



**RESEARCH ARTICLE - BIOLOGY**

## **Isolation and identification of new species *Leuconostoc carnosum* from cauliflower and broccoli**

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Article Info.	Abstract
<p><i>Article history:</i></p> <p>Received 23 June 2024</p> <p>Accepted 9 July 2024</p> <p>Publishing 30 June 2025</p>	<p>A study was conducted on cauliflower and broccoli which were fermented to isolate and characterize lactic acid bacteria that are consumed in these fermented foods by people. One –hundred eighty isolates belong to the lactic acid bacteria were taken from 120 samples of different parts of cauliflower and broccoli were obtained from different markets of Baghdad city. Only 20 isolates were bacteriocin producers thus showed antibacterial activity against indicator bacterial isolates (<i>S. aureus</i>, <i>S. agalactiae</i>, <i>E. coli</i> and <i>P. aeruginosa</i>). The lactic acid bacteria (LabBr no. 28) isolate had the highest activity against indicator bacteria with inhibition zones of (22 mm) against <i>S. aureus</i>, (16.5 mm) against <i>S. agalactiae</i>, (18mm) against <i>P. aeruginosa</i> and (19mm) against <i>E.coli</i>. This isolate was identified by using conventional methods then by VITEK®2 System. The identification was confirmed by 16sRNA sequencing to characterize and describe the new species <i>Leuconostoc carnosum</i>.</p> <p><b>The aim of this study:</b> Recognition of lactic acid bacteria species that found in cauliflower and broccoli, which have ability to produce the bacteriocin by detection their ability to inhibit growth of pathogenic bacteria.</p>

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**Keywords:** Lactic acid bacteria; *Leuconostoc carnosum*; bacteriocin; antibacterial activity; 16sRNA sequencing;

### **1. Introduction**

Broccoli and cauliflower act as anti-proliferative effects on a wide variety of tumour cell lines due to have phytochemical compounds. It's fermentation seems to be an ideal processing step. As it improves organoleptic properties; increases the level of safety and extends shelf life. Lactic acid bacteria are able to give extra nutritional value to these raw vegetables and benefits of which constitute a portion of the microbiota. Raw vegetables may be subjected to spontaneous lactic acid fermentation When providing the positive conditions of anaerobiosis, water activity, salt concentration, and temperature [1],[2]. LAB are a kind of Gram- positive bacteria that can ferment carbohydrates lead to the acidification (lower than pH 4.0) due to the production lactic acid, and are currently widely used in the fermented food industry due to its useful effect dependent on its safety, nutritional, organoleptic and preservative properties [3],[4]. The genus *Leuconostoc* placed within the family of

Lactobacillaceae. All species within this genus are heterofermentative. Which it was metabolizing the carbohydrates during pentose phosphate and phosphoketolase pathway; yielding lactic acid, CO<sub>2</sub>, ethanol and/or acetic acid [5]. The *Leuconostoc carnosum* frequently occurs in the microbiota of foods. Mostly meat-based products and have been isolated from processed vegetables. It have been able to produce of bacteriocins. [6], [7], [8]. Bacteriocins of LAB have significant applications of biotechnology, since they are simple to produce, constant at low pH, non-toxic to human, and susceptible to proteases [9]. The 16s rRNA gene analysis is molecular method used for the detection of genetic polymorphism of lactobacilli at the strain level. Phenotypic characters (morphological and biochemical characters) of lactic acid bacteria is not appropriate to differentiate them properly. For this reason, molecular characterization based on genetic characterization is very important and also beneficial for tracing new strains [10].

## **2. Experimental work**

### **Isolation of Lactic acid bacteria**

One hundred twenty of small pieces were taken out of 30 samples of fresh Vegetables (cauliflower and broccoli) were collected randomly from Baghdad markets, Iraq during the period from November 2022 to January 2023 and transported in an box to the food microbiology lab., gently washed with distilled water and cut in to small pieces, 1.0 g of vegetable was suspended in tube containing 1.0 mL sterile saline; then incubated at room temperature for 24 hours. The Lactic acid bacteria were isolated by using tubes containing 9 ml of MRS broth were inoculated with 1 ml of the upper layer of saline containing samples separately and incubated anaerobically at 30°C for 48 hours .After incubation, serial dilutions were made for each culture by using physiological saline solution. Spread-plate method was used with 0.1 ml samples from appropriate dilutions were spread on MRS agar plates and incubated at 30°C for 48 hours under anaerobic conditions. After incubation ,large and small pure colonies were selected , transferred and purified by streaking method on MRS agar and incubated under the same incubation conditions above before being subjected to identification tests [11],[12].

### **Identification**

#### **-Macroscopic Examination of colonies**

The appearance of colonies on solid media was studied with respect to form, color, size, opacity, and margin as described by [13].

#### **-Microscopic Examination**

The microscopic examination was made for all bacterial isolates .The bacterial cells were studied with respect to their morphological characteristics (Gram's staining, shape, arrangement, and spore formation) [13].

#### **-Biochemical Tests**

##### **Catalase Test**

On the clean glass microscopic slide the fresh bacterial colony have been placed by sterile wooden stick and rubbed, a drop of 3% hydrogen peroxide reagent was added to perform catalase test. A positive result occurs when release of gas bubbles within 5-10 sec seconds [14].

##### **Oxidase Test**

An 18-hours old bacterial colony transferred to the filter paper which was saturated with oxidase reagent, then rubbed onto the reagent with a sterile wooden stick. A positive result appearance during 30 seconds with purple colour [15].

### **Gelatinase Test**

An 18-hours old bacterial isolates with 1% were cultured in tubes of gelatine medium (except control tubes) and incubated for 48 hours at 37°C. Then, all tubes were placed in refrigerator and positive result appearance during 30 minutes with liquefaction of medium [16].

### **Production of Ammonia from Arginine**

An 24-hours old bacterial isolates with 1% were cultured in tubes of MRS-arginine broth medium (except control tubes) and incubated for 24 hours at 30°C. Then, 1 ml of Nessler's reagent was added to 1 ml of each bacterial isolate, the tubes were gently shaken. The development of orange-brown color indicates positive result [17].

### **Growth at Different Temperatures**

Tubes of MRS broth were cultured (except control tubes) with 1% of fresh bacterial isolates and incubated for 24 hours at (10 and 45) °C. The development of turbidity indicates positive result [18].

### **Growth on Blood Agar**

Blood agar plates were cultured (except control plates) with an fresh bacterial isolates and incubated for 24 hours at 30°C. Then, colony appearance was studied according to [19].

### **Production of CO<sub>2</sub> from Glucose Fermentation**

Tubes containing MRS broth supplement with durham tube were inoculated with 1% of 24 h old bacterial isolates and incubated at 30°C for 24 h [20].

### **-Detection of bacteriocin Production by Lactic acid bacteria**

LAB was cultured in MRS medium for 24 hours at 30 °C. Cell-free supernatant extracted by centrifuging the cultures for 30 minutes at 4 °C / 4000 rpm. The supernatants were filtering through a 0.22 µm filter (Millipore filter) to be sterilized. The pH of supernatant was adjusted using 1N NaOH to 6.0 and used as crude bacteriocin [21]. The activity of bacteriocin produced by LAB was measured as antimicrobial against some pathogenic bacteria according to agar well diffusion method. Pathogenic isolates, including (*Escherichia coli*, *Pseudomonas aeruginosa*, *Streptococcus agalactiae*, and *Staphylococcus aureus*) were inoculated in nutrient broth, followed by incubation at 37°C overnight. The microbial concentration was adjusted to 0.5 McFarland standard and sub-cultured on Mueller Hinton agar when made a 6 mm diameter well by cutting a hole with sterile cork borer were filled with 100 µl of the culture supernatant. The plates were incubated at 37°C for 24 h. Inhibition was detected by a zone of clearing around the supernatant well [22], [23]. The bacterial isolate that caused largest inhibition zone was chosen for further experiments.

### **-Detecting of bacteriocin producing isolates**

One hundred eighty isolates of lactic acid bacteria were isolated and diagnosed then the most producer isolate of bacteriocin was selected after testing the ability of isolates to produce of bacteriocin by forming inhibition zone against pathogenic bacteria through agar well diffusion assay.

**-Identification of the producer isolates by VITEK®2 System**

Lactic acid bacterial isolates produced bacteriocin were identified at the species level using VITEK® 2 systems. Identification-Gram positive bacteria (ID-GBB) cards were used according to manufacturer's instructions. The system contains of a printer, a computer and a VITEK® 2 instruments. The VITEK® 2 Compact system comes with software that includes analysis and data processing tools.

**-Selection the most efficient producer isolate**

The most efficient bacteriocin producer isolate was selected to study morphology, microscopically and biochemical characteristics, then identified by 16SrRNA sequencing.

**-Identification the most efficient bacteriocin producer isolate by 16SrRNA sequencing****Genomic DNA Extraction.**

DNA of selected isolate was extracted and purified using procedure of DNA extraction kit designed for the isolation of DNA from Gram positive bacteria as follows

- 1 ml of overnight Gram positive bacteria was transferred to a 1.5 ml tube and centrifuge at 12000 rpm for 1 minute. The supernatant discarded and the bacteria resuspended with 500µl of 70% ethanol, incubated on ice for 20 minutes and then centrifuge at 10000rpm for 1 minute, the supernatant discarded.
- The bacteria re-suspended with 200µl of re-suspended buffer (containing 4mg lysozyme) and incubated at 37oC for at least 60 minutes then centrifuged at 12000 rpm for 1 minute, the supernatant discarded.
- The bacteria re-suspended with 100µl of lysis buffer and 20µl of proteinase k by vortex and Incubated at 55oC for 15 minutes for made clear solution.
- 20µl of RNase added, mixed and incubated at room temperature for 2 minutes.
- Binding buffer was added with 400µl and vortex for 30 seconds , then transferred it to spin column and centrifuged at 12000 rpm for 30 sec, discarded the flow-through.
- 500µl of clean buffer added and centrifuged at 12000 rpm for 30 sec, discarded the flow-through. Repeated this step once.
- 500µl of wash buffer added and centrifuged at 12000 rpm for 30 sec, discarded the flow-through. Repeated this step 7 times.
- The spin column put in a 1.5 sterilized tube of microcentrifuge and addition 50-200µl of elution buffer was of then incubated at room temperature for 2 minutes and centrifuged at 12000 rpm for 1 minute to elute genomic DNA. Repeated this step once. The isolated DNA stored at -20°C.

**Measurement Purity and Concentration of DNA:**

The Purity of DNA was measured by using a nanodrop UV spectrophotometer, the optical density of DNA (1.5 µl) was measured at two wavelengths (260 and 280 nm). In most samples, DNA preparation gave A260/A280 ratio between 1.8 and 2.0, which is considered to be suitable for further analysis .The measurement of DNA concentration for the sample was in the range of (25-118) ηg/ml [24].

**Agarose gel electrophoresis of DNA.**

Electrophoresis was done to determine DNA segments following the extraction process. While the ladder is present in order to distinguish the size of bundle in the PCR interaction's result on the Agarose gel. Making an agarose gel usually has been made according to [25] as follow:

1. An amount of 100 ml with (1X) of tris acetate EDTA(TAE) or tris borate EDTA (TBE) buffer prepared from stock solution (10X) of TBE buffer by adding 10 ml from the stock to 90 ml of D.W.
2. In two separate flasks 1 gram and 2 grams of agarose powder respectively were added with amount of TBE or TAE buffer then the volume completed to 100ml of the same buffer.
3. The microwave was used for (1-3) minutes and preferably swirl the flask for each (30-45) second during the heating process and waited for it to boil.
4. At room temperature the gel has been left until it cools down and reaches about 50°C. Ethidium bromide dye was added in the amount of (2-3) µl per 100 ml of gel .the necessary precautions when using the dye, because it is neurotoxic. Then the gel was poured into a tray that previously had a comb fixed.
5. Casting of the Agarose Gel: The agarose solution was poured into the gel box (The gel has been poured gently to prevent air bubbles from forming ) where the comb was placed and left for 30 minutes at room temperature until hardened. The carefully inserted comb was removed carefully and the tank used in the electrophoresis was contain the plate of gel installed to its stand in the Electrophoresis horizontal unit and the tank filled with (1X) of TBE buffer till reached 2-3 mm on the gel surface.

### Preparation of sample

Amount of (3µl) of the processor loading buffer (TRANSGEN Biotech / China) has been mixed with (7µl) of the supposed DNA to be electrophoresis, after the mixing process, the (10µl) of loading mixture was done to the holes of the gel. An electric current of 70 volts has been exposed for 90 minute till the tincture has reached the other side of the gel. The gel has been tested by a source of the UV with a trans-illuminator and then photographed.

### Amplification of 16S rRNA of selected Isolates using PCR

The PCR (polymerase chain reaction) was method an in vitro for forming large amounts of a specific fragment of DNA. It was defined length and sequence from small amounts of a complex template [26].The universal primer (27F: 5' -AGA GTT TGA TCC TGG CTC A-3' and 1492R 5' -GGTTACCTTGTTACGACTT -3') was lyophilized, it was liquefied in the nuclease-free water to give a final concentration of 100 pmol/µl as stock solution. The stock was kept at -20°C, to prepare 10 pmol/µl concentration as work primer suspended 10 µl of the stock solution in 90 µl of the free deionized distilled water to reach a final volume of 100 µl. Fragments of the 16S rRNA genes of the producer bacterial isolate were amplified using the universal primer and other components of PCR reaction in the table 1.

**Table 1.** Reaction components for amplification

NO.	Components	Volume
1	2× Easy Taq PCR Super Mix	12.5 µl

2	Forward primer	1µl
3	Reverse primer	1µl
4	DNA template	5µl
5	Nuclease free water	5.5 µl
Final volume		25µl

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The Easy Taq® PCR super Mix (+dye) components (dNTPs - DNA polymerase -optimized buffer - Gel loading buffer) and -20°C was optimum temperature for it storage. The temperature program and the cycle of reactions were as initial denaturation step at 94°C for 5 min., followed by 35 cycles of denaturation at 94°C for 60 sec, primer annealing at 58°C for 30 sec, and primer extension at 72°C for 60 sec with a final extension at 72°C for 5min. [27], [28]

### **Agarose gel electrophoresis of PCR products:**

PCR products are transferred onto the agarose gel 2% and sample is loaded with a quantity (5µl) directly without adding a loading dye and finally it is relayed at a voltage of 70 for about an hour and a half. Then staining with Ethidium Bromide Stain, the PCR products were exposed to UV light (302 nm) for observation after being separated on a (2%) agarose gel electrophoresis.

### **Sequencing of PCR product**

The primers and products of PCR used in this study were sent to the Macrogen, a South Korean company (dna.macrogen.com) for sequencing analysis using ABI (Applied Biosystem) automated DNA sequences. The sequencing results of the PCR products of the targeted fragments were edited, aligned, and analysed as long as with the respective sequences in the reference database using BioEdit Sequence Alignment Editor Software Version 7.1.

The sequences were identified by searching for sequence homology between published reference sequences using the Basic Local Alignment Search Tool (BLAST) which is accessible online at (National Center for Biotechnology Information (NCBI), <http://blast.ncbi.nlm.nih.gov/>). Homologies with 99–100% a type strain were considered as excellent identifications [29], [30]

## **3. Results and discussion**

### **Isolation and Identification of lactic acid bacteria from cauliflower and broccoli**

One –hundred eighty isolates belong to the lactic acid bacteria were taken from 120 samples of various parts of cauliflower and broccoli were obtained from different markets of Baghdad city during period at 15 November 2022 to 15 February 2023. The microscopically investigating of lactic acid bacteria isolates was occurred under compound light microscope at 40X and 100X by using Gram stain examination, the Gram stain was appeared all isolates were positive to Gram stain and some isolates were rods, single , chain bacteria or in pairs and others were spherical, single or chain and all non-spore forming bacteria. These findings were agreement with the study of [31]. The cultural characteristics of some lactic acid bacterial colonies were large, raised, smooth, greyish, transparent, and others were white or milky color, round, large or small, opaque, flat or convex on MRS agar media. These results agreed with the result showed by [32], [33]. For characterization of lactic acid bacteria different biochemical tests were performed. The results were appeared that the bacterial isolates were

negative for oxidase, catalase, gelatinase, non-motile, anaerobic, and some isolate positive for gas production but other negative. These results agreed with the result presented by [34]

### Detection of Bacteriocin Production by Lactic acid bacteria

Table (2) shows the differences of inhibitory spectra between Lactic acid bacteria isolates by the agar well diffusion method. Crude filtrate of 180 lactic acid bacterial isolates was tested to investigate the activity as antibacterial against indicator bacterial isolates (*S. aureus*, *S. agalactiae*, *E. coli* and *P. aeruginosa*). As antibacterial activity showed with only 20 isolates at inhibition zone diameter between 8.5-22 mm. The three isolates of lactic acid bacteria (LabBr no. 26, 27 and 28) were showed highest inhibition zone of antibacterial activity against all indicator bacteria isolates. The lactic acid bacteria (LabBr no. 28) had the highest activity against indicator bacteria with inhibition zones of (22 mm) against *S. aureus*, (16.5 mm) against *S. agalactiae*, (18mm) against *P. aeruginosa* and (19mm) against *E. coli*. One study found that the antibacterial activity of lactic acid bacteria on *Listeria innocua* (resistance zone of 19.24 mm), *S. aureus* (resistance zone of 23.17 mm), and *E. coli* O157 (resistance zone of 21.16 mm) [35]. Bacteriocins have been used in food preservation due to their antibacterial action against food-borne pathogenic and spoilage microorganisms [36].

**Table 2:** Inhibitory effect of bacteriocin producer isolates against indicator bacterial isolates

Isolates	Diameters of inhibition zone around (mm)			
	<i>S. aureus</i>	<i>S. agalactiae</i>	<i>P. aeruginosa</i>	<i>E.coli</i>
LabBr1	12mm	11mm	0	0
LabBr2	13mm	14mm	0	0
LabBr4	11.5mm	12mm	0	0
LabBr6	0	9mm	10mm	0
LabCa7	15.5mm	0	0	0
LabCa8	14mm	0	0	0
LabCa9	14.5mm	0	0	9mm
LabCa11	17.5mm	8.5mm	0	10mm
LabCa26	14mm	12mm	15mm	16.5mm
LabBr27	13mm	9mm	13.5mm	17mm
LabBr28	22mm	16.5mm	18mm	19mm
LabCa74	10mm	12mm	0	0
LabCa97	9mm	0	0	0
LabCa101	10mm	0	0	0
LabBr112	0	0	12.5mm	11mm
LabBr116	15mm	0	0	12.5mm
LabCa124	11mm	0	0	0
LabBr131	13.5mm	11mm	12mm	10
LabBr 137	11.5mm	10mm	11mm	12mm
LabCa148	12mm	-	-	9mm

-well diameter 6.0 mm, LabBr: lactic acid bacteria isolated from broccoli, LabCa: lactic acid bacteria isolated from cauliflower

### -Identification of the producer isolates by VITEK®2 System

Biochemical assays of LAB isolates which produced the bacteriocin were investigated using the VITEK 2 Compact system. The isolates cultured on MRS agar and produced positive findings from biochemical testing were verified using the VITEK2 compact system.

Results of the identification isolates of the study recorded as 5 (25%) isolates of *Leuconostoc mesenteroides* ssp. *mesenteroides*, 4 (20%) isolates of *Leuconostoc mesenteroides* ssp. *dextranicum*, 3(15%) isolates of *Lactococcus garvieae*, 7 (35%) isolates of *Leuconostoc citreum* and 1(5%) isolate of *Leuconostoc carnosum* as show in Fig.1. *Leuconostoc mesenteroides* ssp. *mesenteroides* and *Leuconostoc mesenteroides* ssp. *dextranicum* isolates were isolated from cauliflower while *Leuconostoc citreum*, *Leuconostoc carnosum* and *Lactococcus garvieae* were isolated from broccoli. The study reported the *Lactococcus garvieae* isolates from radish and broccoli sprouts [37]. Species belonging to genus *Leuconostoc* (*Lc. argentinum*, *Lc. carnosum*, *Lc. citreum*, *Lc. fallax*, *Lc.ficulneum*, *Lc. fructosum*, *Lc. gasicomitatum*, *Lc. gelidum*, *Lc. inhae*, *Lc. kimchii*, *Lc. lactis*, *Lc. mesenteroides*, *Lc. pseudomesenteroides*) can be found mainly in vegetables, cereals, silage, fruits, wine, fish, meat, and dairy products [38]. Figure -1 shows the results of the identification of the bacterial isolates by VITEK 2 System and ID GP card. The VITEK 2 system's GP card has biochemical assays to measure enzyme activity, carbohydrate consumption, and resistance to certain compounds, all of which can be used to identify GP, non-spore-forming bacteria [39].

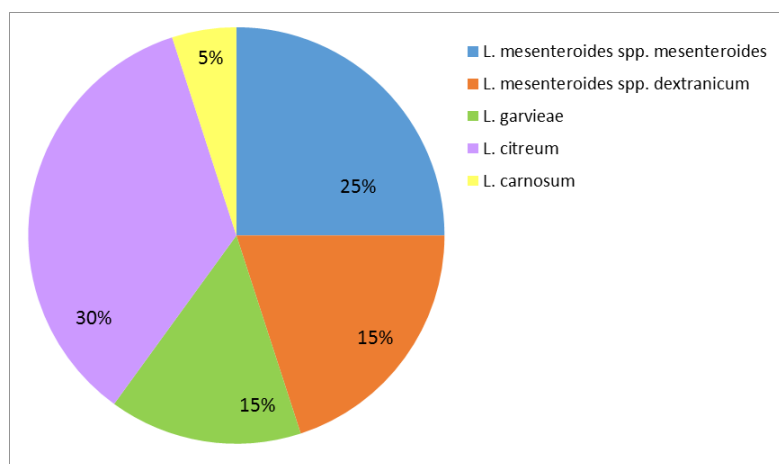
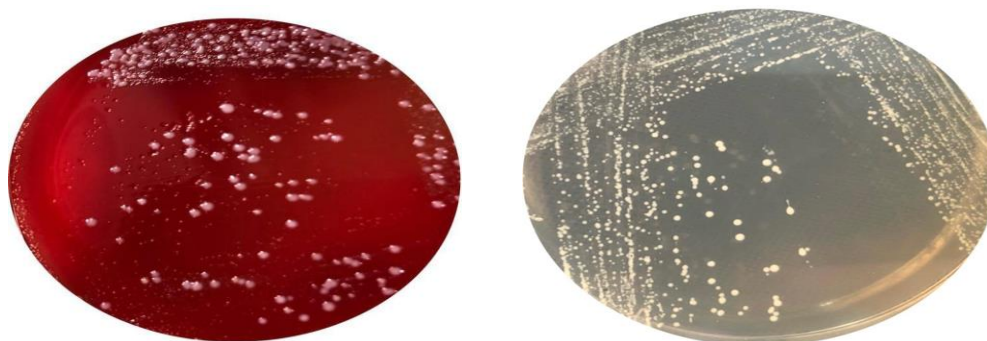


Fig. 1. Identification of LAB isolate by using VITEK 2 System

### Selection the most efficient producer isolate

During the study, the *Leuconostoc carnosum* (LabBr28) was the highest bacteriocin producer among other LAB isolates and it was isolated for the first time from broccoli because it was not predominant in the broccoli while the genus *Lactobacillus* occupied the dominant position of the broccoli juice, (abundances of 79.0 %) as showed with search by [40]. *Lactobacillus curvatus*, *Leuconostoc carnosum*, and *Leuconostoc mesenteroides* were also identified as the main LAB in kimchi was explained by [41] whereas *L. carnosum* 4010, which was isolated from the surface of sliced vacuum-packed ham as reported with the study of [42]. Morphological characteristics of *L. carnosum* on MRS agar and blood agar showed creamy, round colonies, convex and large as shows in Fig.2. The genus *Leuconostoc* ssp. round colonies have smooth edges, a convex surface, 1-4 mm in size, and a whitish or cream colour [43].





A. Blood agar

B. MRS agar

Fig. 2. Colony morphology of *Leuconostoc carnosum* (LabBr28) on A: Blood agar , B: MRS agar

The microscopic and biochemical characteristics of *L. carnosum* were summarized in Table (3) which appeared gram positive, ovoid cocci, arranged singly, in pairs or forming chains, negative for oxidase, catalase, gelatinase, production of CO<sub>2</sub> there for it was belonged to hetero fermentative lactic acid bacteria, non-producer of ammonia from arginine, non-motile, non-spore forming, and growth at 10°C but not growth at 45°C with anaerobic condition. These results agreed with the result presented by [44], [45], [46].

**Table 3.** Biochemical tests of the *L. carnosum* isolates

Biochemical and other tests	result
Gram stain	+
Catalase test	-
Oxidase test	-
gelatinase test	-
Gas from glucose	+
Producing ammonia from arginine	-
Growth at 10°C	+
Growth at 45°C	-
Spore forming	-
motility	-

Symbols: + = positive result; - = negative result

### -Identification the *Leuconostoc carnosum* (LabBr28) by 16SrRNA sequencing

#### Genomic DNA Extraction

Genomic DNA was successfully extracted from LabBr28 isolate and analysed by agarose gel electrophoresis as shows in fig.3.

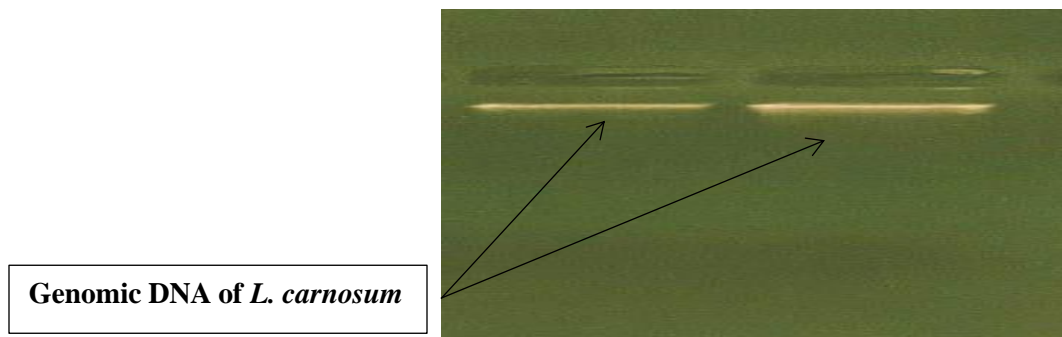


Fig.3. Gel electrophoresis for Extracted DNA, (Agarose 1%, at 100 volts, 60min.). Visualized under U.V light after staining with ethidium bromide.

### Measurement of DNA Purity and Concentration:

The concentration and purity of DNA were measured by using Nano Drop spectrophotometer. DNA concentration showed (57.5 ng $\mu$ l) at 260 nm wavelength which optimum to absorb of the nucleic acids. The ratio of absorption at 260 nm wavelength to absorption at 280 nm wavelength which represented protein contaminants appeared (~1.82) purity of DNA. The A260/A280 ratio must be within the range 1.7-1.9.

### Amplification of 16S rRNA of selected Isolates using PCR

The identification of LabBr28 isolate to determine the isolate carried out based on the 16S rRNA gene. The amplification process to form more copies of the 16S rRNA gene for the next step using the PCR method and the PCR of the 16S rRNA gene of LabBr28 isolate provides an amplicon of about ~1507 bp as shows in Fig. 4 and this result agreed with [46].



Fig. 4. Agarose gel (2%) electrophoresis showing amplified 16S rRNA gene of LabBr28 isolate. A: PCR product~ 1507pb; B: DNA marker ladder (100–1500bp)

### The Sequencing of Amplified Product

The sequencing reactions for LabBr28 isolate indicated the exact identity after performing NCBI blast for these PCR amplicons. The NCBI BLAST engine also showed 97% of sequences similarities between the sequenced sample and *Leuconostoc carnosum* reference sequences as showed in Fig.5. Depending on the morphological, microscopic and biochemical tests as well as molecular identification, the isolate was identified as *Leuconostoc carnosum* by using the basic local alignment search tool (BLAST) of the

GenBank. The nucleotide sequence of the 16S rRNA gene found in all microbes as housekeeping genetic marker for taxonomic and bacterial phylogeny analysis moreover, the 16S rRNA genes (1500 bp) are huge enough for informatics and genetic analysis purposes therefore it was one of the molecular detection techniques used to determine the kinship relationship between bacteria [31],[47].

*Leuconostoc carnosum* strain HT1 16S ribosomal RNA gene, partial sequence

Sequence ID: MH633696.1 Length: 1507 Number of Matches: 1

Range 1: 337 to 1459 GenBank Graphics Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand	Plus/Minus
1914 bits(1036)	0.0	1101/1131(97%)	10/1131(0%)		
Query	7	ATCTGTTCTGCAATTAGACGGT	-	CCTCCTTACGGTTAGGCCACCGGCTTTGGGCATTACA	64
Subject	1459	ATCTGTCTCTGCCTTAGACGGTTCCTCCTTACGGTTAGGCCACCGGCTTTGGGCATTACA			1400
Query	65	AACCTTCATGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTACCGCGGCGTG			124
Subject	1399	AACCTTCATGGTGTGACGGGCGGTGTGTACAAGACCCGGGAACGTATTACCGCGGCGTG			1340
Query	125	CTGATCCGCGATTACTAGCGATTCCGACTTCGTGCAGTTCGAGTTGCAGACTGCAGTCCGA			184
Subject	1339	CTGATCCGCGATTACTAGCGATTCCGACTTCGTGCAGTTCGAGTTGCAGACTGCAGTCCGA			1280
Query	185	ACTGAGACGTACTTTAAGAGATTAGCTCACCTTCGCAGGTTGGCAACTCGTTGTATACGC			244
Subject	1279	ACTGAGACGTACTTTAAGAGATTAGCTCACCTTCGCAGGTTGGCAACTCGTTGTATACGC			1220
Query	245	CATTGTAGCACGTGTGTAGCCAGGTCATAAGGGGCATGATGATCTGACGTCGTCGCCCGC			304
Subject	1219	CATTGTAGCACGTGTGTAGCCAGGTCATAAGGGGCATGATGATCTGACGTCGTCGCCCGC			1160
Query	305	CTTCCTCCGGTTTGTACACCGGCAGTCTCGCTAGAGTGCCTATCTGAATGCTGGCAACTAA			364
Subject	1159	CTTCCTCCGGTTTGTACACCGGCAGTCTCGCTAGAGTGCCTATCTGAATGCTGGCAACTAA			1100
Query	365	CAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAAACATCTCACGACACGAGCTGACGAC			424
Subject	1099	CAATAAGGGTTGCGCTCGTTGCGGGACTTAACCCAAACATCTCACGACACGAGCTGACGAC			1040
Query	425	GACCATGCAACCACCTGTCACTTTGTCTCCGAAGAGAACACTTCTATTTCTAAAAGCTTCA			484
Subject	1039	GACCATGCAACCACCTGTCACTTTGTCTCCGAAGAGAACACTTCTATTTCTAAAAGCTTCA			980
Query	485	AAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAACCATGCTCCAC			544
Subject	979	AAGGATGTCAAGACCTGGTAAGGTTCTTCGCGTTGCTTCGAATTAACCATGCTCCAC			920
Query	545	CGCTTGTGCGGGTCCCGCTCAATTCCTTTGAGTTTCAACCTTGCGGTCTACTCCCCAGG			604
Subject	919	CGCTTGTGCGGGTCCCGCTCAATTCCTTTGAGTTTCAACCTTGCGGTCTACTCCCCAGG			860
Query	605	CGGAACACTTAATGCGTTAGCTTCGGCACTAAGAGGGCGGAGACCTCCTAACACCTAGTGT			664
Subject	859	CGGAACACTTAATGCGTTAGCTTCGGCACTAAGAGGGCGGAAACCTCCTAACACCTAGTGT			800
Query	665	TCATCGTTTACGGTGTGGACTACCAGGGTATCTAATCCTGTTTGCTACCCACACTTTTCA			724
Subject	799	TCATCGTTTACGGTGTGGACTACCAGGGTATCTAATCCTGTTTGCTACCCACACTTTTCA			740
Query	725	GCCTCAACGTCAGTTACAGTCCAGTAAGCCGCGCTTCGCGCTGGTGTCTTCCATATATC			784
Subject	739	GCCTCAACGTCAGTTACAGTCCAGTAAGCCGCGCTTCGCGCTGGTGTCTTCCATATATC			680
Query	785	TACGCATTCCACCGCTACACATGGAGTTCCACTTACCTCTACTGCACTCAAGTTGACCAG			844
Subject	679	TACGCATTCCACCGCTACACATGGAGTTCCACTTACCTCTACTGCACTCAAGTTGACCAG			620
Query	845	TTTCCAATGCCTTTCCGGAGTTGAGCTCCGGGCTTTACATCAGACTTAACCAACCGTCT			904
Subject	619	TTTCCAATGCCTTTCCGGAGTTGAGCTCCGGGCTTTACATCAGACTTAACCAACCGTCT			560
Query	905	GCGCTCGCTTTACGCCCAATAGATCCGGATAACGCTCGGGACATACGTATTACCGCGGCT			964
Subject	559	GCGCTCGCTTTACGCCCAATAAATCCGGATAACGCTCGGGACATACGTATTACCGCGGCT			500
Query	965	GCTGGCACGTATTTAGCCGTCCCTTTCTGGGAAGGGTACCGTCAAGGCTAAAGGTCATTCC			1024
Subject	499	GCTGGCACGTATTTAGCCGTCCCTTTCTGGTATGG-TACCGTCAAGGCTAA-GGTCATTCC			442
Query	1025	CTACCTTAAACTTTTCTTCCCATACAAGAGGGGTTTAAAGACCCGAAAAGCCTTCTTCAC			1084
Subject	441	CTACCTTAA-CTTTTCTTCCCATACAACAGTGCTTTA-CGACCCG-AAAGCCTTCTTCAC			385
Query	1085	AAACGCGGCGTGTCTTTCTTTACAGGGTTTTCGCCCTTTGGGGGAAAAATCCC			1135
Subject	384	AACGCGGCGT-TGCTCCATCAGGCTTT-CGCCCA-TTGTTGGAAGATTCC			337

Fig. 5. Sequencing of 16sRNA gene of *Leuconostoc carnosum*

#### 4. Conclusion

New species of lactic acid bacteria *Leuconostoc carnosum* was isolated for the first time in this study from broccoli and cauliflower. This species was diagnosed by classical and VITEK®2 system techniques and was able to produce antimicrobial peptides (bacteriocin) efficiently. 16sRNA sequencing has revealed 97% similar to *Leuconostoc carnosum*.

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