTION

In a screening project at 45°C, two rod-shaped, non-motile, non-spore-forming, facultative anaerobic, Gram-stain positive lactic acid bacteria, designated as LD0937^T and SCR0063^T, were isolated from grass and corn silage. Polyphasic approach characterisation identified these as novel species of the *Lacticaseibacillus* genus [1].

MATERIAL & METHODS

- A core gene phylogenetic tree was constructed using the UBCG ver3.0 tool [2] and default options (Figure 1). The tree was visualized using the MEGA 11 software (version 11.0.3.) [3].
- For phenotypic characterization, the novel strains and all reference bacteria were cultivated on MRS agar plates at 37°C for 24 h under semi-anaerobic conditions in an anaerobic box with anaerogen bags. Growth tests were conducted in MRS broth with a range of parameters, including temperature (5 to 55°C), pH (3.0 to 10.5) and NaCl salt concentrations (4% w/v to 10% w/v). Using the commercially available test kit API 50 CH system (bioMèrieux), the capacity for carbohydrate metabolism was measured (Table 1).

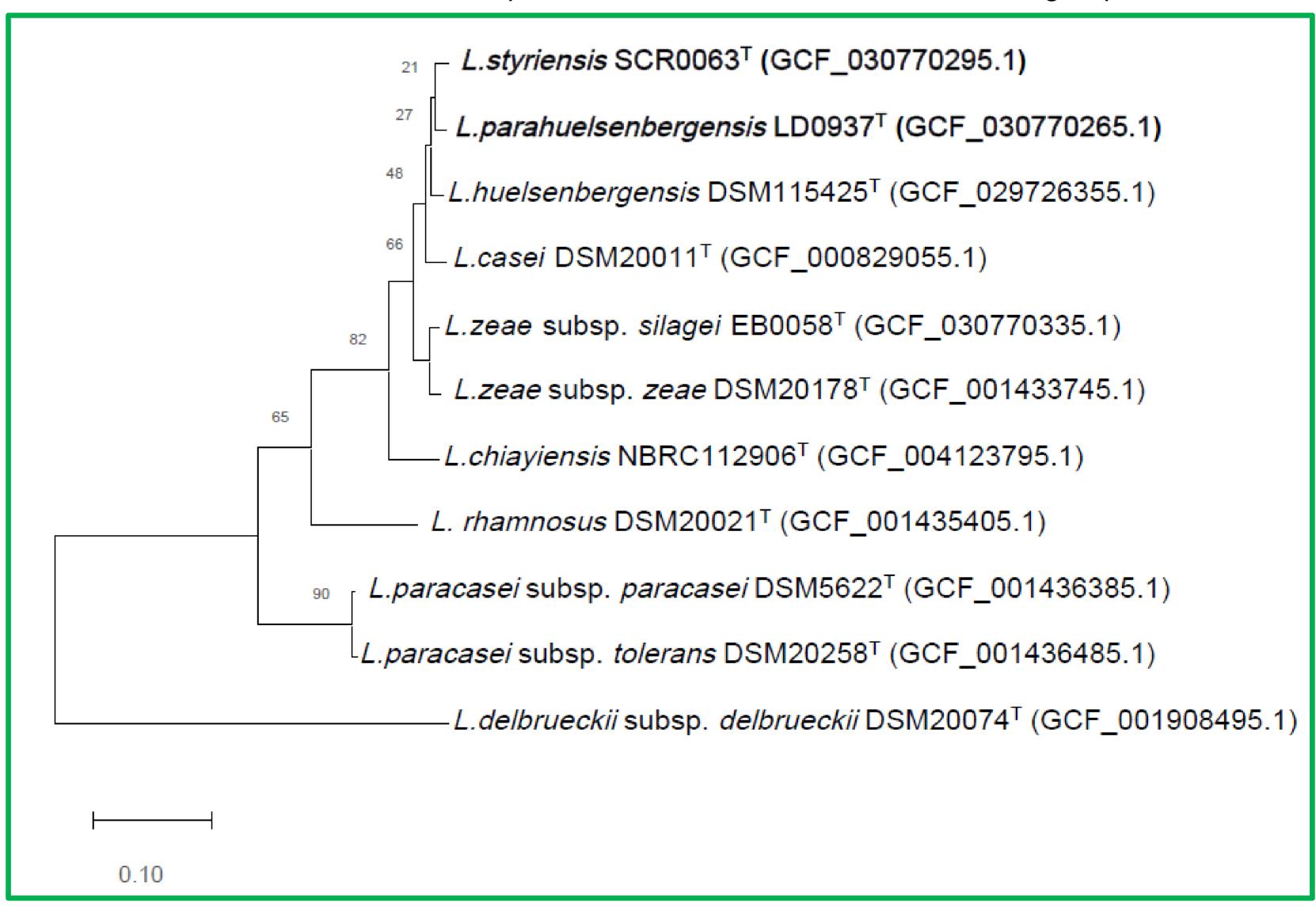
RESULTS & DISCUSSION

According to the analysis of the core genome, the isolates LD0937^T and SCR0063^T can be identified as novel species, *L. parahuelsenbergensis* LD0937^T and *L. styriensis* SCR0063^T (Figure 1).

Strain LD0937^T showed weak growth at pH 3.5 and good growth at pH 10.0 and in medium containing 8% w/v NaCl, whereas SCR0063^T showed weak growth in medium containing 8% w/v NaCl and good growth at pH 3.5 to pH 10.0, in contrast to the closest related strains. Both novel isolates could produce acid from L-Arabinose, LD0937^T from L-Sorbose and SCR0063^T from α -methyl-D-Mannoside, which was confirmed with functional genomics.

Table 1. Differential phenotypic and growth characteristics of the two isolates and their phylogenetically closest related type strains L. huelsenbergensis DSM 115425^T and L. casei DSM20011^T.

Figure 1. Phylogenetic analysis of the novel isolates LD0937^T and SCR0063^T core genome using UBCG tool. Reference strains are the phylogenetically closest related *Lacticaseibacillus* type strains. *Lactobacillus delbrueckii* subsp. *delbrueckii* DSM 20074^T served as outgroup.



	Growth at:			Acid production from:			
Strain	pH 3.5	pH 10.0	8% NaCl	L-Arabinose	α-methyl-D- Mannoside	L-Sorbose	Dulcitol
	pi 1 3.3	pi 10.0	070 NaCi	L-Alabiliose	Mailioside	L-301003E	Duicitoi
LD0937 ^T	W	+	+	+	_	+	_
SCR0063 ^T	+	+	W	+	+	_	_
L. huelsenbergensis							
DSM115425 ^T	+	_	W	_	_	_	+
L. casei DSM20011 ^T	-	_	-	_	_	-	-

+ ... good growth, w ... weak growth, - ... no growth



CONCLUSION

Based on this polyphasic approach, using genomic, phylogenetic, and phenotypic analysis, LD0937^T and SCR0063^T represent two novel species within the *Lacticaseibacillus* group: *Lacticaseibacillus parahuelsenbergensis* with the type strain LD0937^T (=DSM 116105 =NCIMB 15471) and *Lacticaseibacillus styriensis* with the type strain SCR0063^T (=DSM 116297 =NCIMB 15473).

References: