# Characterization of a Cryptic Plasmid Isolated from the Antilisterial Bifidobacterium longum A24

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#### Introduction

Bifidobacterium is gram-positive, non-spore-forming, nonmotile, irregular rod-shaped bacteria that often resemble Y or V shapes. They are strictly anaerobic fermentative organisms that utilize glucose by a very characteristic shunt pathway typified by the enzyme fructose-6-phosphate phosphoketolase and produce primarily acetic and lactic acids. Bifidobacteria is inhabited in the intestines of humans, some animals, and insects, where they are considered as beneficial organism, with a large number of potential health benefits attributed to them. The benefits include prevention and treatment of diarrhea, establishment of a healthy flora in premature infants, alleviation of constipation and symptoms of lactose intolerance, enhancement of immune function, suppression of tumorigenesis, and cholesterol reduction. The wide probiotic activities of bifidobacteria point to their vast potential for improving human health. Because of this potential they are frequently included in fermented dairy products as probiotic adjuncts. However, the lack of molecular tools for studying this group of high G+C gram-positive bacteria has limited our ability to understand what characteristics of these bacteria are important for probiotic activities. To date, plasmids have only been detected in the five species as such as B. longum and B. breve (human), B. globosum (pig), and B. indicum and B. asteroides (honeybee). Some plasmids have been characterized at the sequence level, and two plasmids were reported to replicate via a rolling circle replication mechanism. Recently, the complete genome sequence of a strain of B. longum was deciphered.

In this study, we isolated and analyzed a cryptic plasmid from the antilisterial *B. longum* A24 from infants feces. The plasmid was named pBIFA24 and compared its nucleotide sequence with NCBI database after sequenced using the primer walking approach. Secondary structure of 3 ORF was analyzed using both PHD and prosite program.

## Materials and Methods

#### 1. Plasmid Isolation and Purification

Plasmid DNA preparations from *E. coli* and *Bifidobacterium longum* A24 were carried out using Miniprep kit(Qiagen, Valencia, CA) with slight modification according to the manufacturer's recommendations.

#### 2. Southern Hybridization and Single-Stranded DNA Detection

Southern hybridization was performed using a DIG DNA Labeling and Detection kit (Roche, Indianapolis, IN) according to the manufacturer's instructions. The accumulation of single-stranded DNA intermediates, indicative of rolling circle replication, was evaluated by the effect of S1 nuclease digestion on *B. longum* A24 plasmid, according to Leenhouts (1991).

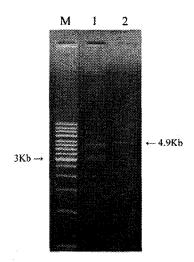
#### 3. DNA Sequencing and Analysis

DNAstar (DNAstar, Inc., Madison, WI) was used for assembly of contigs, and primer walking was used to fill in gaps in the plasmid sequences. Basic DNA and amino acid sequence analyses were performed using DNAstar and PHD (http://www.public.iastate.edu/~pedro/pprotein\_query.html) programs. The BLAST server at the National Center for Biotechnology Information was used for sequence similarity searches and open reading frame (ORF) predictions. The PROSITE at the SWISS-PROT server were used for conserved domain searches. Multiple sequence alignments were performed using CLUSTAL W of DNAstar.

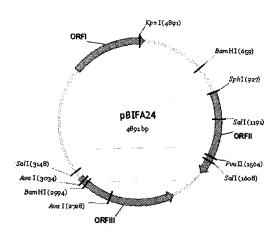
## Results and Discussion

#### 1. Plasmid DNA of Bifidobacterium longum A24

The plasmid DNA of *B. longum* A24 verified one band when treatment as *Kpn* I and size was about 4.9kb.

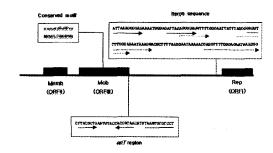


## 2. Restriction Endonuclease Map of pBIFA24



## 4. Schematic Presentation of the Nucleotide Sequence of pBIFA24

The plasmid of pBIFA24 harbored three ORF and mode of replication of pBIFA24 was predicted to be rolling circular replication.



## Conclusion

- 1. The complete plasmid sequence of pBIFA24 consisted of 4.891 bp, with a [G+C] content of 62.0%.
- 2. It was predicted to encode 3 putative (ORFs), involved in replication (Rep), transmembrane domain, and mobilization gene.
- 3. The ori sequences upstream of ORF I consist of directed repeated sequence of 3 set: this structure is identical of typical DNA iteron in the majority of bacterial plasmid.
- 4. The plasmid pBIFA24 contains a putative oriT structure downstream of ORFIII and the putative oriT consists of an inverted repeat and a conserved DNA sequence.
- 5. The mode of replication of pBIFA24 was predicted to be rolling circular replication.

## References

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