

# **Python Program Development for the Detection of four Antimicrobial Resistance (AMR) Genes in specific *Lactiplantibacillus plantarum* (*L. plantarum*) strains**

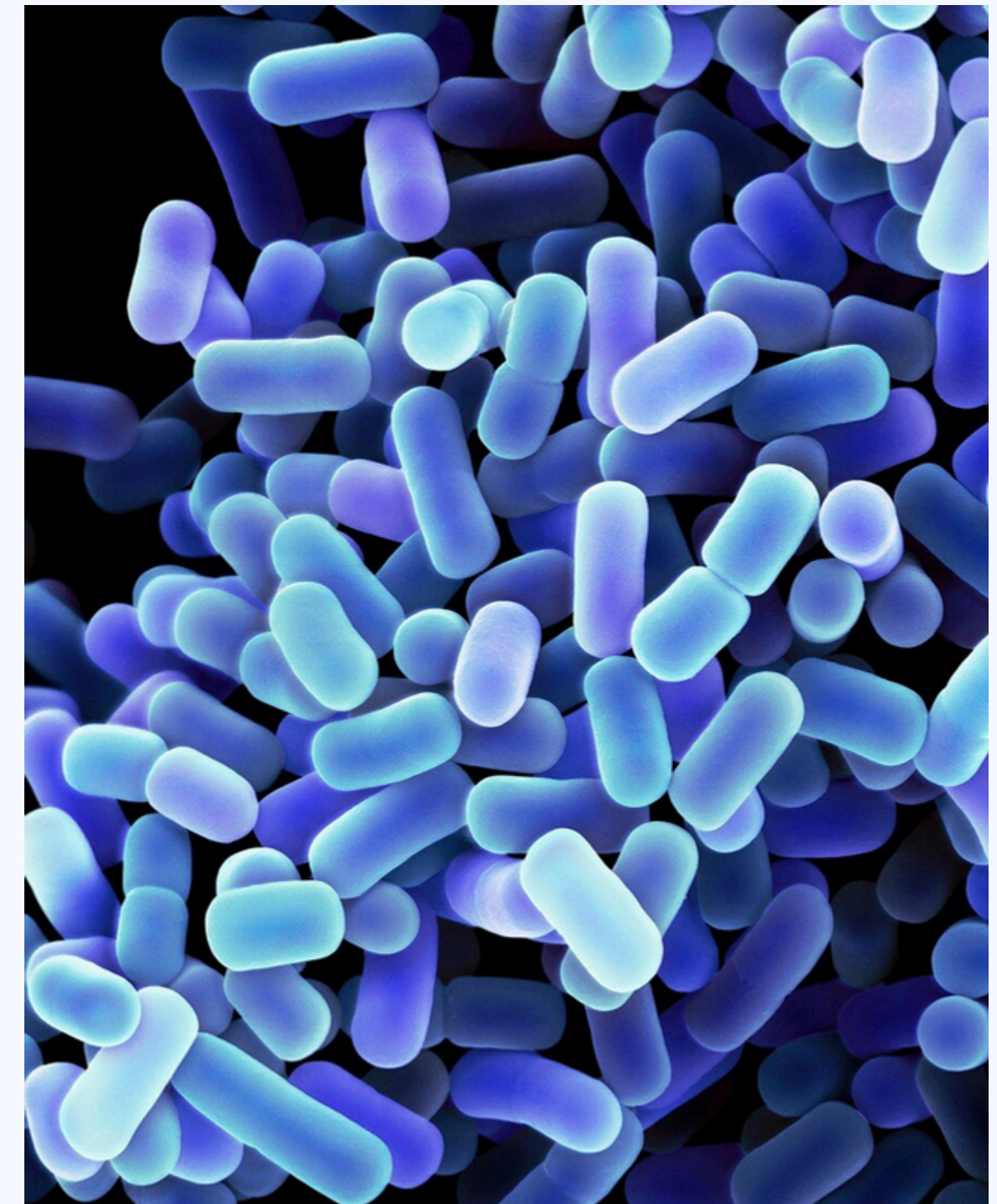
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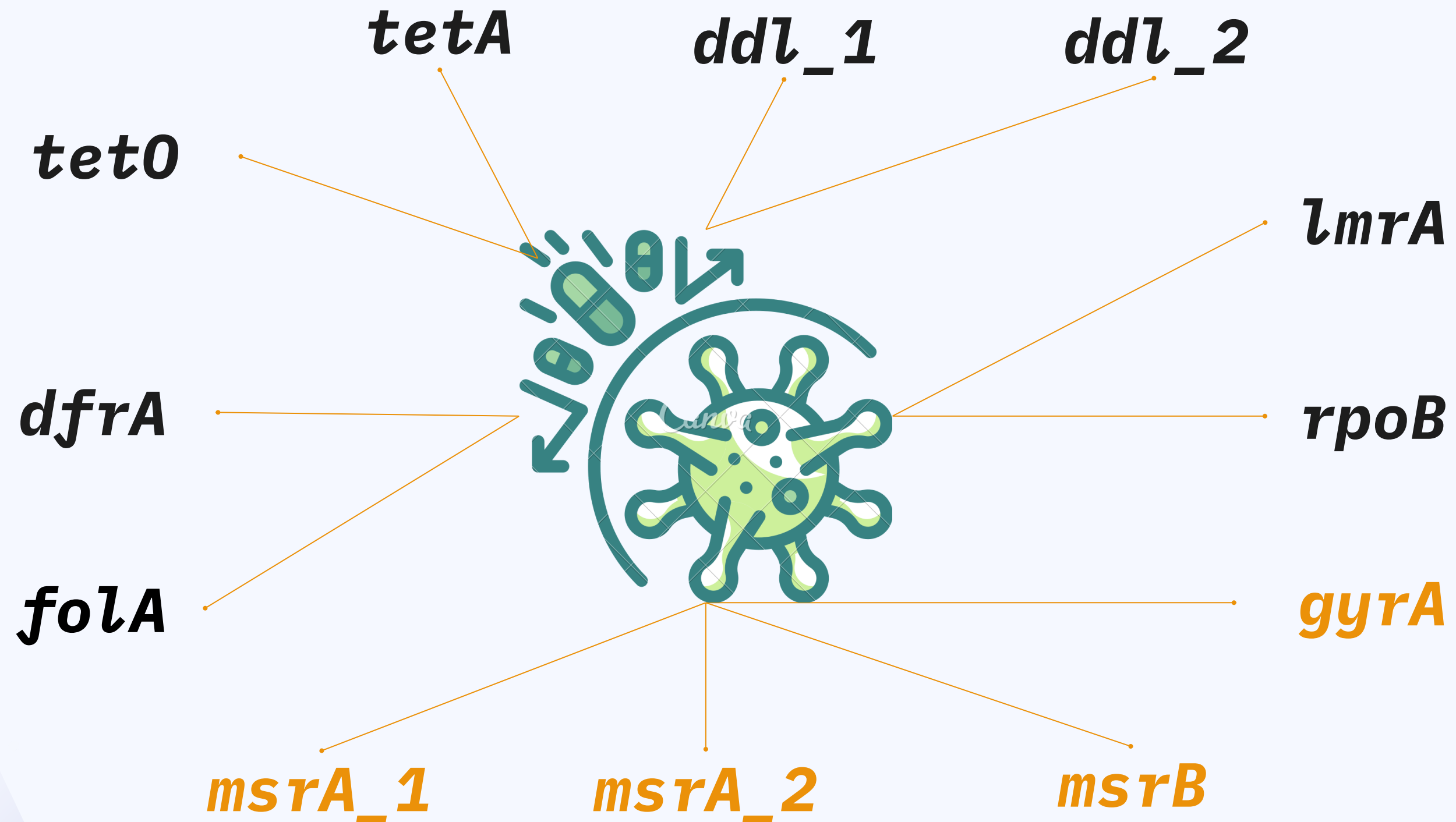
# *Lactiplantibacillus plantarum* (*L. plantarum*)

*L. plantarum* is acknowledged as a **safe microorganism** and belongs to the group of Gram-positive lactic acid bacteria (LAB) species. It has been shown to **exhibit numerous essential probiotic traits**, is **extremely adaptable**, and can effectively **establish and thrive** in the **human gastrointestinal tract** (Fidanza et al., 2021). Hence, it serves various purposes, including **enhancing immunity, promoting nutrient absorption, and preserving the equilibrium of the intestinal flora** (Yang et al., 2022).



**Figure 1.** *Lactiplantibacillus plantarum* bacteria as seen in a colored scanning electron micrograph (SEM) from SCIENCEphotoLIBRARY.

# Antimicrobial Resistance (AMR) genes Present in the Reference Genome (ASM991365v1)



# FUNCTION OF AMR GENES

## ***gyrA***

Protein: **DNA gyrase subunit A**

Confers resistance to?

**Ciprofloxacin** (Pell et al., 2021)

## ***msrA\_1***

Protein: **DNA gyrase subunit A**

Confers resistance to?

**Macrolides, lincosamides, and streptogramins** (Ammor et al., 2007)

## ***msrB***

Protein: **Peptide methionine sulfoxide reductase MsrB**

Confers resistance to?

**Macrolides, lincosamides, and streptogramins** (Ammor et al., 2007)

## ***msrA\_2***

Protein: **DNA gyrase subunit A**

Confers resistance to?

**Macrolides, lincosamides, and streptogramins** (Ammor et al., 2007)



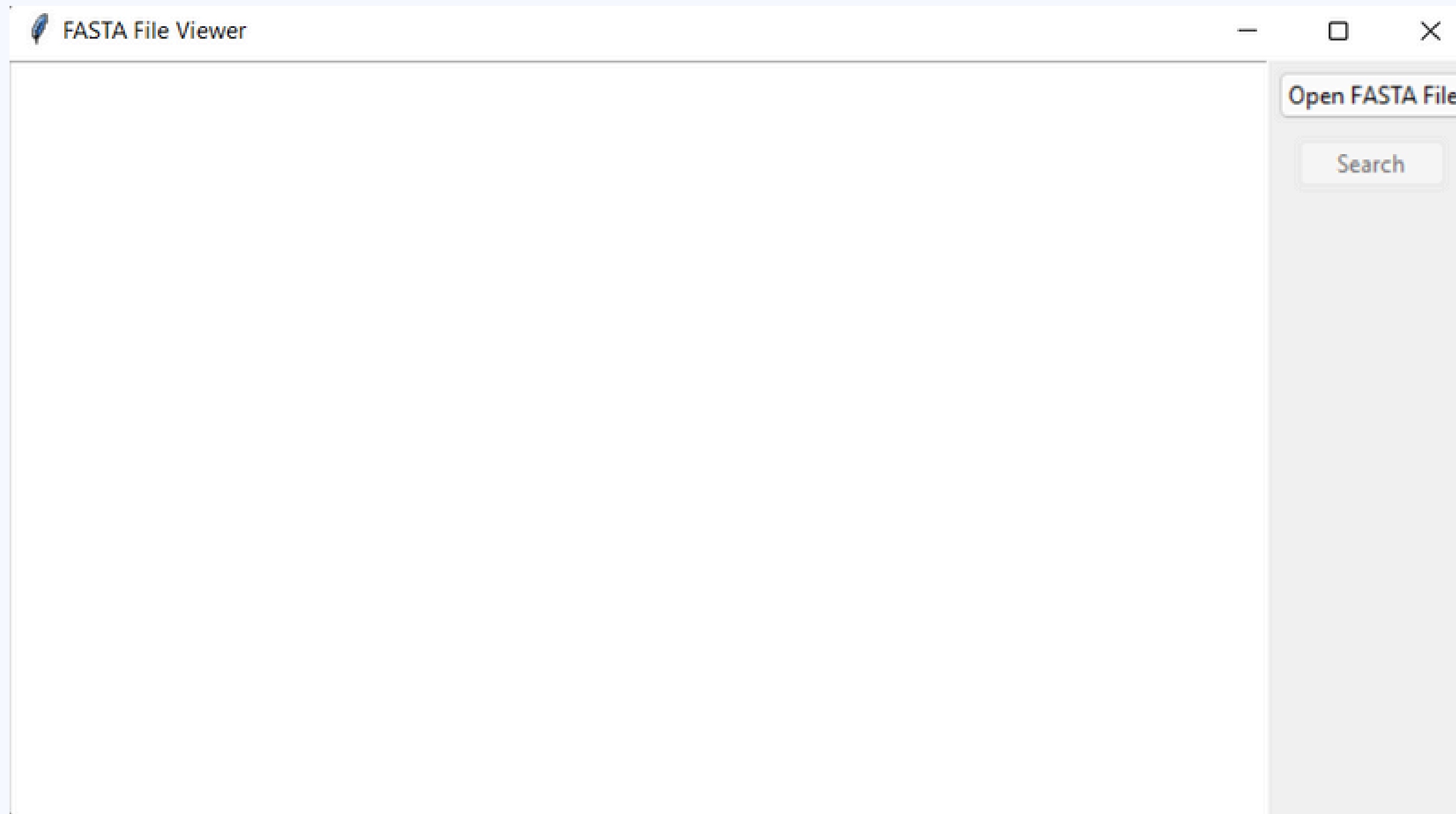
# SIGNIFICANCE

- 01**—— Understand resistance epidemiology
- 02**—— Verification of non-susceptible phenotypes
- 03**—— For identification of resistant strains, when genes are weakly expressed *in vitro*
- 04**—— For understanding the underlying mechanisms and the epidemiology of antimicrobial resistance

# Objectives

- 1.To identify highly conserved Antimicrobial Resistance (AMR) genes across five *L. plantarum* strains from an established reference genome
- 2.To develop a program for the detection of the highly conserved AMR genes present in specific *L. plantarum* strains
- 3.To run a sequence of *L. plantarum* strain in the program for validation of gene detection

# Concept of the Program



# Concept of the Program



The screenshot shows a window titled "FASTA File Viewer". The main area displays a long DNA sequence in a monospaced font. On the right side, there is a panel with the following elements:

- An "Open FASTA File" button.
- A "Search" button.
- Four radio buttons for selecting a gene:   
☐ gyrA   
☐ msrA\_1   
☐ msrA\_2   
☐ msrB

The DNA sequence shown is:

```
ATGGAAGGGATTACTAATTTACGGTCACTAGGTGGTTATCGCAATAAAAAATCAGCAAGTAATCAAAGATGGTTTAATTT  
ACCGGTCAGGACAATTGGATCAATTAACACCGGCACAGACGCAGTATCTAGCAACCACGCTTGGCATTACGCGAATCGTG  
GACATGCGTAGTGCTGATGAGCGTCATCAATTTCCAGATGCGACATGGCCACACGTCCAGTATCACGTGCTGGATGTGCT  
AGCACAAGTCATGACGAACGACGCAAGTTTACAATCGATGATTAGTAGTACGGGGGCGGTCCATGACCGCATGGTTTCAGT  
TATATGAACAGCTAGCGTTAGATCCTACTGCCCGTCAAAGTTATTGTCAATTTATACAGCTTACTACTGGTTCCAGATCA  
GCCACTACTGTTCCATTGTTTTATGAATAAAGAGCGTAAGTCGGTGATGCCGCTATCACAACGACATCATATGACAATTC  
CATGGAAGGACTTTATCCGTAATGAAGATGTTCCCGCTAAGCATGCTAGCTTACAAGAGCGAACATCAATTGTTGGTCGA  
GTTGGCATTTTAATGTTGTCTGTGGGACGGGAGCGTGGCGGGTTCGTGATGCGATGAATAAGATTGCTCGCAGCCTGAA  
TTTAACGTGCTCGGCAGATATCGGGTTGATTTGATTTCAGTACACGTGTTTTTCATCATGAACGTAGTTATACGCAAGTAT  
TATCGATACCAAATACTGGTGTAATAACGGATAAACTAAATATTCTTGAACAGTTTGTCAAAGACTTTGATGCGAAATAT  
GCACGGTTAACGGTGGCACAAGTGCATGCAGCAATTGATGAAGTTCAGACGCGTCCTAAACAGTATTCGCCACTGGTTCT  
TGGGTTGGCAGCTGGCTTAGCCTGTAGTGGATTTATCTTCTTACTTGGTGGGGTATTCCCGAGATGATTTGTTCCTTTTT  
GGGCGCGGGTCTTGGTAACTATGTTTCGGGCGCTGATGGGTAAACGGTCGATGACGACGGTTGCCGGGATTGCGGTCAGCG  
TTGCGGTAGCGTGTTTGGCTTATATGGTTAGTTTTAAGATTTTTGAATATAATTTCCAAATTCTTGCCCAGCATGAGGCG  
GGGTATATTGGTGCCATGTTATTCTGTGATTCCGGGTTTTCCGTTTATTACGAGTATGTTGGATATCTCTAAGTTGGATAT  
GCGCTCAGGACTGGAGCGCTTAGCTTACGCGATTATGGTTACCCTGATTGCAACTCTCGTCGGCTGGCTAGTCGCGACAC  
TGGTGAGCTTCAAGCCAGCTGATTTCTTACCGCTAGGACTTTTACCGTTAGCGGTACTTTTATTACGATTACCAGCTAGT  
TTTTGCGGTGTTTACGGGTTCTCAATAATGTTTAATAGCTCGCAAAAAATGGCCATTACCGCGGGATTATTGGGGCCAT  
TGCGAATACATTGCGCCTTGAAGTAGTTGACTTGACAGCAATGCCACCGGCCGCGGCCCTTTTGTGGGGCGCTCGTTG  
CCGGCTTGATCGCATCGGTGGTTAATCGTTATAACGGCTATCCCGGATTTCATTGACGGTACCTTCAATCGTAATTATG  
GTTCCGGGATTATATATTTATCGTGCAATTTATAGTATTGGCAATAATCAAATTGGTGTCGGTTCACTATGGCTGACGAA  
GGCCGTGTTAATCATCATGTTTTTACCGCTCGGGCTATTTGTAGCGCGTGCGTTGTTGGATCACGAATGGCGACACTTTG  
ATTAAATGTGCACTAGTCTAACTTATACAAATAGTCATGGAGGCCACTTCTTAGCTCGTACAATGGATTTTAACGTTGAC  
TTTGAGCCCCGTATTATGTTTCATGCCTCGACATTACCGCGTGACGGGTGACCTTGGTGATTTTACCACGACTTATGGCTT
```



# Methods: Selection of Genes

	Genome Assembly	Link to NCBI
Reference Genome	ASM991365v1	<a href="https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_009913655.1/">https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_009913655.1/</a>
Strain 1	ASM1058694v1	<a href="https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_010586945.1/">https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_010586945.1/</a>
Strain 2	ASM1413173v1	<a href="https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_014131735.1/">https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_014131735.1/</a>
Strain 3	ASM473096v1	<a href="https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_004730965.1/">https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_004730965.1/</a>
Strain 4	ASM170433v1	<a href="https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_001704335.1/">https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_001704335.1/</a>
Strain 5	ASM170431v1	<a href="https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_001704315.1/">https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_001704315.1/</a>

# Methods: Selection of Genes

<i>Gene</i>	<i>Protein</i>	<i>Location</i>
<i>ddl_1</i>	D-alanine--D-alanine ligase	complement(263558..264670)
<i>ddl_2</i>	D-alanine--D-alanine ligase	2417923..2418984
<i>dfiA</i>	Dihydrofolate reductase	complement(3020120..3020611)
<i>folA</i>	Dihydrofolate reductase	601383..601922
<i>gyrA</i>	DNA gyrase subunit A	1342980..1345541
<i>lmrA</i>	Multidrug resistance ABC transporter ATP-binding and permease protein	complement(719708..721465)
<i>msrA_1</i>	Peptide methionine sulfoxide reductase MsrA	complement(2988326..2988841)
<i>msrA_2</i>	Peptide methionine sulfoxide reductase MsrA	complement(3123072..3123601)
<i>msrB</i>	Peptide methionine sulfoxide reductase MsrB	complement(2988869..2989301)
<i>rpoB</i>	DNA-directed RNA polymerase subunit beta	2244147..2247752
<i>tetA</i>	Tetracycline resistance protein, class B	1997263..1998459
<i>tetO</i>	Tetracycline resistance protein TetO	1419223..1421241

# Thanks!

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