



## GENOMIC EXPLORATION OF *Enterobacter hormaechei* OYAS29: A POTENTIAL ALLY FOR SUSTAINABLE PLANT GROWTH

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### INTRODUCTION & AIM

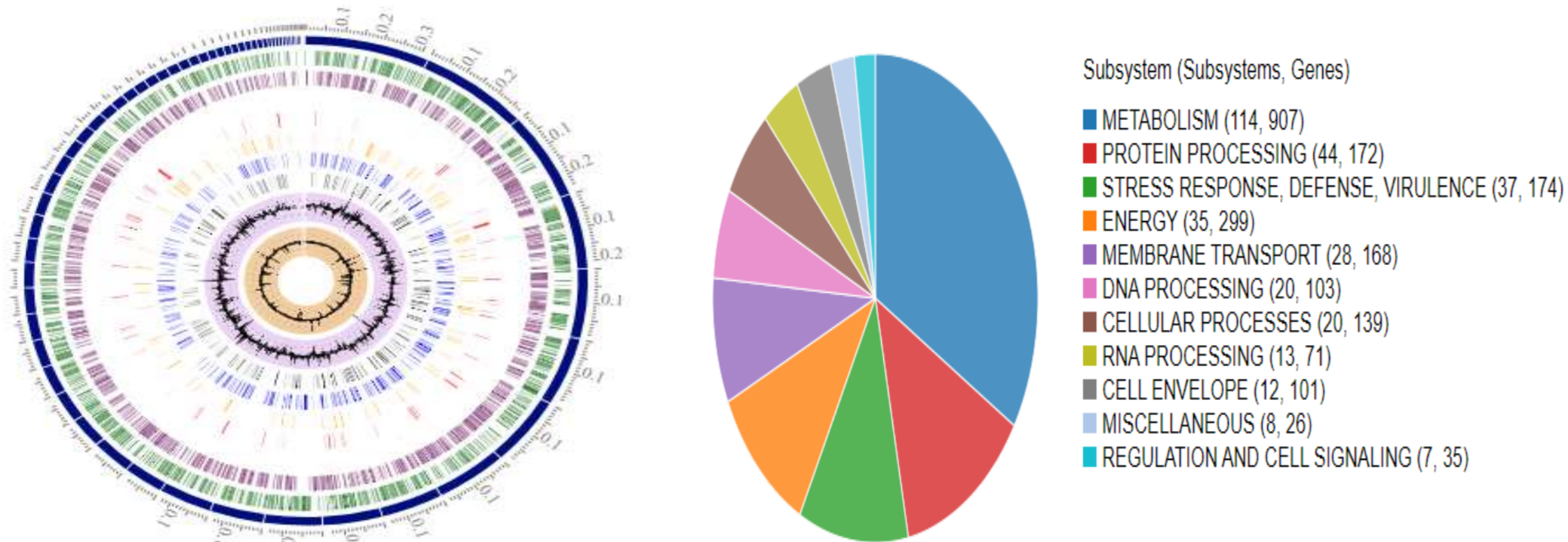
- The future of agriculture demands solutions beyond chemical fertilizers, which degrade ecosystems and threaten soil health. *Enterobacter hormaechei* OYAS29, an indigenous plant growth-promoting rhizobacterium (PGPR), offers a promising alternative. Despite its potential, this microbe remains underexplored compared to its well-known relatives.
- This study unravels the genomic blueprint of OYAS29, highlighting its ability to enhance plant growth, improve nutrient cycling, and withstand environmental stress. Our goal is to position this native strain as a sustainable tool for transforming modern agriculture.

### METHOD

- Isolation of *Enterobacter hormaechei* OYAS29:** OYAS29 was isolated from pristine soil sample at Federal University Oye-Ekiti, Nigeria [7°46'22.5"N, 5°18'57.4"E], an area known for its natural agricultural practices.
- Genomic DNA Extraction:** Genomic DNA was extracted using the ZymoBIOMICS™ DNA Miniprep Kit, ensuring high-quality material for sequencing.
- Next-Generation Sequencing (NGS):** Illumina NovaSeq 6000 generated 2x151 bp paired-end reads, providing comprehensive genome coverage.
- Genome Assembly & Annotation:** Fastq data was assembled with Unicycler v0.4.8 and annotated using PGAP and RAST to identify genes linked to plant growth and stress resilience.
- Functional Analysis:** KEGG and GO databases were used to explore pathways involved in nutrient acquisition, hormone regulation, and stress tolerance.

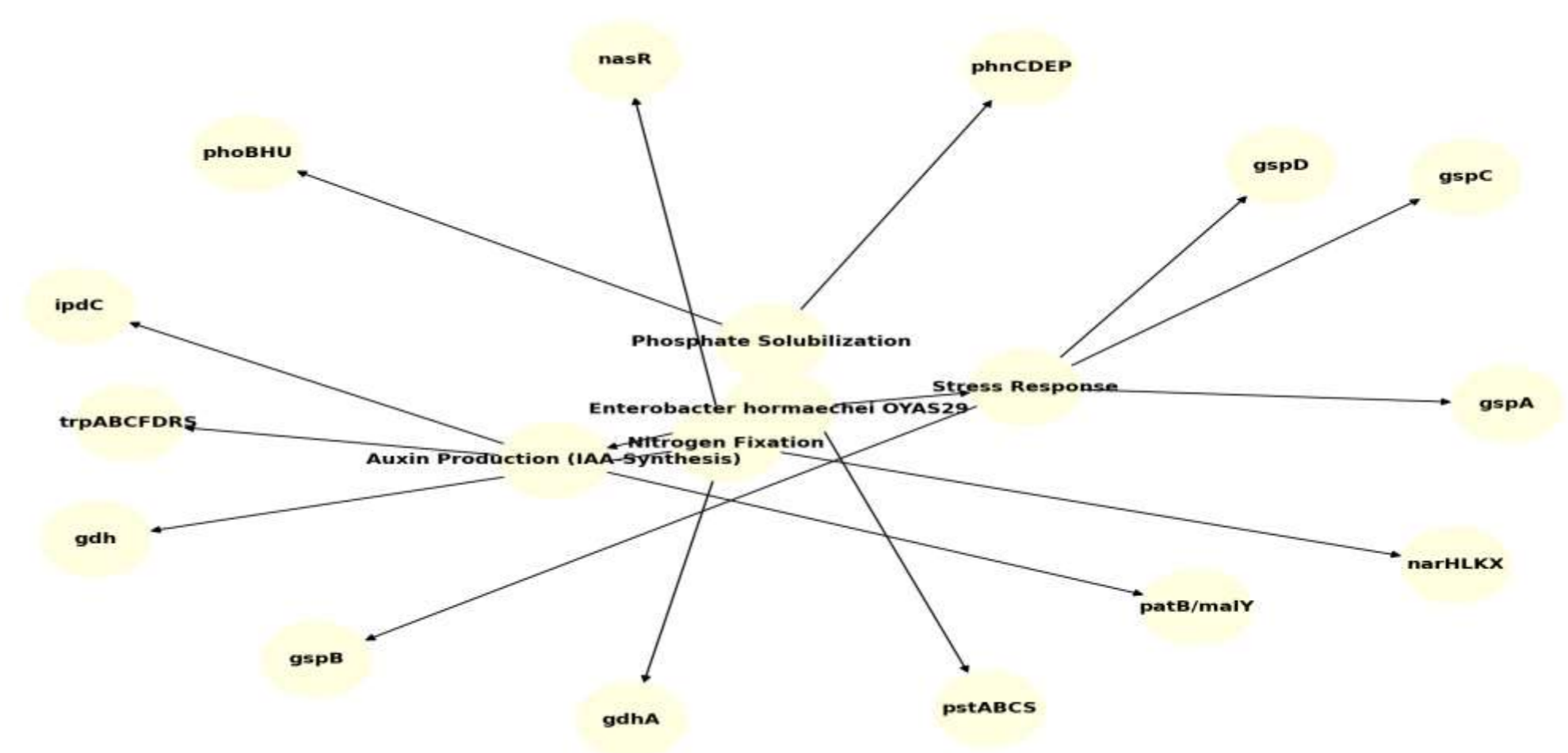
Name	<i>Enterobacter hormaechei</i> OYAS29
Locus	JAXCLF010000000 93rc DNA linear, BCT-11-Dec-2023
BioProject	PRJNA1030784
BioSample	SAMN37915848
Accession	JAXCLF000000000
Assembly Method	Unicycler v.0.4.8
Genome Representation	Full
Sequencing Technology	Illumina Novaseq
Annotation Provider	NCBI Refseq
Annotation Pipeline	NCBI Prokaryotic Genome Annotation Pipeline (PGAP)
Annotation Method	Best-Placed reference protein sets; Genemarks-2+
Annotation Software Revision	6.6
Genes (Total)	4240
CDS (Total)	4143
Genes (Coding)	4068
CDS (with Protein)	4068
Genes (RNA)	97
rRNAs	7,2,5 (5s, 16s, 23s)
Complete rRNAs	6 (5s)
Partial rRNAs	1,2,5 (5s, 16s, 23s)
tRNAs	77
ncRNAs	6
Pseudo genes (Total)	75
CDSs (without Protein)	75
Pseudo genes (Ambiguous residue)	0 of 75
Pseudo genes (Frame shifted)	21 of 75
Pseudo genes (Incomplete)	45 of 75
Pseudo genes (Internal stop)	20 of 75
Pseudo genes (Multiple problems)	9 of 75
Pseudo genes (Short Proteins)	1 of 75
CRISPR Arrays	1
WGS Scaffold	JAXCLF010000001—JAXCLF010000093
Genome Quality	Good

### RESULTS & DISCUSSION



**Figure 1:** *Enterobacter hormaechei* OYAS29's circular genomic map shows a tiered pattern of characteristics from outer to inner rings. These characteristics include contigs, forward and reverse strand protein-coding sequences (CDS), RNA genes, CDS that resemble known virulence factors and antibiotic resistance genes, GC content, and GC skew.

PGPR Mechanism	Key Genes	Description
Auxin Production	<i>trpABCFDRS</i> , <i>ipdC</i> , <i>patB/malY</i>	Involved in auxin synthesis, promoting plant growth.
Nitrogen Fixation	<i>gdh</i> , <i>gdhA</i> , <i>narHLKX</i> , <i>nasR</i>	Facilitates nitrogen fixation, enhancing soil fertility.
Phosphate Solubilization	<i>phoBHU</i> , <i>phnCDEP</i> , <i>pstABCS</i>	Solubilizes phosphate, making it available for plant uptake.
Stress Response	<i>gspA</i> , <i>gspB</i> , <i>gspC</i> , <i>gspD</i>	Responds to environmental stress, ensuring survival.



**Figure 2:** shows the phylogenetic tree for *Enterobacter hormaechei* OYAS29

### REFERENCES

- Jiang L, et al. Genome insights into *Saccharibacillus brassicae* ATSA2T. *AMB Express*. 2023; 13(1):1-16.
- Malgigliolo G, et al. Plant-microbe interaction in sustainable agriculture. *Sustainability*. 2022; 14(4):2253.
- Akinola AO, et al. Growth enhancement potentials of indigenous PGPR on sweet pepper through seed bacterization. 2022.

### CONCLUSION

- Enterobacter hormaechei* OYAS29 shows potential as a plant growth-promoting rhizobacterium (PGPR) with genes for auxin production, phosphate solubilization, and stress tolerance, making it a valuable candidate for sustainable agriculture.
- Future research will focus on validating key genes in plants, conducting field trials, and exploring microbial interactions that enhance plant health.