REPORT

on the implementation of the individual plan of work graduate student of 2 years of study

LIN WU

Supervisor:
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Theme of dissertation work:

FACTORS OF NOSOCOMIAL INFECTIONS RESISTANCE AS A BASIS FOR THE DEVELOPMENT OF MODERN ANTIMICROBIALS

Purpose:

to establish the factors and mechanisms of resistance of selected pathogens and the development of antimicrobial agents of targeted action against these factors

The work is performing

at the Department of Industrial Biotechnology and Biopharmacy Igor Sikorsky KPI and Hainan Medical University (Haikou, China).

Tasks of the work:

■- selection of actual pathogens and analysis of their features by modern genetic methods, comparative study of resistance and virulence of clinical strains;

■- establishment of factors and mechanisms of resistance of selected pathogens that may be targets for the action of antiseptics;

■- obtaining a sample of antibiotic from *Streptomyces albus*, analysis of its spectrum, mechanism of action and effective doses concerning the studied pathogens;

■- development of targeted antiseptic compositions based on antibiotics and enzymes from *Streptomyces albus*;

■- creation of recommendations on directions of development of the newest effective antiseptics which are not promoting of pathogens antibiotic resistance.

Completed tasks for 2 years of study according to the work plan (scientific component):

- writing a review of the literature on the research topic and publishing an article on these materials
- study of the conditions of biosynthesis and isolation of the antibiotic drug from *Streptomyces albus*, obtaining a sample for further research
- genome sequence and annotation of *Bacteroides sp aff. Thetaiotaomicron* strain isolated from blood
- report at an online conference with the publication of abstracts

Genome sequence and annotation of *Bacteroides sp aff. Thetaiotaomicron* strain isolated from blood

Background

Bacteroides thetaiotaomicron

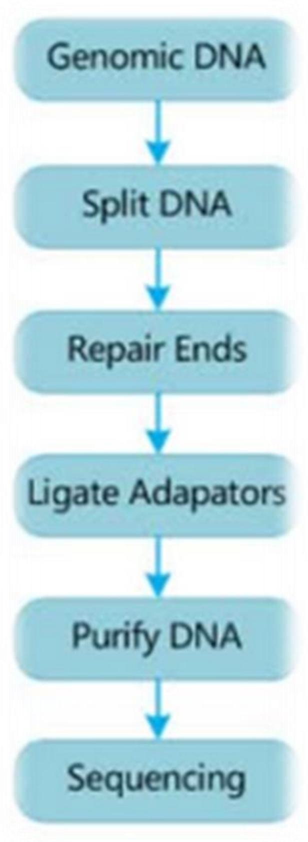
-a dominant member of normal human colonic flora

-an opportunistic pathogen

What is the pathogenic mechanism of *B. thetaiotaomicron* ?

By sequencing the genetic structure, it is possible to quickly predict the function of a gene and, thus, the subsequent pathogenic mechanism.

Method



Analysis content	Software	Functional description	version
QC*	cutadapt	Filter low quality data and remove linker sequences	1.9.1
Assembly	kmergenie	Estimated genome size	1.7039
	velvet	Build contig	1.2.10
	SSPACE	Building scaffold	v3.0
	GapFiller	Fill up gap	v1-10
gene finding	prodigal	Gene prediction	v2.6.3
ncRNA analysis	cmscan	Aligning genomic sequences to the Rfam library	1.1.2
gene annotation	diamond	Nr comment	0.8.15
	blast	Kegg comment	2.2.28+
	blast2go	Go Comment	v2.5
	hmmscan	Cog comment	3.1b2
repeat analysis	RepeatModeler	Repeat sequence analysis	1.0.8
	RepeatMasker		4.0.6

Results

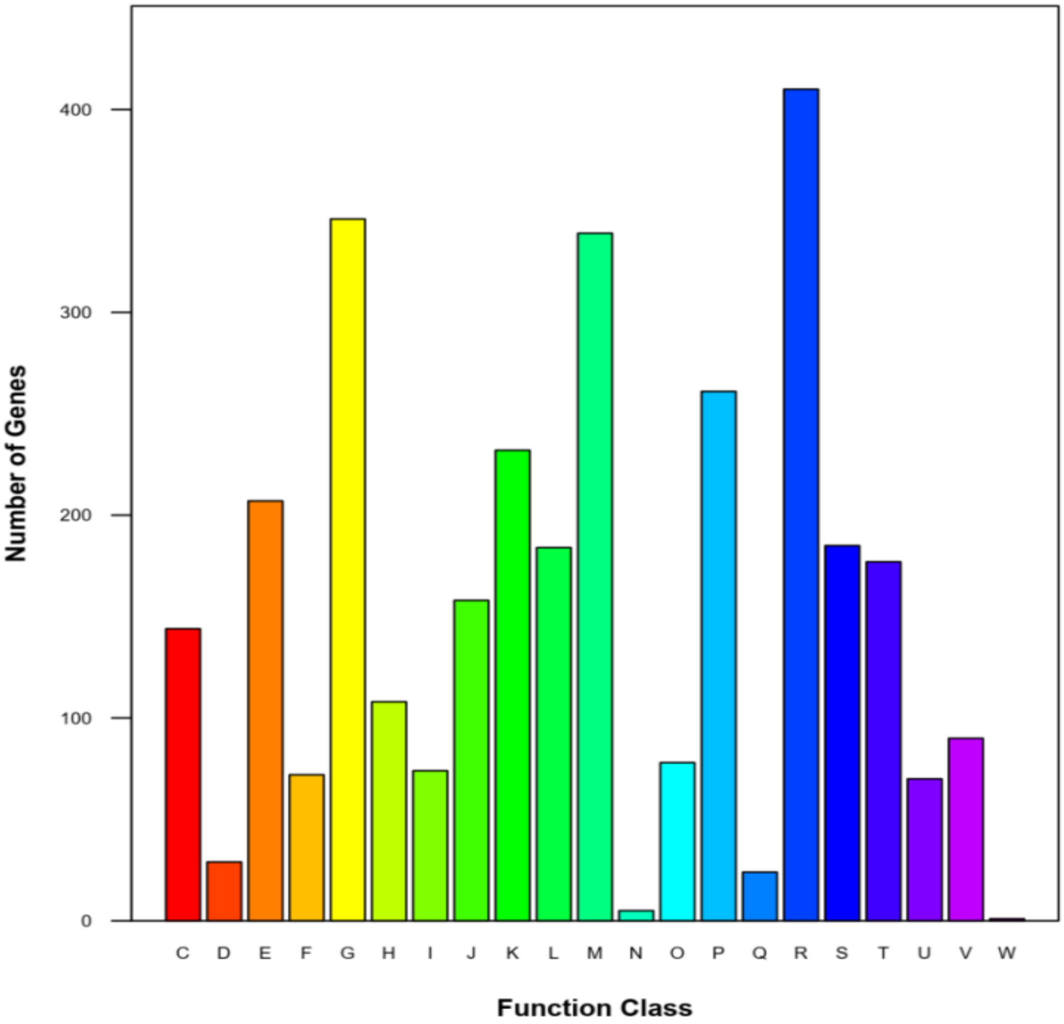
Genes enrichment in *Bacteroides sp. aff. thetaiotaomicron strain* according to the KEGG pathway database

-Bacteroides thetaiotaomicron revealed the presence of genes associated with pathway 199.

--the division of biological metabolic pathway into six categories

Results

Annotation of genes in *Bacteroides sp. aff. thetaiotaomicron* in the COG database.



C: Energy production and conversion
D: Cell cycle control, cell division, chromosome partitioning
E: Amino acid transport and metabolism
F: Nucleotide transport and metabolism
G: Carbohydrate transport and metabolism
H: Coenzyme transport and metabolism
I: Lipid transport and metabolism
J: Translation, ribosomal structure and biogenesis
K: Transcription
L: Replication, recombination and repair
M: Cell wall/membrane/envelope biogenesis
N: Cell motility
O: Posttranslational modification, protein turnover, chaperones
P: Inorganic ion transport and metabolism
Q: Secondary metabolites biosynthesis, transport and catabolism
R: General function prediction only
S: Function unknown
T: Signal transduction mechanisms
U: Intracellular trafficking, secretion, and vesicular transport
V: Defense mechanisms
W: Extracellular structures

Conclusions

Incorporate 199 pathway assciated genes

The capacity of metabolizing a varity of polysaccarides

expanded repertoire of enzymes for the hydrolysis

Build a nomal microbiota of the gut

Completed tasks for 2 years of study according to the work plan (educational component):

Title of the subjects	Credits	Attestation	Mark
Organization of scientific-innovative and scientific-pedagogical activity	4	Test	91
Pedagogical practice	2	Test	95
Scientific and managerial principles of ecological expertise	4	Test	92
Problem issues of biochemistry, molecular biology, cytology and bioengineering	8	Exam	96
Problem issues of pharmaceutical biotechnology	5	Test	92
Innovative finished forms of biopreparations	5	Exam	96

Publication during 2nd year of study

(2 Article, 1 Abstract)

1. Zhi Cheng Wu, **Lin Wu**, Meng Zhang, WeiLan Zhou. Genome sequence and annotation of Bacteroides sp aff. Thetaiotaomicron strain isolated from blood / Infection, Genetics and Evolution, 2021, 91:104816

2. **L. Wu**, Z.C. Wu, T.S. Todosiichuk, O.M. Korneva. NOSOCOMIAL INFECTIONS: PATHOGENICITY, RESISTANCE AND NOVEL ANTIMICROBIALS /Innov Biosyst Bioeng, 2021, vol. 5, no. 2, 73–84. doi: 10.20535/ibb.2021.5.2.228970

3. Korneva O.M., Ryzhkova T.S., Wu Lin. Peculiarity of Streptomyces albus antimicrobial complex′s biosynthesis / Проблеми та досягнення сучасної біотехнології: матеріали I міжнародної наук.-практ. інтернет-конф. (25 березня 2021 р., м. Харків). – Електрон. дані. – Х. : НФаУ, 2021. – С.12.

MINISTRY OF HEALTH OF UKRAINE

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CERTIFICATE

of participation

№062

This is to certify that

Lin Wu

participated in the I International Scientific and Practical Internet Conference

«PROBLEMS AND ACHIEVEMENTS OF MODERN BIOTECHNOLOGY»

(duration - 8 hours)

March 25, 2021, Kharkiv, Ukraine

Rector of the NUPh, prof. Alla KOTVITSKA

Vice-Rector for Research and Development, prof. Inna VLADIMIROVA

Head of the Department of Biotechnology, prof. Natalia KHOKHLENKOVA