



ELSEVIER

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib



CrossMark

Data Article

Nucleotide sequence alignment of *hdcA* from Gram-positive bacteria

Maria Diaz, Victor Ladero*, Begoña Redruello,
Esther Sanchez-Llana, Beatriz del Rio, Maria Fernandez,
Maria Cruz Martin, Miguel A. Alvarez

Instituto de Productos Lácteos de Asturias, IPLA-CSIC, Paseo Río Linares s/n, 33300 Villaviciosa, Spain

ARTICLE INFO

Article history:

Received 3 December 2015

Received in revised form

22 December 2015

Accepted 9 January 2016

Available online 18 January 2016

ABSTRACT

The decarboxylation of histidine –carried out mainly by some gram-positive bacteria– yields the toxic dietary biogenic amine histamine (Ladero et al. 2010 [\[1\]](http://dx.doi.org/10.2174/157340110791233256), Linares et al. 2016 [\[2\]](http://dx.doi.org/10.1016/j.foodchem.2015.11.013)). The reaction is catalyzed by a pyruvoyl-dependent histidine decarboxylase (Linares et al. 2011 [\[3\]](http://dx.doi.org/10.1080/10408398.2011.582813)), which is encoded by the gene *hdcA*. In order to locate conserved regions in the *hdcA* gene of Gram-positive bacteria, this article provides a nucleotide sequence alignment of all the *hdcA* sequences from Gram-positive bacteria present in databases. For further utility and discussion, see [\[4\]](http://dx.doi.org/10.1016/j.foodcont.2015.11.035).

© 2016 Elsevier Inc.. Published by Elsevier Inc. This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0/>).

* Corresponding author.

E-mail address: ladero@ipla.csic.es (V. Ladero).

Specifications table

Subject area	<i>Microbiology</i>
More specific subject area	<i>Food microbiology</i>
Type of data	<i>Figure</i>
How data was acquired	<i>Retrieved from databases</i>
Data format	<i>Analyzed</i>
Experimental factors	<i>The nucleotide sequences were retrieved from NCBI database shown below</i>
Experimental features	<i>Sequences were aligned using ClustalW software and visualized using Jalview v.2 programme.</i>
Data source location	<i>N/A</i>
Data accessibility	<i>Data with article</i>

Value of the data

- Identification of Gram-positive bacteria *hdcA* gene present at databases.
- Sequence alignment defines conserved and variable regions within the *hdcA* sequence.
- Obtained data allowed to design primers within *hdcA* conserved regions -flanking variable ones- that can be used to identify histamine-producing species in food matrices by PCR-DGGE.

1. Data

Full-length *hdcA* sequences of the histamine-producing Gram-positive bacteria strains present in Genbank database were aligned using ClustalW software [5]. Based on the alignment of these sequences Fig. 1 was made and primers used in Diaz et al. 2016 [4] were designed. For reasoning and further utility and discussion, see [1–4].

2. Experimental design, materials and methods

Sequence data were obtained from NCBI (<http://www.ncbi.nlm.nih.gov/>) database. Full-length *hdcA* sequences of representative histamine-producing Gram-positive bacteria strains present in database were selected for the alignment (Table 1). The sequences were aligned by DNA multiple sequence alignment ClustalW software using default parameters [5]. The visualization, which included the percentage of conservation of each residue was obtained using Jalview v.2 programme [6].

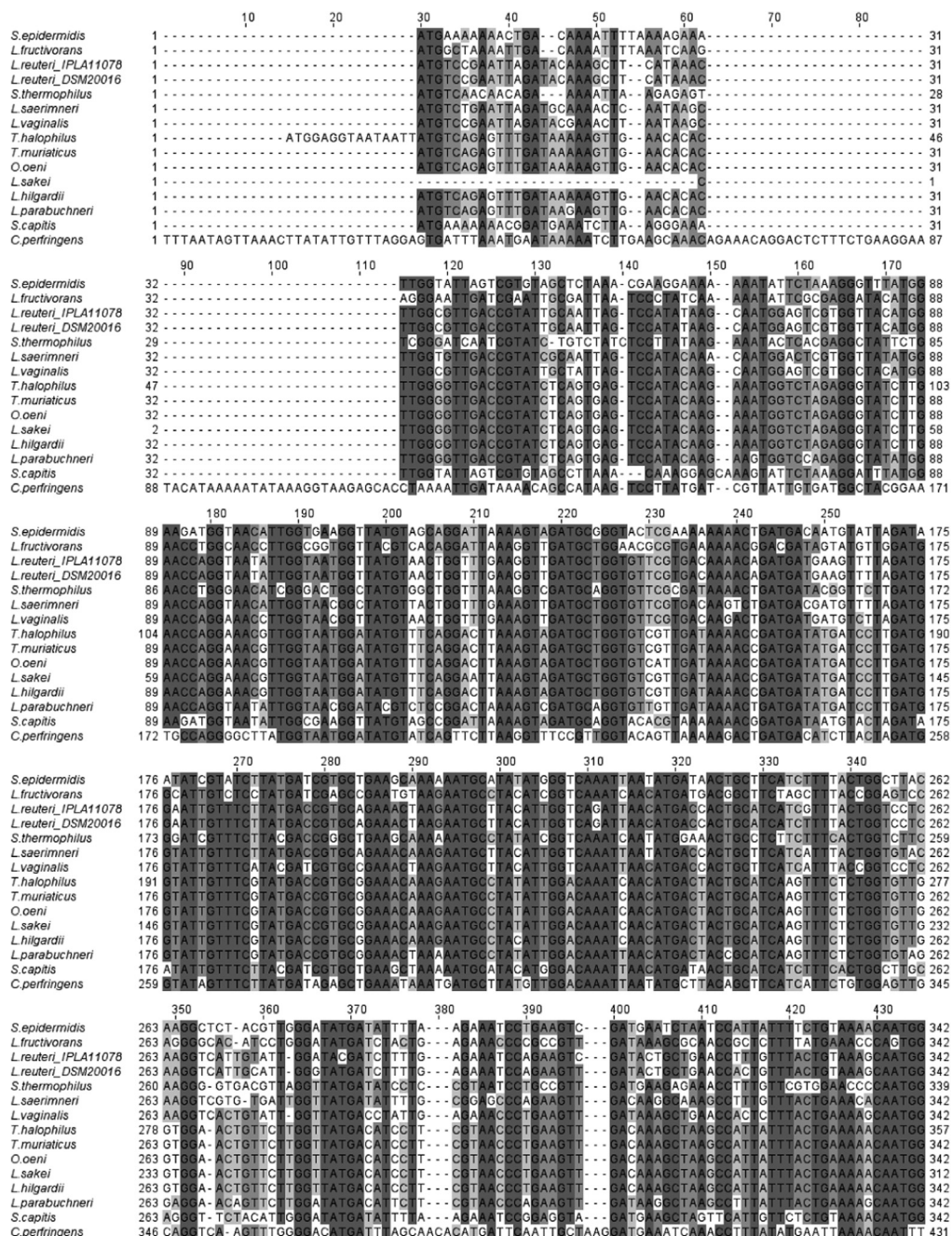


Fig. 1. hdaA sequences of Gram-positive bacteria strains, which are indicated in Table 1, were aligned using ClustalW software. The bacterial species are indicated at the left of each sequence. The gray tones correspond to the percentage of residues in each column that agree with a hypothetical consensus sequence: > 80%, > 60%, > 40%, < 40%. Selected regions for primer design are indicated with a box.

	440	450	460	470	480	490	500	510	520	
<i>S.epidermidis</i>	343	GATGGCAGTAAATACCAATTTATGATTTAAATACGCTTAAATGACACTTGTGAAATTTGGTACTGACACAGAGAGAGAT	428							
<i>L.fructivorans</i>	343	GATGGTTCCAAGCTTCCCAATCTATGACGGGAGGCGCTGCAAGATTACAGTGGTGAGTTTCGGAGCGGCTGTATACGGGACCA	428							
<i>L.reuteri_IPLA11078</i>	343	GATGGTTGTAACATTCGAATCTATGATGTTAGGCGGTACCAAGATTGCTTAGTGTAAACTTTGGTACTAATATACCGCGTCA	428							
<i>L.reuteri_DSM20016</i>	343	GATGGTAGTGAACATTCGAATCTATGATGTTAGGCGGTACCAAGATTGCTTAGTGTAAACTTTGGTACTAATATACCGCGTCA	428							
<i>S.thermophilus</i>	340	GATGGATCAAAATACCGATCTATGATGGCAAACTTACCAAGATGGCTTAGTGTAAATATTTGGCAGCGATCA-BATCGTGTCA	425							
<i>L.saeirneri</i>	343	GATGGCAGTAAATACCAATTTACGATGGTAGGCAATACCAAGATGGCTTAGTGTAAATATTTGGTACTGACAC-BATCGTGTCA	428							
<i>L.vaginalis</i>	343	GATGGCAGTAAATACCAATTTACGATGGTAGGCAATACCAAGATGGCTTAGTGTAAATATTTGGTACTGACAC-BATCGTGTCA	428							
<i>T.halophilus</i>	358	GACGGTAGTGAACITCCCAATTTACGATGGTAGGCGTTTACCAAGATGCTTAGTGTAAATCTTTGGTACTAATATACCGATATGGGTCA	443							
<i>T.muriaticus</i>	343	GACGGTAGTGAACITCCCAATTTACGATGGTAGGCGTTTACCAAGATGCTTAGTGTAAATCTTTGGTACTAATATACCGATATGGGTCA	428							
<i>O.oeni</i>	343	GACGGTAGTGAACITCCCAATTTACGATGGTAGGCGTTTACCAAGATGCTTAGTGTAAATCTTTGGTACTAATATACCGATATGGGTCA	428							
<i>L.sakei</i>	313	GACGGTAGTGAACITCCCAATTTACGATGGTAGGCGTTTACCAAGATGCTTAGTGTAAATCTTTGGTACTAATATACCGATATGGGTCA	398							
<i>L.hilgardii</i>	343	GACGGTAGTGAACITCCCAATTTACGATGGTAGGCGTTTACCAAGATGCTTAGTGTAAATCTTTGGTACTAATATACCGATATGGGTCA	428							
<i>L.parabuchneri</i>	343	GACGGTAGTGAACITCCCAATTTACGATGGTAGGCGTTTACCAAGATGCTTAGTGTAAATCTTTGGTACTAATATACCGATATGGGTCA	428							
<i>S.capitis</i>	343	GATGGCAGTAAATACCAATTTATGATTTAAATACGCTTAAATGCTCTTTGTAATATTCGGAACCTGACACAGAGAGAGAGCA	428							
<i>C.perfringens</i>	432	GATGGACCCCACTTAAGCTTTATGATGGCAAACTTTATTAGAACGTTGGTAAGAACCTTTCCGTACA-GAATAAATAGAGCTTT	517							
	530	540	550	560	570	580	590	600		
<i>S.epidermidis</i>	429	TCCTTTAACTCCAGGAGCAATGTC--ATTTGTGCTATTAAGGTGTTGTGGGCTCAGAAC--	509							
<i>L.fructivorans</i>	429	TCTTCCGACACCGG--TAGTTTCAITGTCTGTGTGGCAAGGAGTACAGGGGACAGAC--	509							
<i>L.reuteri_IPLA11078</i>	429	CTATCCAGCTCGTGGTTTGA--TTTCAITGTTTGTGCTAATAAGGTGTTACTGTGTAACCTCC--	509							
<i>L.reuteri_DSM20016</i>	429	CTATCCAGCTCCAGGTTTGA--TTTCAITGTTTGTGCTAATAAGGTGTTACTGTGTAACCTCC--	509							
<i>S.thermophilus</i>	426	CAATTTAGTTCCTGGCBCC--AGGGTGGTTGTGCTAACAAAGGTGTAGCTGGATATGCGGCCAAGGGATCCGCTTCCA--	507							
<i>L.saeirneri</i>	429	CTATCCAGCTCCAGGTTTGA--TTTCAITGTTTGTGCTAACAAAGGTGTACTGTGTAACCTCC--	509							
<i>L.vaginalis</i>	429	CTATCCAGCTCCAGGTTTGA--TTTCAITGTTTGTGCTAACAAAGGTGTACTGTGTAACCTCC--	509							
<i>T.halophilus</i>	444	CTATCCGTCCTCCAGGTGGA--TTTGTATGCTGTGGCAACAAAGGTGTACTGTGTAACCTCC--	524							
<i>T.muriaticus</i>	429	CTATCCGTCCTCCAGGTGGA--TTTGTATGCTGTGGCAACAAAGGTGTACTGTGTAACCTCC--	509							
<i>O.oeni</i>	429	CTATCCGTCCTCCAGGTGGA--TTTGTATGCTGTGGCAACAAAGGTGTACTGTGTAACCTCC--	509							
<i>L.sakei</i>	399	CTATCCGTCCTCCAGGTGGA--TTTGTATGCTGTGGCAACAAAGGTGTACTGTGTAACCTCC--	479							
<i>L.hilgardii</i>	429	CTATCCGTCCTCCAGGTGGA--TTTGTATGCTGTGGCAACAAAGGTGTACTGTGTAACCTCC--	509							
<i>L.parabuchneri</i>	429	TTATCCAGCTCTGGTGGT--TTTGTATGCTGTGGCAACAAAGGTGTACTGTGTAACCTCC--	509							
<i>S.capitis</i>	429	TCCTTTAACTCCAGGAGCA--AGTCAATCTGTGGCAATAAGGATTTTAGGCTCAGAAC--	509							
<i>C.perfringens</i>	518	TCAACTGCTCCAGGTGGA--CATGTAATATGTGGCAATAAGGATTTTAGGCTTATAGC--	598							
	610	620	630	640	650	660	670	680	690	
<i>S.epidermidis</i>	510	TGAATAAGAGGATATGGCTTTTGGTCAGATTTGGTATTTGATTCGAGAGGATAATATAAAGATTTCAGATATGTTTGTGAAGA	596							
<i>L.fructivorans</i>	510	TCCGGTGAAGCCCTATGGATTTTGGTCGGCATTTGGGATCTGAAATGGGAAGATCCGGTCTTACTGTTCCGATGTTTATCGAAGA	596							
<i>L.reuteri_IPLA11078</i>	510	ACCGGTCGAGGATATGGGTATGGTCAGGCAATGGCTTTGATTCGTAAGATACCTGCTGAAAGAGTTTCAAGCATGTTTATGAAGA	596							
<i>L.reuteri_DSM20016</i>	510	ACCGGTCGAGGATATGGGTATGGTCAGGCAATGGCTTTGATTCGTAAGATACCTGCTGAAAGAGTTTCAAGCATGTTTATGAAGA	596							
<i>S.thermophilus</i>	508	GCC-GGTGAAGGCTATGGTGCTGTGTCAGGCAATGGTATCTGCTTTGCAAGCAGATGGTATGTTATTCAGATATGTTTGAAGA	593							
<i>L.saeirneri</i>	510	GCGAGCTCAAGGTTATGGGTATGGTCAGGCAATGGTATCTGCTTTGTAAGGATCTGCTAGTAACTTCAGCATGTTTGTGAAGA	596							
<i>L.vaginalis</i>	510	GCGTGTGCAAGGCTATGGGTATGGTCAGGCAATGGTATCTGCTTTGTAAGGATCTGCTAGTAACTTCAGCATGTTTGTGAAGA	596							
<i>T.halophilus</i>	525	GCGTGTGCAAGGATATGGGTATGGTCAGGCAATGGTATCTGCTTTGTAAGGATCTGCTAGTAACTTCAGCATGTTTGTGAAGA	611							
<i>T.muriaticus</i>	510	GCGTGTGCAAGGATATGGGTATGGTCAGGCAATGGTATCTGCTTTGTAAGGATCTGCTAGTAACTTCAGCATGTTTGTGAAGA	596							
<i>O.oeni</i>	510	GCGTGTGCAAGGATATGGGTATGGTCAGGCAATGGTATCTGCTTTGTAAGGATCTGCTAGTAACTTCAGCATGTTTGTGAAGA	596							
<i>L.sakei</i>	480	GCGTGTGCAAGGATATGGGTATGGTCAGGCAATGGTATCTGCTTTGTAAGGATCTGCTAGTAACTTCAGCATGTTTGTGAAGA	566							
<i>L.hilgardii</i>	510	GCGTGTGCAAGGATATGGGTATGGTCAGGCAATGGTATCTGCTTTGTAAGGATCTGCTAGTAACTTCAGCATGTTTGTGAAGA	596							
<i>L.parabuchneri</i>	510	GCGAGTCGAGGCTATGGGTATGGTCAGGCAATGGTATCTGCTTTGTAAGGATCTGCTAGTAACTTCAGCATGTTTGTGAAGA	596							
<i>S.capitis</i>	510	TGAATAAGAGGATATGGGTATGGTCTTTTAGGCTATAGCATTAATAATAGGAGGATCTGTGTGACTAATTCATGAAGA	685							
<i>C.perfringens</i>	599	AGAAAGAGGCTATGGGTATGGTCTTTTAGGCTATAGCATTAATAATAGGAGGATCTGTGTGACTAATTCATGAAGA	685							
	700	710	720	730	740	750	760	770	780	
<i>S.epidermidis</i>	597	TGCAAGTAATGG--ATAGATCG--AGTGTGGTAATATAGCAATATTTAAATGAAAAAGCTCTCTTAACTTAATGAGTAAG	680							
<i>L.fructivorans</i>	597	CCGAGGACCTGG--ATTCCGCG--AAATAGGACATTTACAGAGCTTTCTTACTGGCGGAGCGCTGCTCTCTCTTTG	680							
<i>L.reuteri_IPLA11078</i>	597	TGCTGGGTAAG--GAAACGCG--TAACCAAGATGAATTAATGATATCTTAAGGTGTGCTGATAGCAATTCCTAAAGTCAATTTG	680							
<i>L.reuteri_DSM20016</i>	597	TGCTGGGTAAG--GAAACGCG--TAATBAAGATGAATTAATGATATCTTAAGGTGTGCTGATAGCAATTCCTAAAGTCAATTTG	680							
<i>S.thermophilus</i>	594	CCGCGTGTGTTGGACGAATAATGATACCAAGAGCTGATTTGACCTTGGCTGCTACTGTGCTCAAAAGGTTTGCACAACTCTTGG	680							
<i>L.saeirneri</i>	597	TGCTGGGTTTGG--GAAACTCC--TAACCAAGATGAATTAATGATATCTTAAGGCGGTGCTAATGCAAGGCTCAATTTG	680							
<i>L.vaginalis</i>	597	TGCTGGGTTTGG--GAAACTCC--TAACCAAGATGAATTAATGATATCTTAAGGCGGTGCTAATGCAAGGCTCAATTTG	680							
<i>T.halophilus</i>	612	TGCTGGGTTTGG--GAACTCCG--TAACCAAGATGAATTAATGATATCTTAAGGCGGTGCTAATGCAAGGCTCAATTTG	695							
<i>T.muriaticus</i>	597	TGCTGGGTTTGG--GAACTCCG--TAACCAAGATGAATTAATGATATCTTAAGGCGGTGCTAATGCAAGGCTCAATTTG	680							
<i>O.oeni</i>	597	TGCTGGGTTTGG--GAACTCCG--TAACCAAGATGAATTAATGATATCTTAAGGCGGTGCTAATGCAAGGCTCAATTTG	680							
<i>L.sakei</i>	567	TGCTGGGTTTGG--GAACTCCG--TAACCAAGATGAATTAATGATATCTTAAGGCGGTGCTAATGCAAGGCTCAATTTG	650							
<i>L.hilgardii</i>	597	TGCTGGGTTTGG--GAACTCCG--TAACCAAGATGAATTAATGATATCTTAAGGCGGTGCTAATGCAAGGCTCAATTTG	680							
<i>L.parabuchneri</i>	597	TGCTGGGTTTGG--GAACTCCG--TAACCAAGATGAATTAATGATATCTTAAGGCGGTGCTAATGCAAGGCTCAATTTG	680							
<i>S.capitis</i>	597	TGCTGGTAATGG--ATAGATCG--TAGTBAAGATTAATAGGCAATCTGAATGAAAGAGCTGCTGATAGCTCACTGAAGAG	680							
<i>C.perfringens</i>	686	TGCTGGACTTTGGACAAATAATGATATCCAGAGATTTAGAGAAATCTTAGCAATATATAAAGCTGTAAGTTGGTCAGTAAT	772							
	790	800	810	820	830	840	850	860		
<i>S.epidermidis</i>	681	AGAGTGTGGGAGATTA-----ACCTGTCTGCT-----ATAAATCTTCATGGATGGATTGGCATATAAATGATGGAAG	752							
<i>L.fructivorans</i>	681	CCAGTGTGGGAGGACGCT-----AGCCTCTCTGCT-----TGCTAGTTCATGGATGCGTTTGGTCACTCATGATGAAGAG	752							
<i>L.reuteri_IPLA11078</i>	681	TBAGTGTGGGAGATGCT-----AATACCTTCATG-----TAAGGTTTCATGGATTGGCTTGGTCAATGGAATGATGAAG	752							
<i>L.reuteri_DSM20016</i>	681	TBAGTGTGGGAGATGCT-----AATACCTTCATG-----CAAGGTTTCATGGATTGGCTTGGTCAATGGAATGATGAAG	752							
<i>S.thermophilus</i>	681	AGAAATGGTTCAGATAGG-----CATGCTCGCT-----GCCAAGATAATATTTGGCTTGGCCATGACATGATGAAG	752							
<i>L.saeirneri</i>	681	TBAATGTGGTTCAGATAGG-----CATGCTCGCT-----TGAAAGTCTTGGATTTGGCTTGGCTCAATGATGATGAAG	752							
<i>L.vaginalis</i>	681	AGAGTGTGGTTCAGATAGG-----AATACCTTCATG-----CAAGGATTCATGGATTGGCTTGGCTCAATGATGATGAAG	752							
<i>T.halophilus</i>	696	AGCCCTGTGGCGAAACACTGCTGCCGCGGAAATGGTGGTGGCGTATTCACAAGCTCATGGATTGGATTGGACATGGAATGATGAAG	782							
<i>T.muriaticus</i>	681	AGCCCTGTGGCGAAACACTGCTGCCGCGGAAATGGTGGTGGCGTATTCACAAGCTCATGGATTGGATTGGACATGGAATGATGAAG	767							
<i>O.oeni</i>	681	AGCCCTGTGGCGAAACACTGCTGCCGCGGAAATGGTGGTGGCGTATTCACAAGCTCATGGATTGGATTGGACATGGAATGATGAAG	767							
<i>L.sakei</i>	651	AGCCCTGTGGCGAAACACTGCTGCCGCGGAAATGGTGGTGGCGTATTCACAAGCTCATGGATTGGATTGGACATGGAATGATGAAG	737							
<i>L.hilgardii</i>	681	AGCCCTGTGGCGAAACACTGCTGCCGCGGAAATGGTGGTGGCGTATTCACAAGCTCATGGATTGGATTGGACATGGAATGATGAAG	767							
<i>L.parabuchneri</i>	681	AGCCCTGTGGCGAAATACCGCGGCGGAAATGGTGGTGGCGTATTTAGTATGCTGAGATTCGGATTGGACATGGAATGATGAAG	767							
<i>S.capitis</i>	681	AGAAATGGTTCAGATAGG-----ACCTGCTTACAAATC-----TTACATGGATTGGCTTTGGCTATGAATGATGAGGAG	752							
<i>C.perfringens</i>	773	TBAATGTGGTACAGATTCT-----CAGTGTGTT-----TTGAAAGAAATTCACAGAGCTTTGGTTATGTAATATGAAGAG	844							

Fig. 1. (continued)

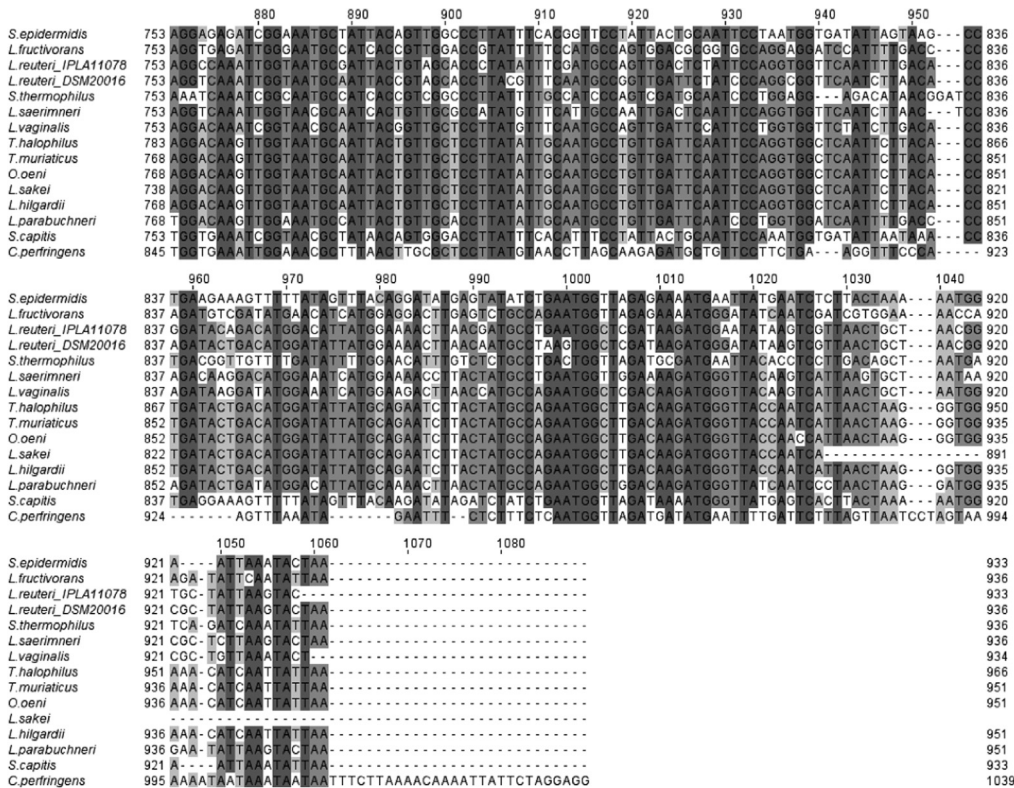


Fig. 1. (continued)

Table 1
Accession numbers of the *hdcA* gene sequences of representative histamine-producing Gram-positive bacteria strains present in database used for the alignment.

<i>hdc+</i> species	Accession number
<i>Staphylococcus epidermidis</i>	GeneBank: AB583189
<i>Lactobacillus fructivorans</i>	GeneBank: NZ_JQJ201000009
<i>Lactobacillus reuteri</i> IPLA11078	GeneBank: LN877767
<i>L. reuteri</i> DSM20016	GeneBank: NC009513
<i>Streptococcus thermophilus</i>	GeneBank: FN686789
<i>Lactobacillus saerimneri</i> 30a	GeneBank: NZ_ANAG0000000
<i>Lactobacillus vaginalis</i>	GeneBank: LN828720
<i>Tetragenococcus halophilus</i>	GeneBank: AB362339
<i>Tetragenococcus muritatus</i>	GeneBank: DQ132889
<i>Oenococcus oeni</i>	GeneBank: DQ132887
<i>Lactobacillus sakei</i>	GeneBank: DQ132888
<i>Lactobacillus hilgardii</i>	GeneBank: AY651779
<i>Lactobacillus parabuchneri</i>	GeneBank: LN877764
<i>Staphylococcus capitis</i>	GeneBank: AM283479
<i>Clostridium perfringens</i>	GeneBank: BA000016

Acknowledgments

This work was performed with the financial support of the Spanish Ministry of Economy and Competitiveness (AGL2013-45431-R) and the Plan for Science, Technology and Innovation 2013-2017 of the Principality of Asturias, which is co-funded by the European Regional Development Fund (GRUPIN14-137). M.D. was a beneficiary of an FPI fellowship from the Spanish Ministry of Economy and Competitiveness.

Appendix A. Supplementary material

Supplementary data associated with this article can be found in the online version at <http://dx.doi.org/10.1016/j.dib.2016.01.020>.

References

- [1] V. Ladero, M. Calles-Enríquez, M. Fernández, M.A. Alvarez, Toxicological effects of dietary biogenic amines, *Curr. Nutr. Food Sci.* 6 (2010) 145–156. <http://dx.doi.org/10.2174/157340110791233256>.
- [2] D.M. Linares, B. del Rio, B. Redruello, V. Ladero, M.C. Martin, M. Fernandez, P. Ruas-Madiedo, M.A. Alvarez, Comparative analysis of the in vitro cytotoxicity of the dietary biogenic amines tyramine and histamine, *Food Chem.* 197 (2016) 658–663. <http://dx.doi.org/10.1016/j.foodchem.2015.11.013>.
- [3] D.M. Linares, M.C. Martin, V. Ladero, M.A. Alvarez, M. Fernandez, Biogenic amines in dairy products, *Crit. Rev. Food Sci. Nutr.* 51 (2011) 691–703. <http://dx.doi.org/10.1080/10408398.2011.582813>.
- [4] M. Diaz, V. Ladero, B. Redruello, E. Sanchez-Llana, B. del Rio, M. Fernandez, M.C. Martin, M.A. Alvarez, A PCR-DGGE method for the identification of histamine-producing bacteria in cheese, *Food Control.* 63 (2016) 216–223. <http://dx.doi.org/10.1016/j.foodcont.2015.11.035>.
- [5] M.A. Larkin, G. Blackshields, N.P. Brown, R. Chenna, P.A. McGettigan, H. McWilliam, F. Valentin, I.M. Wallace, A. Wilm, R. Lopez, J.D. Thompson, T.J. Gibson, D.G. Higgins, Clustal W and Clustal X version 2.0, *Bioinformatics* 23 (2007) 947–2948.
- [6] A.M. Waterhouse, J.B. Procter, D.M.A. Martin, M. Clamp O, G.J. Barton, Jalview Version 2 – a multiple sequence alignment editor and analysis workbench, *Bioinformatics* 25 (2009) 1189–1191.