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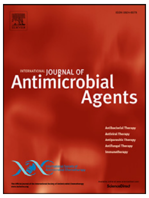

LABiocin database: A new database designed specifically for Lactic Acid Bacteria bacteriocins

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ABSTRACT

Bacteriocins from lactic acid bacteria (LAB) are successfully applied as natural alternatives to food preservation and to antibiotics; however, information on these antimicrobial peptides (AMPs) is scattered through the literature and databases. Therefore, we developed the LABiocin database, a specialized database on LAB bacteriocins. The database was stored and compiled using MySQL with NetBeans IDE as the platform. Important data are compiled, including bacteriocin name, class, amino acids and nucleic acid sequences, if available. Target microorganisms, origin, status of the producing strains and their culture conditions and extraction and purification methods are also included in this new database. A phylogenetic tree for the mature peptide bacteriocin sequences has also been created.

LABiocin is an interactive database with a user-friendly interface that integrates several tools and services and comprises up to 517 LAB bacteriocins. Besides data searching tools, a BLAST tool was integrated into the database to enable the user to perform a homology search against mature peptide sequences. Users can be linked to other databases that contain additional information, particularly about predicted bacteriocin structure and mechanisms of action.

The LABiocin database enables comprehensive functional analysis of this special group of AMPs. This would be useful in food preservation and food safety applications and would also have substantial implications for development of new drugs for medical use. LABiocin database is available at labiocin.net.

1. Introduction

Bacteriocins are antimicrobial peptides (AMPs) synthesized by certain bacteria via the ribosomal pathway and are generally active against closely related bacteria. Some bacteriocins have shown a wide range inhibitory spectrum [1]. The discovery of bacteriocins preceded that of antibiotics. Colicin was the first bacteriocin identified, in 1925, from an *Escherichia coli* strain [2]. Numerous bacteriocins have since been identified, leading to a diverse family of proteins in terms of size, target, mode of action, delivery, and immunity mechanisms.

Lactic acid bacteria (LAB) produce antimicrobial molecules, such as organic acids, diacetyl, acetoin, hydrogen peroxide, antifungal peptides, and bacteriocins [3]. Most LAB are Generally Recognized as Safe (GRAS), granted by the American Food and Drug Agency (FDA). The European Food Safety Authority (EFSA) also granted the Qualified Presumption of Safety (QPS) status to most of the LAB genera [4]. Bacteriocins produced by LAB have been successfully

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applied as natural antimicrobial alternatives in food preservation and in antibiotic therapy [5]. Hence, many research studies have been conducted to discover LAB bacteriocins and thoroughly investigate their properties and activities. Unfortunately, the information from these studies is scattered in various databases, thus hampering their availability and use for interested users. Therefore, gathering all LAB bacteriocins and their information in a specific database is an important task. Such a database is a fundamental tool for scientists, food authorities and food industries.

Several databases were created to hold AMPs and bacteriocins. Such databases could deliver information in a well-organized manner and facilitate comparison between stored bacteriocins (peptide sequence, inhibitory spectrum, resistance to extreme conditions, characterization methods, etc). Two databases comprising AMPs and bacteriocins are specialized in bacteriocins: BACTIBASE and BAGEL. BACTIBASE holds 177 bacteriocins in its last release, of which 156 bacteriocins belong to Gram-positive bacteria [6]. BAGEL4 (the latest release of BAGEL) [7], is a mining web server that identifies and visualizes gene clusters in bacteria and archeal genomes involved in biosynthesis of ribosomally-synthesized and post-translationally modified peptides (RiPPs). The database used in BAGEL4 for gene clusters prediction contains 254 bacteriocins from LAB [7]. More specialized databases are becoming increasingly available for the scientific community to enable users to query more homogenous and focalized databases on a particular theme. For example, RegulonDB and *Bacillus*-RegNet are comprehensive resources for transcriptional regulatory networks for *E. coli* and *Bacillus* spp., respectively [8,9].

There is a clear need to gather, filter and critically evaluate this mass of information and store it into smaller, more specialized resources to enhance efficiency. A new database designed specifically for LAB bacteriocins is therefore needed. The microbial, physicochemical and structural properties provided in such a database would enable more comprehensive structural and functional analysis of this special group of AMPs. This would be useful in food preservation and food safety applications and would also have implications for development of new drugs for medical use. The goal for the present work was to develop the LABiocin database, a specialized database on LAB bacteriocins. LABiocin has a user-friendly interface and offers a validated repository of LAB bacteriocins that enables users to extract, analyse and compare data.

2. Materials and Methods

2.1. Data collection

The LAB bacteriocins presented in the LABiocin database were extracted and collected from Scopus, Pubmed/Medline, Science Direct and other databases until August 2017. The keywords used were LAB bacteriocins, and antibacterial peptide. LAB bacteriocins from Bactibase (http://bactibase.hammamilab.org/main.php) and BAGEL3 (http://bagel.molgenrug.nl/) databases were also collected. The latter bacteriocins were verified from their original references to add all missing information. The information on bacteriocins gathered in the literature review were divided into three information groups: (i) general bacteriocin characteristics: class, charge, molecular weight (MW), isoelectric point (IP), solubility, producer organisms, and target bacteriocin organisms; (ii) bacteriocin sequences: full pre-peptide sequence, mature peptide sequence, leader sequence, corresponding accession numbers to UniProt database and to Protein and Nucleotide NCBI databases, and gene sequence (if available or predicted); (iii) in vitro characterization of bacteriocins: extraction, characterization and purification methods and conditions of bacteriocin production (culture medium, pH and temperature). As well as the literature review and the UniProt and Protein databases, NCBI tblastn software was used to retrieve gene sequences coding for peptidic bacteriocin sequences available in the Nucleotide collection (nr/nt) database. Genes were considered only if they had 100% query coverage and 100% identity between peptidic bacteriocin query and database sequences. The NCBI blastp program was used to search homologies in the Non-redundant protein sequences (nr) and UniProtKB/Swiss-Prot(swissprot) databases. If a peptidic database sequence had 100% identity with our query only characterized to a partial level by researchers, the full pre-peptide sequence of the database sequence was extracted and represented in the database. Both sequences (partial and full pre-peptide sequences) were mentioned in the bacteriocin entry in the LABiocin database with a note explaining this issue. Multiple sequence alignment was done using MUSCLE available at: https://www.ebi.ac.uk/Tools/msa/muscle/.

2.2. Database architecture

The LABiocin database was stored and compiled using MySQL (v 6.3), with NetBeans IDE 8.0.2 as the platform. HTML and JSP were used to improve the web interface. This database is available on the following domain: labiocin.net and is hosted at Lille University, France.

The LABiocin database contains 13 tables, with the bacteriocin table the main one. The relationships between these tables are represented in Figure 1 and can be summarized as follows. Each bacteriocin has one producer strain designed by full species name and code. This producer strain is isolated from one (or more) sources that can be human, animal, food or other source. A status, such as probiotic or starter, is given for each producer strain depending on the available information. Each producer strain requires some culture conditions to produce bacteriocin, such as culture medium type, medium pH, incubation time, and temperature. Each bacteriocin was extracted by one or two methods, such as salt precipitation, solvent extraction, or solid phase extraction, and then each was purified via one or two methods, such as Reverse-LC technique. Bacteriocin characterization was divided into several parts: (i) each bacteriocin should be classified in a class and/or subclass, such as Class I, Class II, subclass IIa, etc. In addition, each bacteriocin has (ii) a MW, (iii) an IP, and (iv) a peptide sequence (full sequence, mature sequence, partial sequence and leader peptide sequence). Therefore, many techniques and methods were used to characterize bacteriocins. Bacteriocin characterization methods included mass spectrometry, Edman degradation and SDS-PAGE. Bacteriocin is an AMP and exhibits an antimicrobial spectrum; each bacteriocin has its own antimicrobial spectrum designed by the list of the indicator strains used.

The full name, species and strain codes of the indicator strains were included and to ease classification, indicator strains were classified in several categories, such as Gram stain, fastidious, molds, yeast, etc.

Each bacteriocin has a reference designed by a published article or other. Sometimes, one bacteriocin can be mentioned in several references; thus, all these references are mentioned in the LABiocin database.

2.3. LABiocin data analysis

GraphPad Prism was employed for graph preparation and data analysis.

2.4. Phylogenetic tree

Two phylogenetic trees have been created: one for the 16S *rDNA* gene sequences of bacteriocin-producing LAB and the other for the mature peptide bacteriocin sequences. For the first tree, 16S

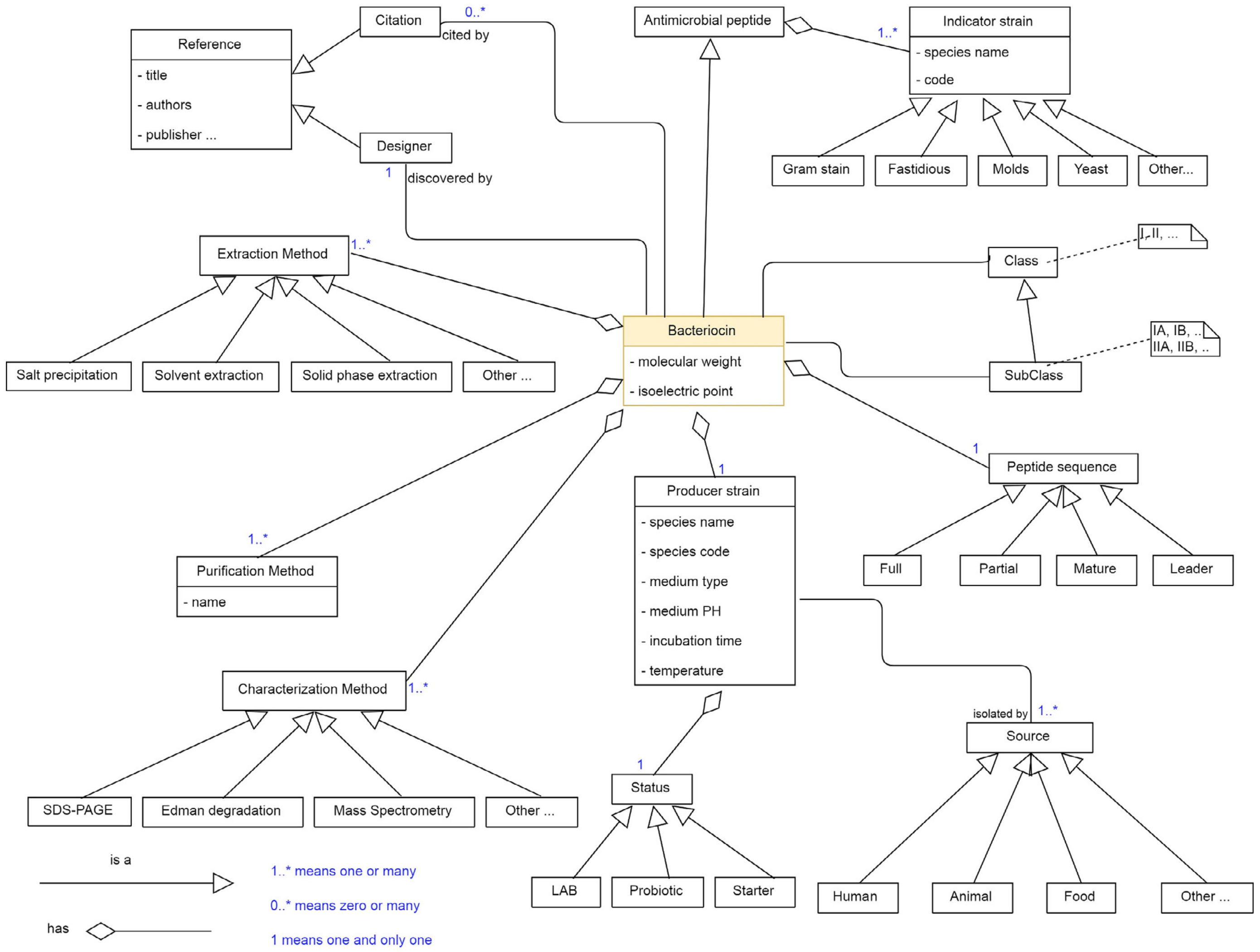


Fig. 1. LABiocin architecture. This figure shows the database tables, the stored data in each table and the relationships between these tables. The bacteriocin table was the main table.

rDNA gene sequences for each bacteriocin-producing LAB species available in our database were extracted from the representative genomes in the Genome database at NCBI. The Software Mega7 was used to construct the phylogenetic tree by Maximum likelihood method (Figure S1) [10]. For the second tree, the mature peptide bacteriocin sequences were aligned using MUSCLE v3.8.31 [11]. The obtained multiple sequence alignment was trimmed using the TrimAl v1.4. method [12]. After that, Protest3 determined the best-fit model of evolution for this datatest [13]. Then, FastTree v2.1.8 inferred the maximum-likelihood phylogenetic tree with WAG (Whelan-And-Goldman) as a model [14]. FastTree support values were calculated from the Shimodaira-Hasegawa test to provide an estimate of reliability of observed clusters. FigTree v1.4.3 was used to graphically display the trees (http://tree.bio.ed.ac.uk/software/figtree/).

3. Results and discussion

3.1. Brief Description

LABiocin is a worldwide free access database. However, the user must register and log in to the database with their proper username and password. The database homepage allows access to the following interfaces: Blast, Phylogeny, data analysis, About us, GeoMap, Contact, and Submit new bacteriocin (Figure 2). The user can also query the database directly from the homepage (discussed below). The results of a search query are given first in a simple table (Figure 2) that provides the user a quick view of some characteristics of the searched bacteriocin. The table shows the LABiocin accession number, the bacteriocin class, the bacteriocin producer strain, the MW, gene names and links to reference article in Pubmed, UniProt and NCBI databases (Protein and GenBank). The user can download the whole information and/or the Fasta format of bacteriocin sequences from a selected bacteriocin.

By clicking the name of a specific bacteriocin in the table, a new entry will show detailed information about this bacteriocin. This entry is divided into seven sections (Figure 2). The first section lists the bacteriocin details, such as bacterial status, IP, MW, electrostatic charge, solubility, full pre-peptide sequence, leader sequences, mature peptide sequence and gene sequence and their corresponding accession numbers to UniProt, NCBI databases and Bactibase, if available. The second section details the producer organism information, such as full name species, food matrix, environmental conditions from the bacterial source, and conditions used to induce bacteriocin production (culture medium, incubation temperature, pH). The third section shows the indicator strains tar-

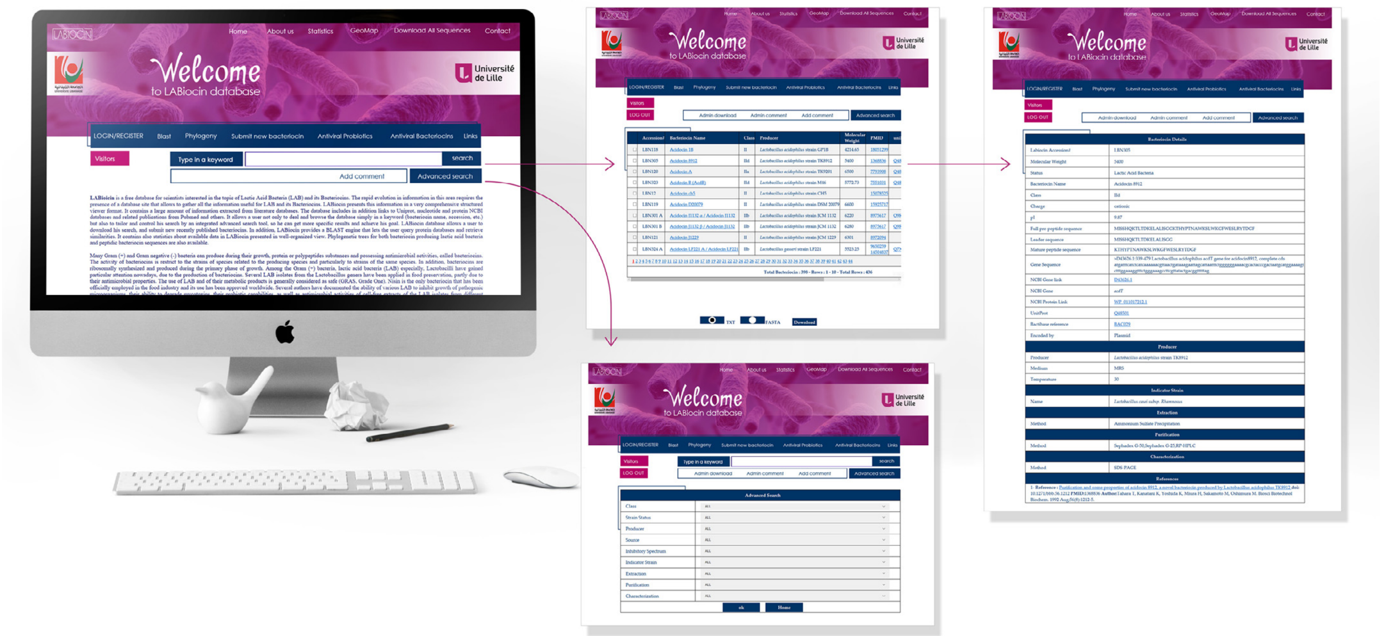


Fig. 2. LABiocin interfaces. **Top left** presents the database homepage that enables access to the following interfaces: Blast, Phylogeny, Statistics, About us, GeoMap, Contact, and Submit new bacteriocin. **Top middle** is a simple table that provides the user with a quick view of some characteristics of the searched bacteriocin. **Top right**, an interface shows detailed information about a specific bacteriocin. **Bottom middle**, an advanced tool search enables the user to perform complex queries and combine up to 9 fields in a single search.

geted by bacteriocins. The fourth, fifth and sixth sections list the extraction, purification, and characterization methods, respectively. The last section of this entry corresponds to the literature review of this bacteriocin.

3.2. Available tools

Various tools have been implemented to query the database. For data searching, two options are available: "type in a keyword" and "advanced search" tools. The "type in a keyword" tool allows the user to quickly query the database using a simple keyword. The keyword may be a bacteriocin name, a LABiocin accession number, antimicrobial spectrum or indicator strains, a producer status (starter culture, probiotic, etc), an extraction or purification method, or the origin of the bacteriocin producer, such as the food matrix. "Advanced search tool" enables the user to perform complex queries and combine up to 9 fields in a single search (Figure 2). The chosen term, within the inhibitory spectrum list, filters the appeared terms in the indicator strains list. For example, when the user chooses the inhibitory spectrum as Gram-positive, the given list in the indicator strain field systematically corresponds to Gram-positive genera. Besides data searching tools, a BLAST tool was integrated into the database to enable the user to perform a BLAST search against mature peptide sequences. Homologous sequences in the LABiocin database that have a high similarity with the query peptide will appear. To assess the similarity between the query and the aligned database sequences, many criteria were used such as the identity, similarity, query coverage, percentage of gaps, and E-value.

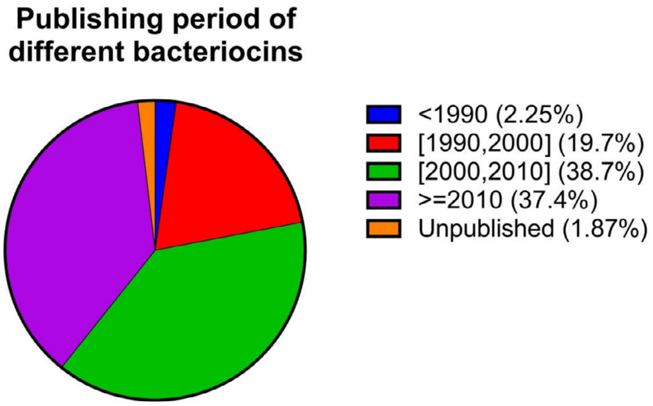


Fig. 3. Publishing period of different bacteriocins.

3.3. Services for users

Several services for users have been integrated into the LABiocin database. A "contact us interface" allows users to communicate with the database curators for any further requests or suggestions. To ensure a continuous update of our data, the user can directly submit the newly identified bacteriocin by sending an email with validated data using the "submit new bacteriocin" interface. The user can also download all available sequences in the database, including mature peptide sequences, full prepeptide sequences, partial sequences, and/or bacteriocin-encoding gene sequences. However, a previous contact with the curators for the commitment of terms and conditions of use of the LABiocin database is needed for download. Finally, a GeoMap interface shows the user popularity by country.

3.4. Phylogenetic trees

Of 517 bacteriocins stored in the LABiocin database, 267 with full mature peptide sequences were selected and analysed by Maximum likelihood phylogenetic tree based on their sequence similarities (Figure S2). If more than one bacteriocin had the same sequence, one bacteriocin sequence was selected to represent these identical bacteriocins in the tree (appendix 1). Several groups with high FastTree support values (more than 70%) were identified in the tree with the potential to identify bacteriocin classes. For class I bacteriocins, lantibiotics form well-defined groups dispersed in the tree and include lacticin 481, nisin, streptin, salivaricin 9, ClyLS, bovicin HJ50, pldA1, salivaricin A, mutacin 1140, and plantaricin w β groups. Moreover, class IIa bacteriocins define groups that are close to each other. These groups include sakacin X, bavaricin MN, mesentericin Y105, pediocin PA-1, and carnobacteriocin BM1. Bacteriocins of class IIb consist of ThmB, BlpM-TIGR4, salivaricin Abp118 β, sakacin T α, BlpN-TIGR4, lafX, lafA, BlpM-23F, enterocin X α, and latococcin G β groups. Bacteriocins of class IIc, IId, III, and IV as well as some divergent members of class I, IIa, and IIb are distributed across the tree. Furthermore, several unclassified or unknown bacteriocins that did not belong to a known bacteriocin class are scattered across the tree. Interestingly, the clustering of these unclassified or unknown bacteriocins with known bacteriocins with high FastTree support values may be explained by insufficient characterization of the bacteriocins or poor sequencing of other novel bacteriocins to constitute distinct groups. For examples, lactacin rm is clustered with enterocin AS-48 belonging to class IIc. Also, bacteriocin J46, a post-translationally unmodified bacteriocin, is clustered with the nisin group belonging to class I. In addition, some poorly characterized class II members grouped with well-defined members, such as Hiracin JM79, which is a Sec-dependent class II bacteriocin, clustered with the bavaricin MN group, a class IIa group. Finally, this sequence similarity-based tree fits well with structure-based sequence fingerprints that identify 12 groups in 107 analysed bacteriocins [15]; although some differences between these 2 trees are observed and are mainly due to the massive number of newly described bacteriocins analysed here. As discussed, phylogenetic trees may provide new horizons and solutions to classify bacteriocins that are insufficiently characterized under the current contradictory classification schemas.

3.5. Relevant results and LABiocin data analysis

The LABiocin database holds 517 LAB bacteriocins collected from scientific research articles up to August 2017. Each bacteriocin in our database is assigned a specific accession number starting with a prefix LBN. The availability of such a number of stored LAB bacteriocins allows deep data analysis that can be accessed by LABiocin users in a specific interface. The LABiocin data analysis (Figure 3) showed that LAB bacteriocins were not studied much up to 1990. Between 1990 and 2000 (19.7%), researchers started looking for new GRAS bacteriocins, such as LAB bacteriocins, for both food and medical applications. The majority of bacteriocins research (38.7%) was conducted between 2000 and 2010, and research continued after 2010 (37.4%).

3.5.1. Bacteriocinogenic potential in lactic acid bacteria

Our findings indicate that the *Lactobacillus* genus is the most bacteriocinogenic genus among the LAB family, accounting for 30.95% of total bacteriocinogenic LAB genera, followed by the *Enterococcus* genus with 24.18% of the total. *Weissella* and *Bifidobacterium* species exhibit the lowest percentages with 2.13% and 0.58%, respectively (Figure 4A). Interestingly, the percentage of bacteriocinogenic probiotic strains is very low (7.72%), based on the published bacteriocinogenic strain status (Figure 4B); however, 58.49% of bacteriocinogenic strains have no published status, therefore LAB status was given to these strains. The bacterial probiotic status of the LAB may change in the future depending on the research investigation.

3.5.2. LAB bacteriocins classification and antimicrobial spectrum

Among these 517 bacteriocins, 19.54% were classified in class IIa, and 17.6% were of unknown class. The “unclassified bacteriocins” (15.28%) are bacteriocins with sequences and/or structures that do not match any known class, whereas the “unknown bacteriocins” are bacteriocins with incomplete information, particularly

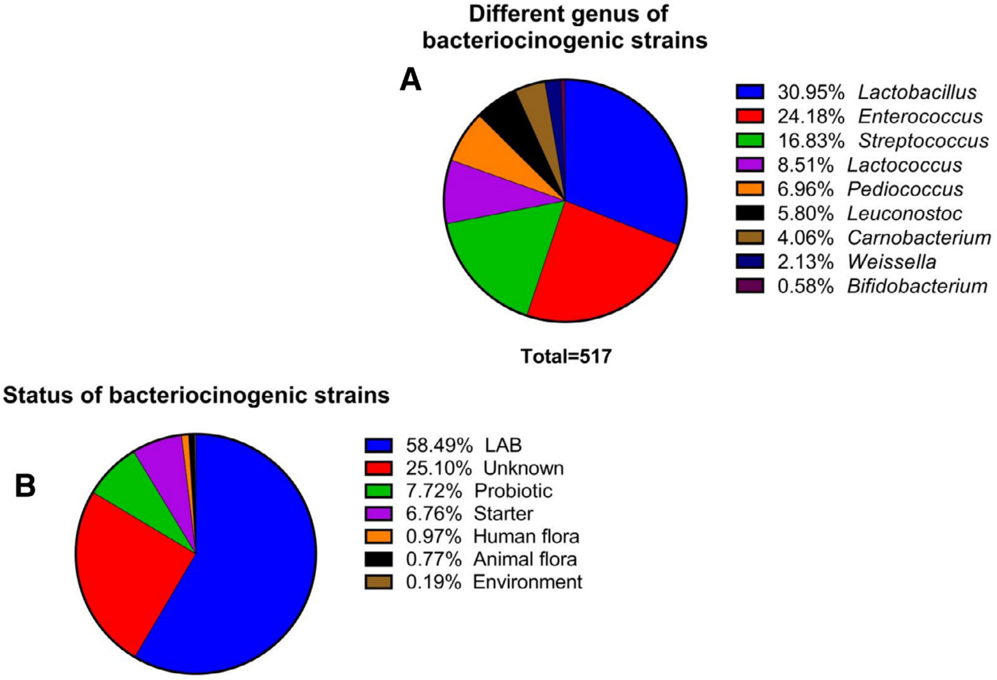


Fig. 4. A: The percentage of genus variability in bacteriocinogenic strains; B: Percentage of bacteriocinogenic strain status.

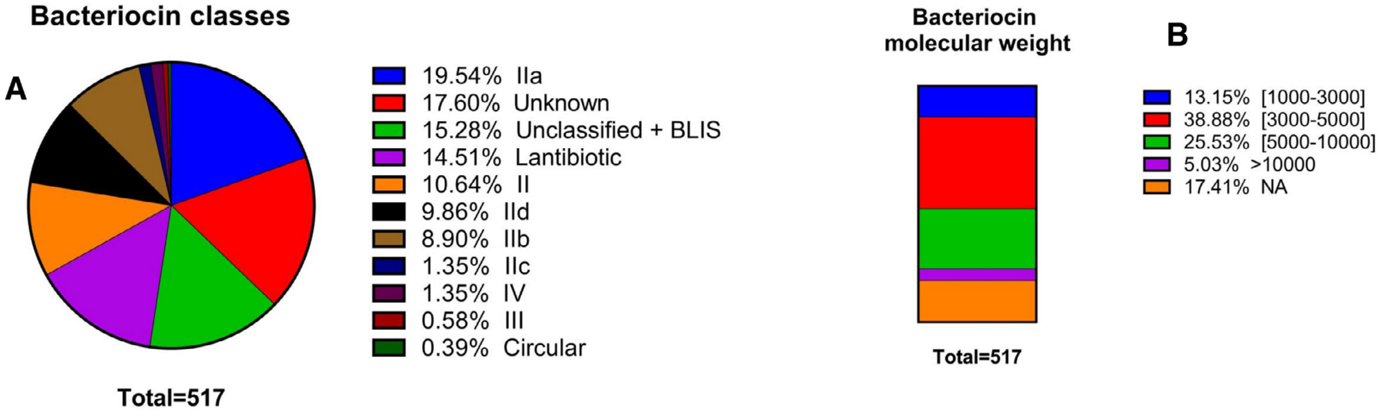


Fig. 5. A: Percentage of bacteriocin classes; B: Percentage of bacteriocin molecular weight.

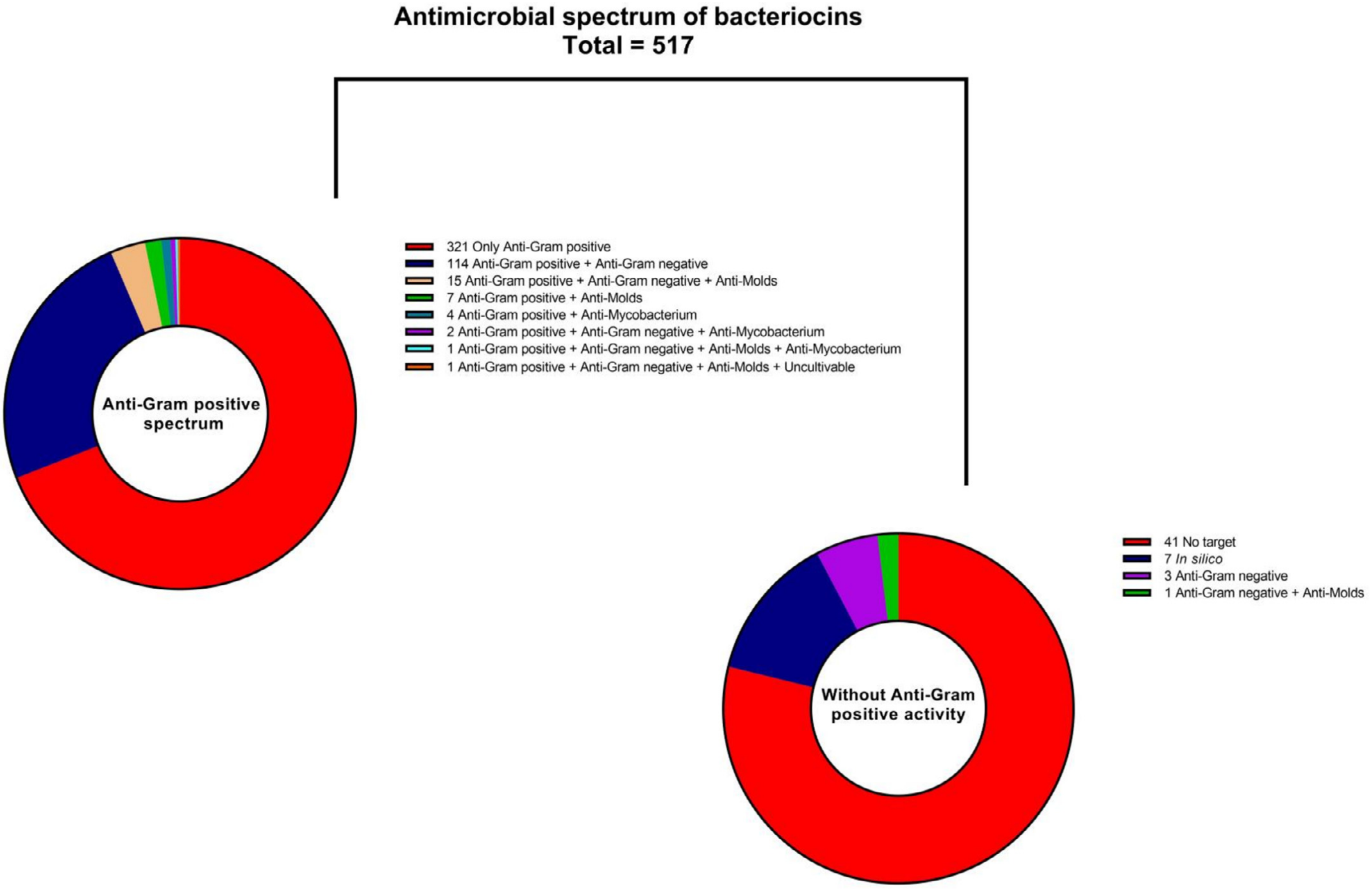


Fig. 6. Antimicrobial spectrum of bacteriocins.

in terms of peptide sequence. Class IIc, IV, III and circular bacteriocins are rare classes found in LAB bacteriocins at the following percentages 1.35, 1.35, 0.58 and 0.39%, respectively (Figure 5A).

Over one-third of LAB bacteriocins (38.88%) have a MW of 3-5 kDa; however, 17.4% of LAB bacteriocins have unidentified MW (Figure 5B). The most important characteristic of bacteriocins is the activity spectrum. Bacteriocins are generally known to be active against closely related bacteria; however, LAB bacteriocins seem to have a wide antimicrobial spectrum. For example, 114 bacteriocins among 517 show antimicrobial activity against both Gram-positive and Gram-negative bacteria. In addition, 24 bacteriocins exhibit anti-mold activity. Furthermore, the following bacteriocins "Bacteriocin VJ13B, Enterocin AS-48, Mutacin C67-1" and "Salivaricin A2, A3, A5 and Salivaricin A4" can inhibit *Mycobacterium* species, such as atypical mycobacteria (4) and *Mycobacterium tuberculosis* (2), respectively (Figure 6). The list of indicator strains was collected for each bacteriocin from published articles. Rare bacteriocins had more than one published article; therefore, all lists of indicator strains were compared and gathered in our database.

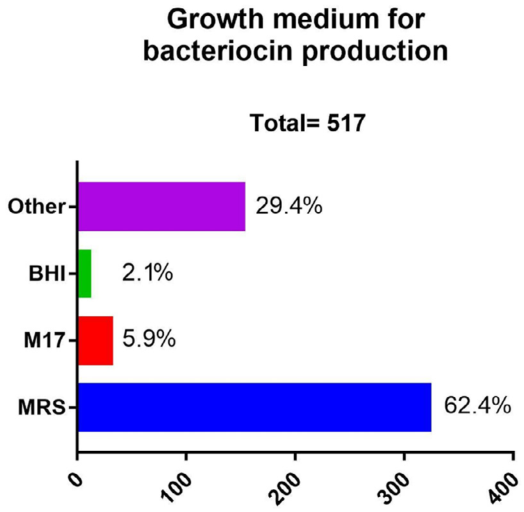


Fig. 7. Growth medium for bacteriocin production.

3.5.3. In silico predicted bacteriocins

Seven bacteriocins have been detected with in silico methods, such as whole genome sequencing of the producer strain followed by identification of bacteriocin gene clusters and characterization of bacteriocins. The methods used to detect and characterize bacteriocins are critical for re-identification and discovery of bacteriocins. These methods enable industries to characterize and produce bacteriocins in large scale for medical or food applications.

3.5.4. Culture conditions, extraction/purification and characterization methods

The LABiocin database summarizes the most important methods for future bacteriocin research. The most common medium used to produce a large amount of bacteriocins from LAB strains is De Man Rogosa Sharp (MRS) medium (62.4%) (Figure 7).

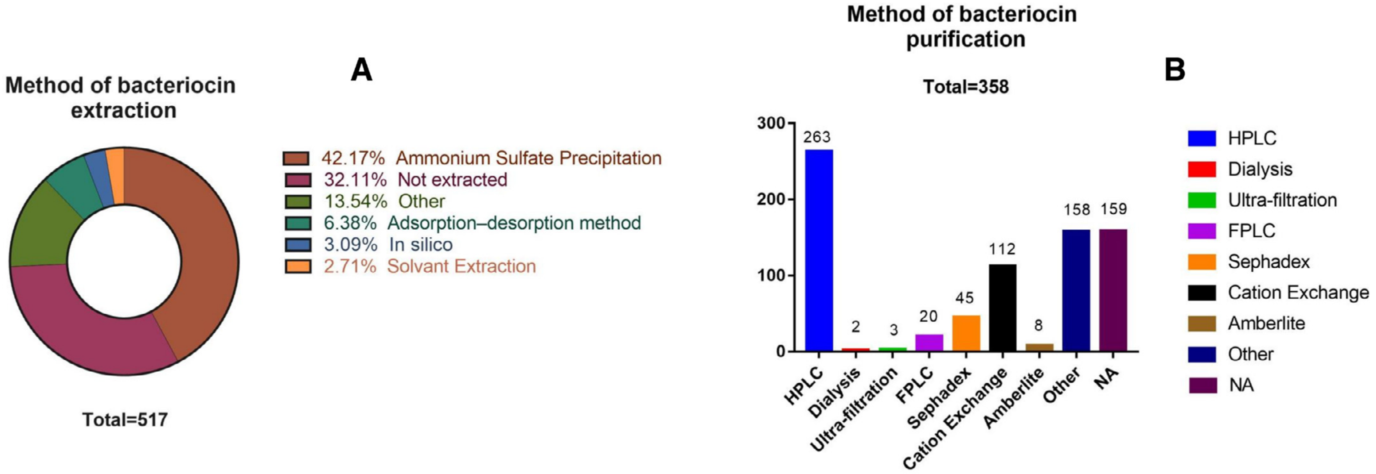
Ammonium sulfate precipitation is the most common method used to extract LAB bacteriocins (42.17%). The Yang method, an “adsorption-desorption” method, is the fourth most common (6.38%). Remarkably, a large number of bacteriocins (32.11%) were directly purified without an extraction step (Figure 8A). The C18-HPLC method was the most common purification method to purify LAB bacteriocins (263/358), followed by the cation exchange method (112/358) (Figure 8B). Bacteriocin characterization methods, such as MW determination and peptide sequencing, were used to identify bacteriocin properties. SDS-PAGE was the most common method used to determine bacteriocin MW (211/384), followed by MALDI-TOF and ESI-MS methods (123/384). The Edman degradation method was the most common method used to sequence LAB bacteriocins (Figure 9).

A sequenced bacteriocin is defined as a bacteriocin with a partial, mature or full pre-peptide sequence with or without a leader sequence. There are a total of 335 sequenced LAB bacteriocins, 292 of which have full pre-peptide sequences (leader and mature peptide sequences). A total of 174 do not have an identified sequence (blocked sequence and/or non-sequenced bacteriocins), and 58 LAB bacteriocins have been partially sequenced (Figure 10). Peptide and DNA sequences of 230 LAB bacteriocins are present in both the NCBI and Uniprot databases, whereas 75 do not appear in either the NCBI or Uniprot databases (Figure 10).

3.6. Comparison with other databases

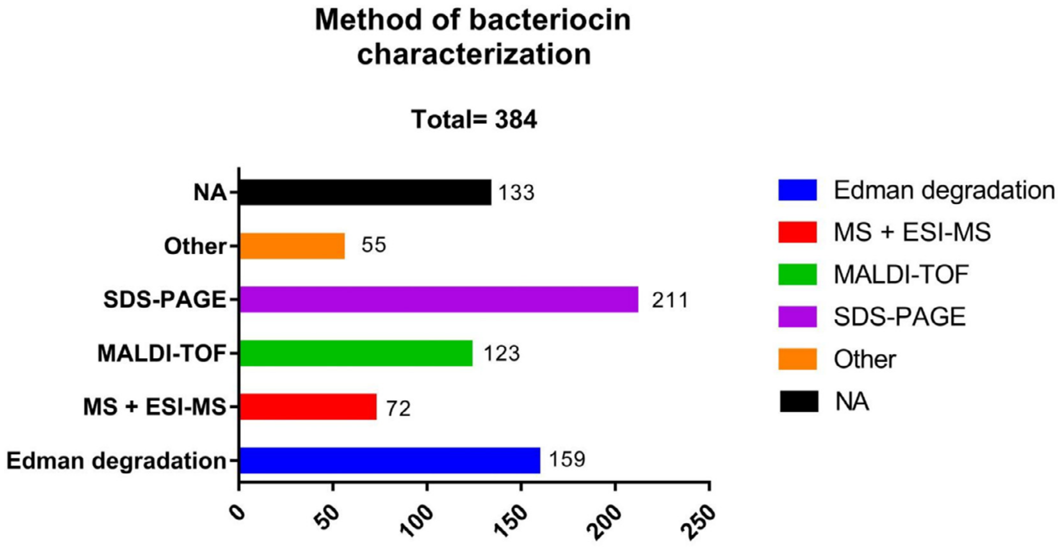
Over 10 thousand AMPs have been studied in the last decade. Several databases were created to gather these AMPs and their information. Each AMP database holds specific information as well as specific tools and statistics. Table 1 shows the comparison between LABiocin and other AMP databases. APD3 [16], CAMPR3 [17], DBAASP [18], LAMP [19], YADAMP [20], BACTIBASE 2 [6] and BAGEL4 [7] are the well-known available AMP databases. Only BACTIBASE 2 and BAGEL4 databases are specific to bacteriocins. The others comprise AMPs from all origins, such as animal, plant, human and microbes. Bacteriocins presented in AMP databases are lacking information and need to be validated. As shown in Table 1, there is less information on bacteriocins included in BACTIBASE than on those included in LABiocin. Furthermore, LABiocin includes GRAS bacteriocins, which are not cytotoxic and are ready to use in any medical or food applications. LABiocin contains 517 bacteriocins, whereas BACTIBASE 2 has only 177 bacteriocins, including non-LAB bacteriocins; however, BACTIBASE 2 contains more information on bacteriocin structure and physico-chemical properties.

BAGEL4 is a genome mining web tool for bacteriocin prediction and contains 814 bacteriocins originating from all bacterial phyla. The majority of BAGEL bacteriocins are predicted from genomic analysis. LABiocin contains the majority of LAB bacteriocins in the literature, including bacteriocins found in BACTIBASE 2 and



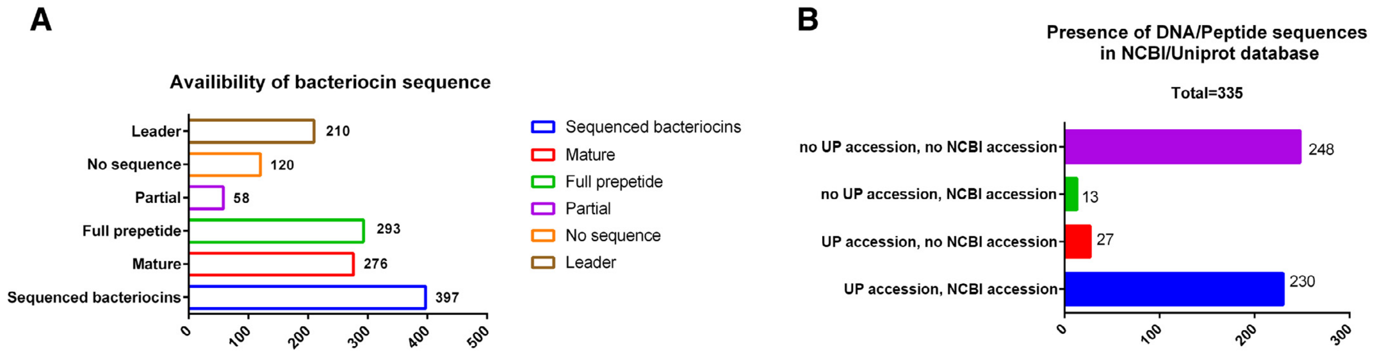
*Some bacteriocins could have several purification methods

Fig. 8. A: Methods of bacteriocin extraction, B: Methods of bacteriocin purification.



*Some bacteriocins could have several characterization methods

Fig. 9. Methods of bacteriocin characterization.



*Some sequences could be present in two databases

Fig. 10. A: Availability of bacteriocin sequence, B: presence of DNA/peptide sequences in NCBI/Uniprot database.

Table 1
Comparison between LABiocin and other AMPs databases, the number of “+” indicates the degree of data availability; “-” corresponding data is absent in the specific database; “nd”: not determined

	LABiocin	BACTIBASE 2	BAGEL 4	APD3	CAMP	DBAASP	LAMP	YADAMP
Non-bacterial origin of AMPs (as) number	-	-	-	2981	1386	11 103	5547	2133
Number of bacteriocins (LAB bacteriocins)	517 (517)	177	814 (nd)	335 (nd)	442 (nd)	813 (nd)	0	nd
Specificity to bacteriocins	+++	+++	+++	+	+	+	-	+
General information (MW and class)	+++	+++	+	+++	++	+	-	+
Spectrum of antimicrobial activity	+++	+++	-	+++	+++	+++	++	+++
Mode of action	-	++	-	-	-	+++	-	-
Chemical and physical properties	++	+++	-	+++	++	++	+	++
3D structure	-	+++	-	+++	+++	+++	+	-
AMP sequence	+++	+++	+++	+++	+++	+++	+++	+++
Source of producer organism	+++	-	-	-	-	-	-	-
BLAST tools	+++	+++	+++	-	+++	-	++	-
Prediction tools	-	++	+++	+++	+++	+++	-	+
Available statistics	+++	+	-	+++	+++	+++	+	-
References	+++	+++	+++	+++	++	++	++	++
Links to other databases	+++	+++	+++	+++	+++	++	+	-
Dynamic phylogenetic trees	+++	-	-	-	-	-	-	-
Producing methods (extraction, purification and characterization)	+++	-	-	-	-	-	-	-
Downloading all data and sequences	+++	+	+	+	+	+	+	+
Easy to submit new data	+++	-	-	-	-	-	-	-

BAGEL4. Furthermore, the BACTIBASE and BAGEL accession numbers are included as hyperlinks in the LABiocin database, and lead users to these databases.

4. Conclusion and future prospects

LABiocin is a comprehensive, easy to access database that compiles all LAB bacteriocins collected up to August 2017. Furthermore, LABiocin contains codes presented as hyperlinks to several other databases, including Pubmed, Uniprot, NCBI, BAGEL and BACTIBASE. Users of the LABiocin database can be directed to other database sites (APD3, CAMP and BAGEL4), which contain several prediction tools. The LABiocin database is a source of information and integrates several tools and services. This interactive database will continue to grow as new data are submitted by researchers and our team. New releases of the database will be published online with new information, data and tools. The next release of LABiocin will contain antiviral bacteriocins as well as antiviral LAB.

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Declarations

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Supplementary material

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.ijantimicag.2019.07.012.

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