

Characterization of the microbiome of breast tissue and gut in Korean breast cancer patients

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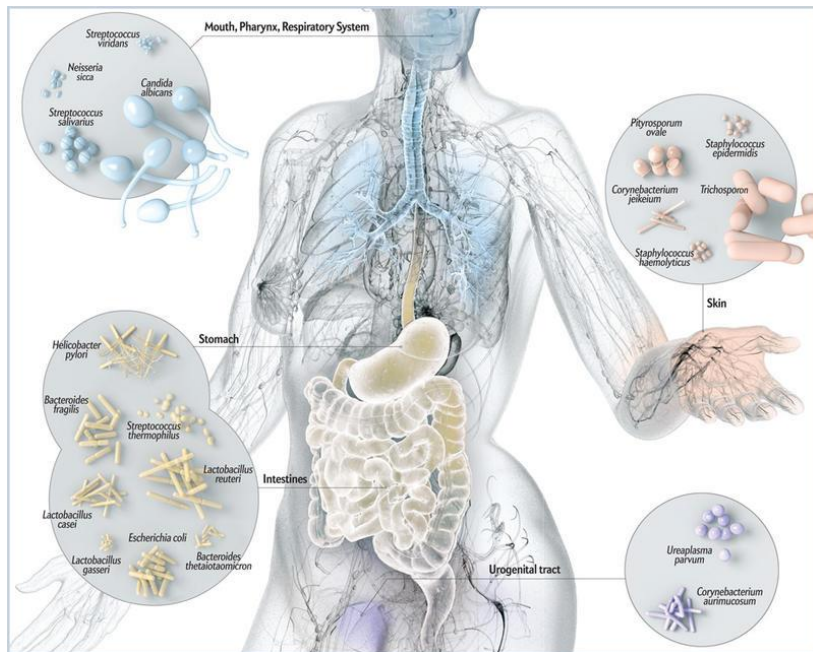
DISCLOSURE

The present research has been
supported by
Korea Breast Cancer Foundation.

Introduction

Human Microbiome In Human Health

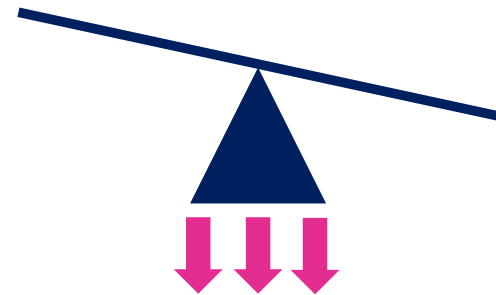
100 trillion microbes



Symbiosis



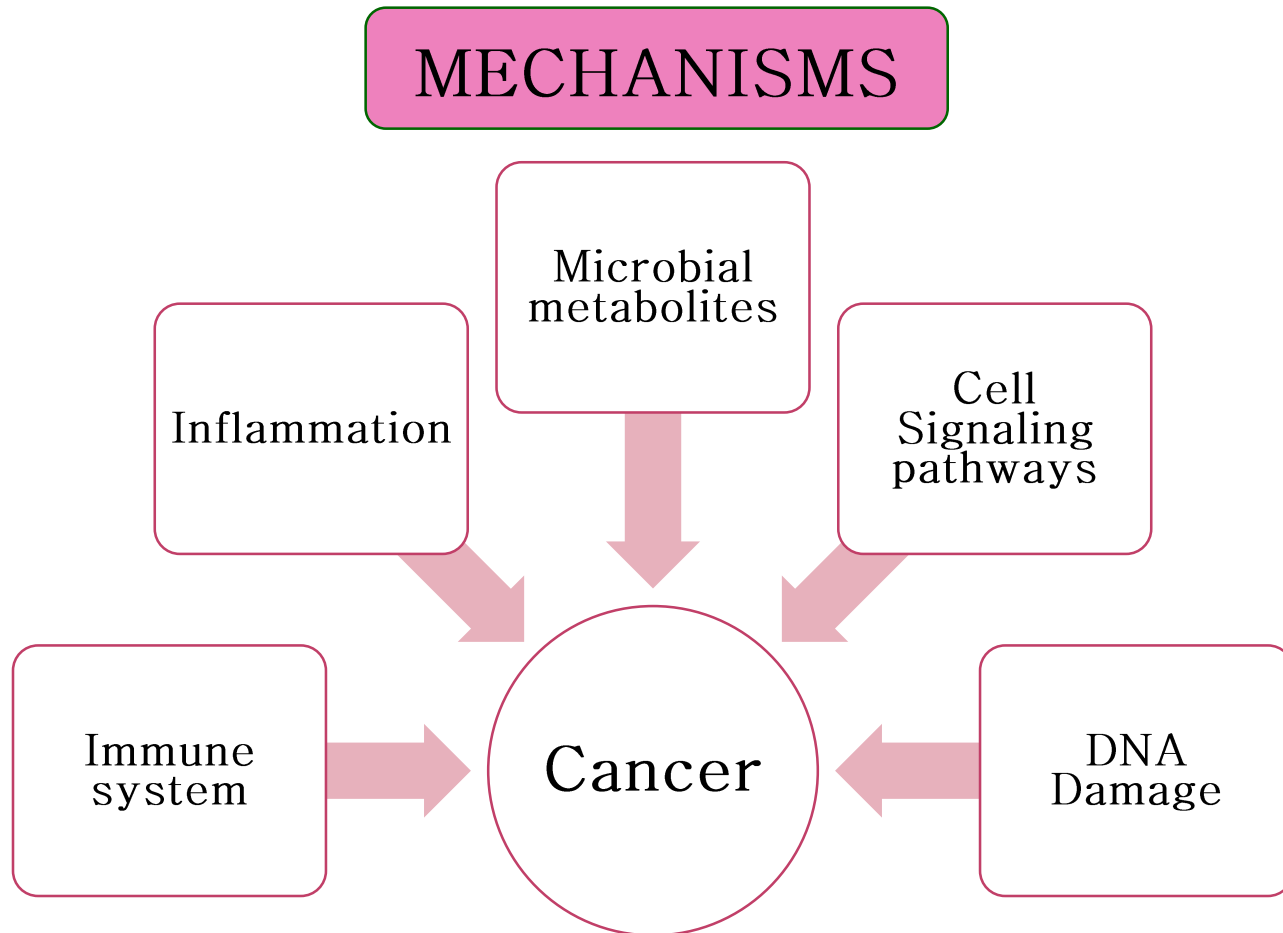
Dysbiosis



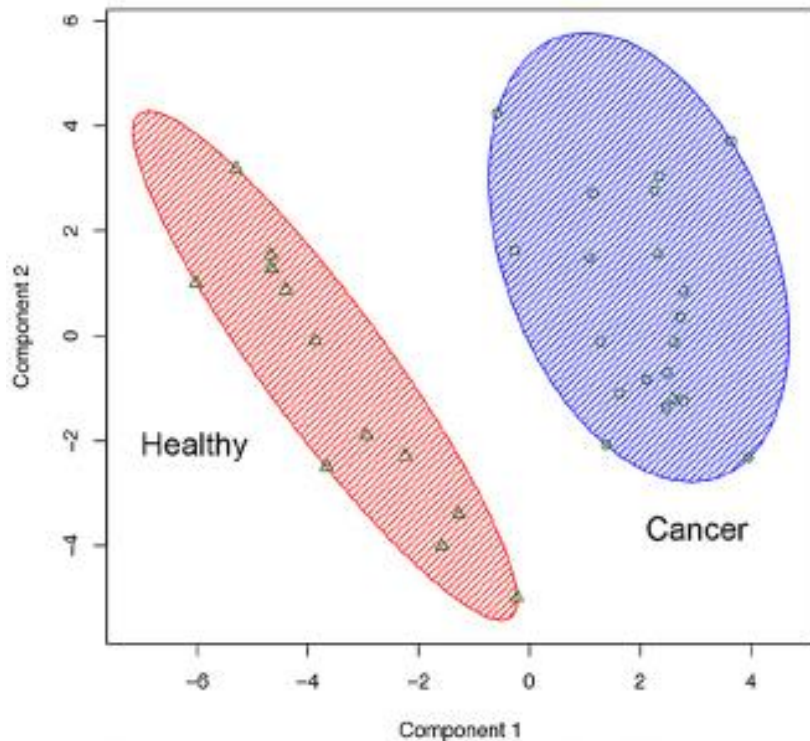
Inflammatory
Bowel dz.
Obesity
Autoimmune dz.
Mental
disorders

Cancer
Colorectal
Stomach
Liver
Nasopharynx
Etc.

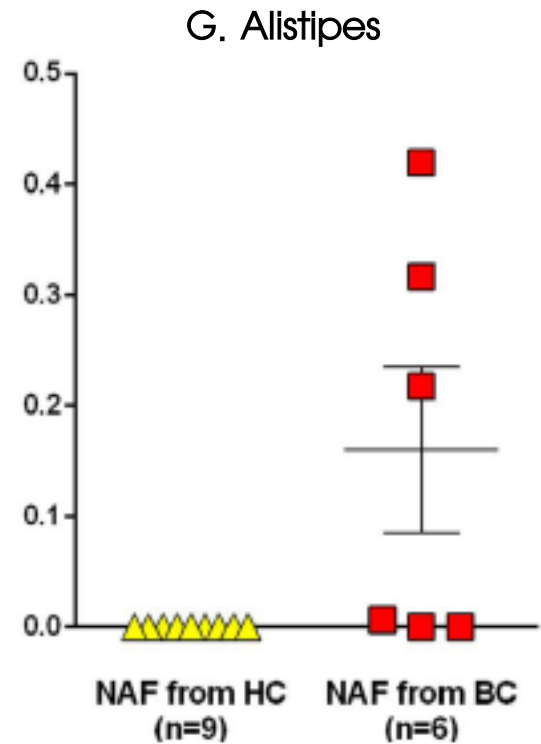
Human Microbiome In Cancer



Breast Microbiome In Breast Cancer



Applied and Environmental Microbiology (2016)



Scientific Reports (2016)

Gut Microbiome In Breast Cancer

- Difference in microbial composition and diversity between breast cancer group and normal group.

JNCI J Natl Cancer Inst

(2015)

- Difference in absolute number and proportions of some species according to the clinical stage and grade.

FASEB J (2015)

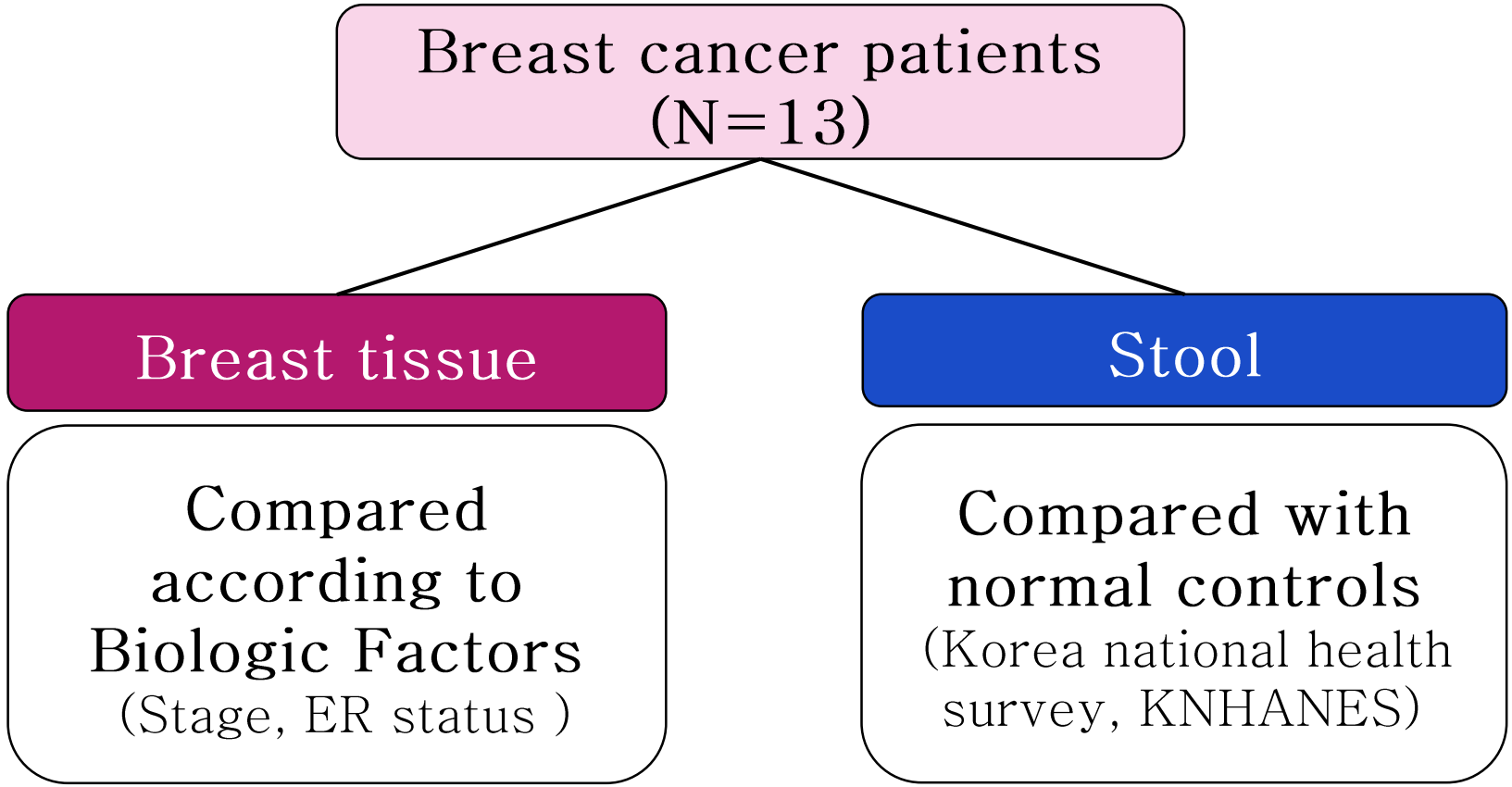
Objective

- The precise roles of microbiome in breast tissue and gut on breast cancer is still unknown
- No studies that investigate the microbiome of breast tissue in Asian woman
- To investigate the microbial community in breast tissue and gut in Korean breast cancer patients

Materials and Methods

Materials

Breast cancer patients
(N=13)



```
graph TD; A[Breast cancer patients (N=13)] --> B[Breast tissue]; A --> C[Stool]; B --> D[Compared according to Biologic Factors (Stage, ER status)]; C --> E[Compared with normal controls (Korea national health survey, KNHANES)]
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Breast tissue

Compared
according to
Biologic Factors
(Stage, ER status)

Stool

Compared with
normal controls
(Korea national health
survey, KNHANES)

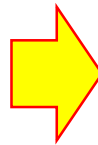
Methods

METAGENOMICS

Study of **genetic material** directly from environmental sample without culturing

Culture Dependent Method

- Traditional method
- Only 10~30% of bacteria are culturable.

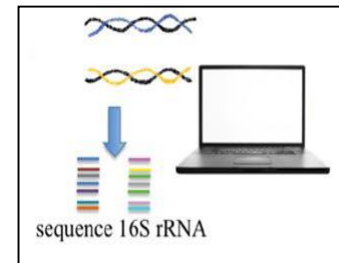


Culture Independent Method

- Metagenomics
- Analyze microbial communities regardless of the culturability

Methods

- Breast tissue (aseptic, 2cm away from the tumor)
- Stool



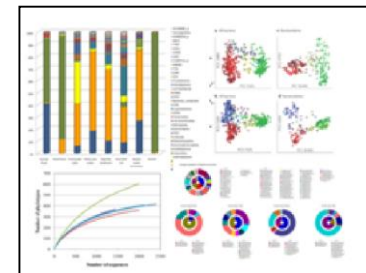
Sample

DNA extraction

PCR amplify 16S rRNA gene

Next generation sequencing

Bacterial community analysis



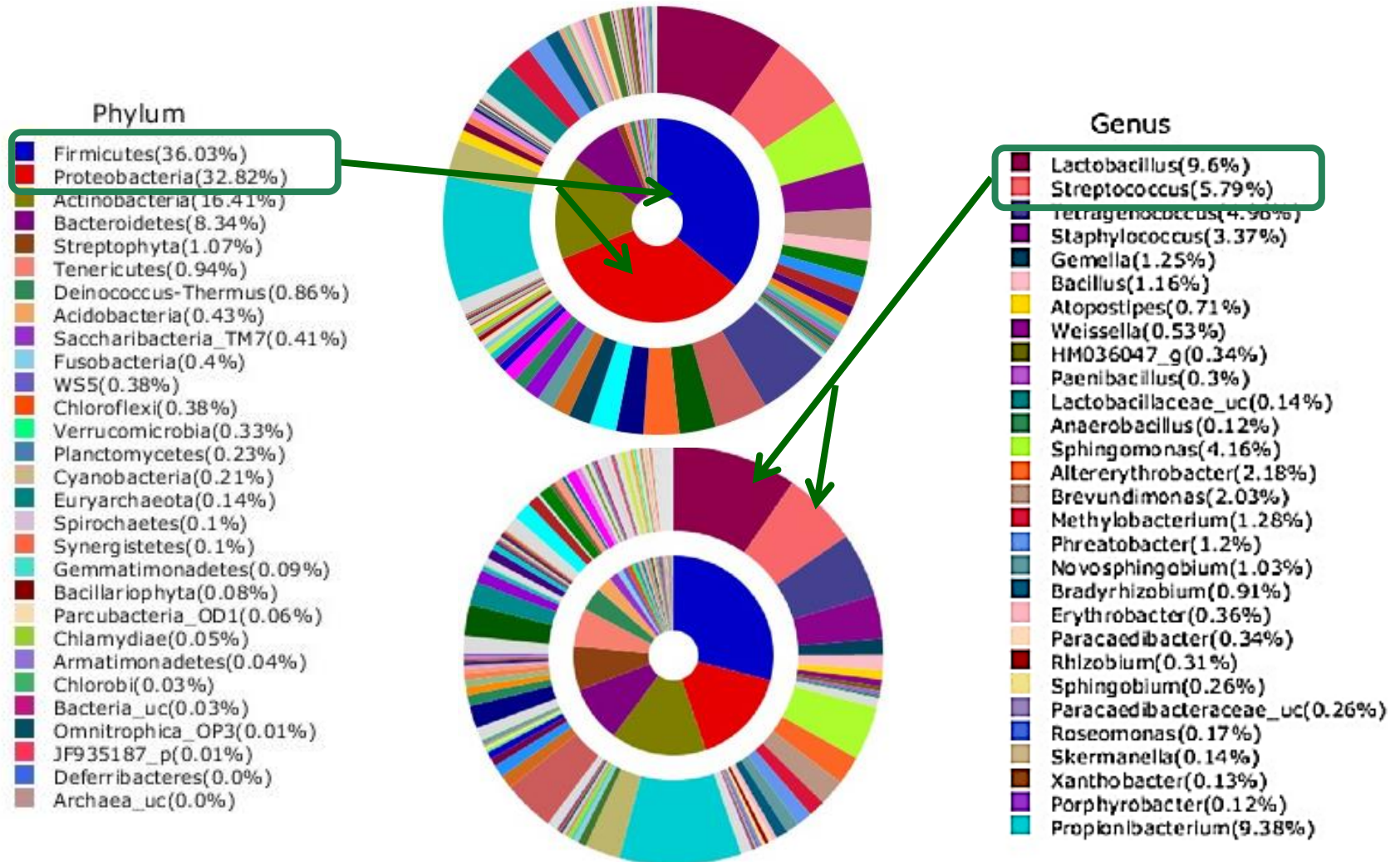
Results

Patients Characteristics

Characteristic	Number (%) or mean \pm SD
Cancer stage	
I	7 (53.8)
II	5 (38.5)
III	1 (7.7)
Menstruation	
Premenopause	8 (66.7)
Postmenopause	4 (33.3)
Pathology	
Invasive ductal carcinoma	11 (90.9)
Mucinous carcinoma	1 (9.1)

Lymph node metastasis	
(+)	2 (16.6)
(-)	10 (83.3)
Estrogen receptor	
(+)	9 (75.0)
(-)	3 (25.0)
Progesteron receptor	
(+)	7 (41.7)
(-)	5 (58.3)
HER2	
(+)	2 (16.7)
(-)	10 (83.3)
Tumor size	2.05 \pm 0.71
BMI (kg/m²)	23.58 \pm 3.64

Breast tissue microbiome analysis



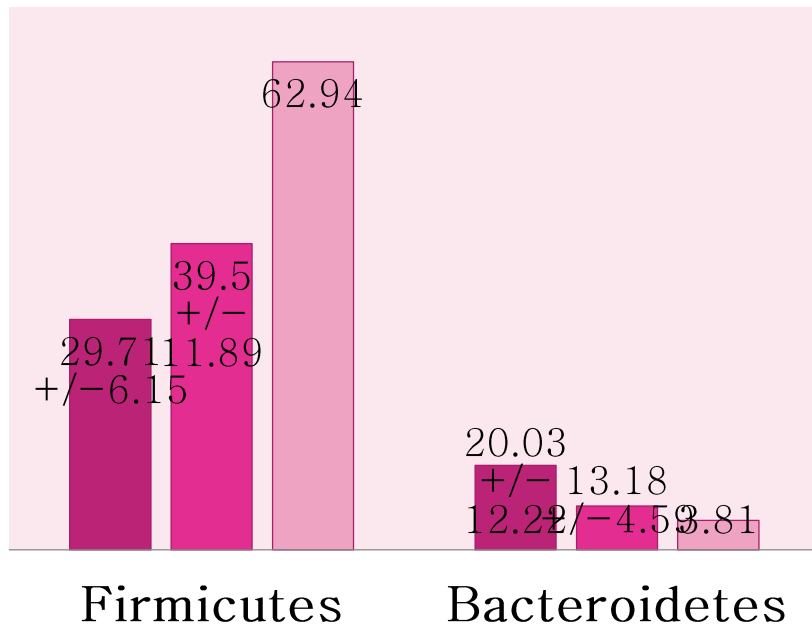
Breast tissue microbiome analysis

Stage

Stage I (n=7), II (n=5), III (n=1)

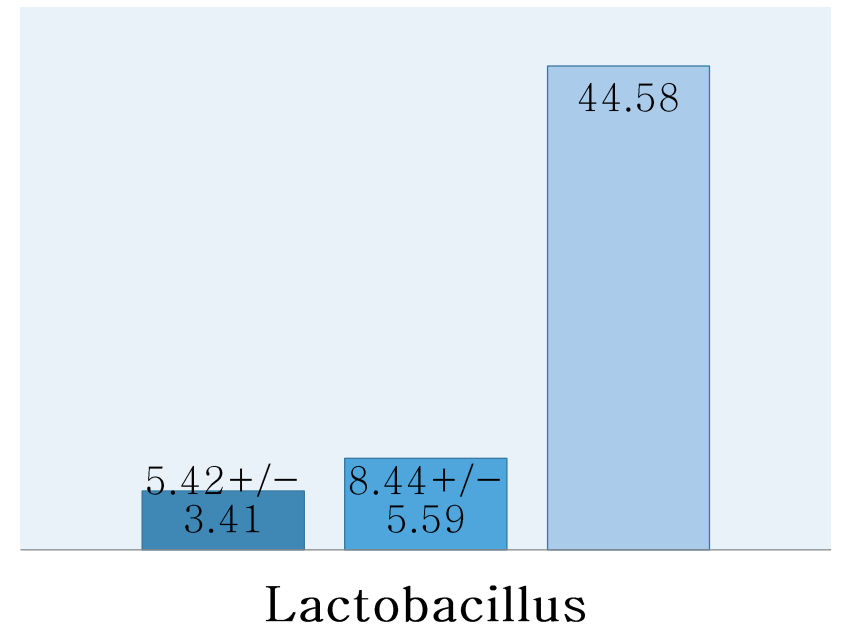
Phylum

■ Stage I ■ Stage II ■ Stage III



Genus

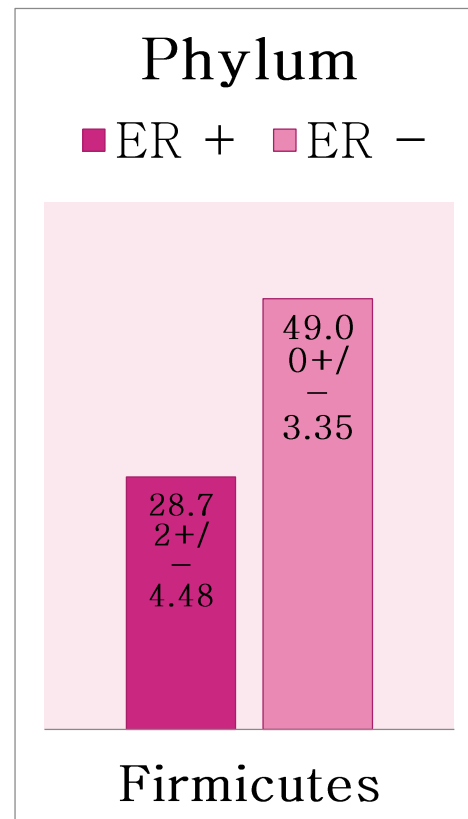
■ Stage I ■ Stage II ■ Stage III



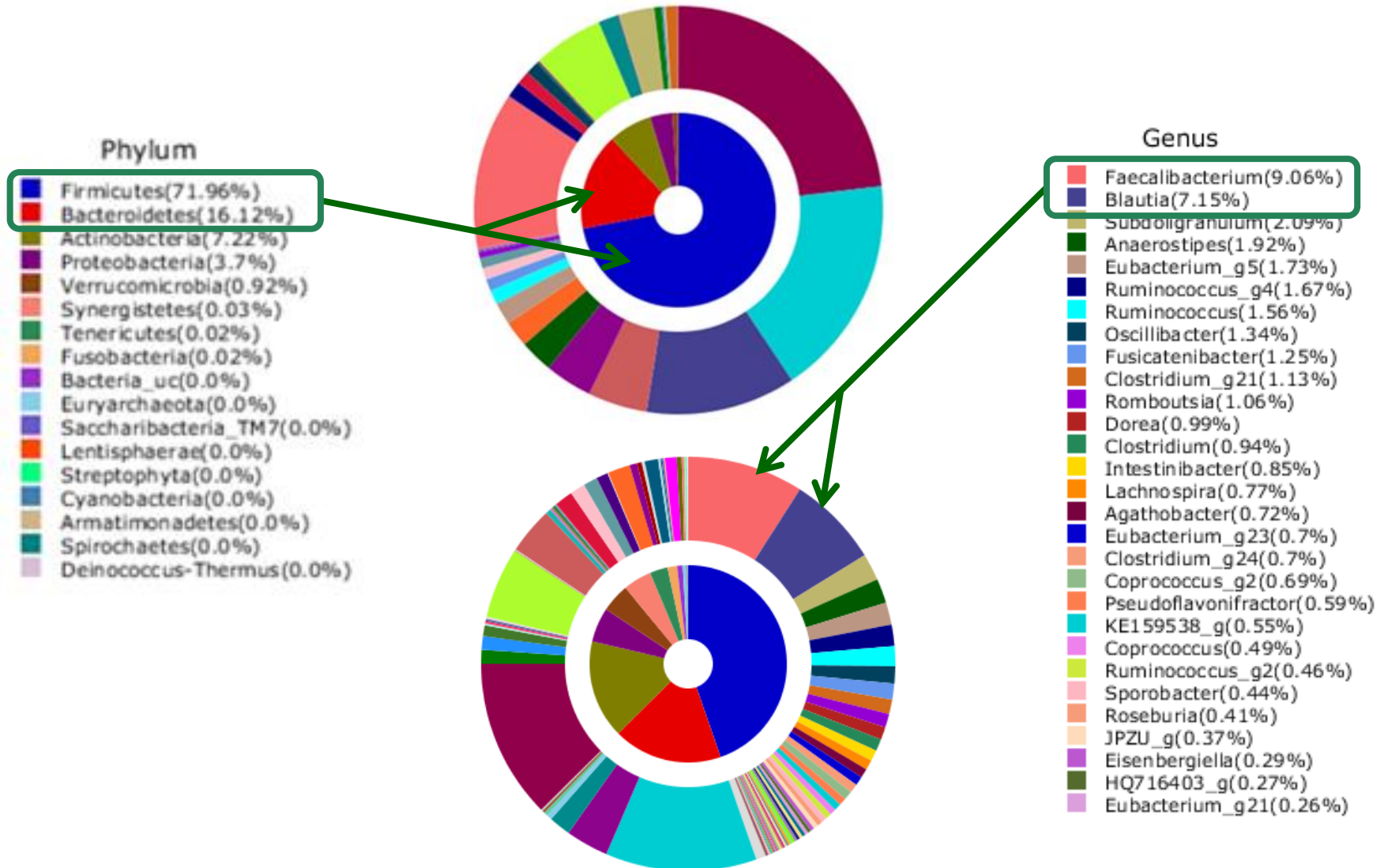
Breast tissue microbiome analysis

ER status

ER positive(n=9) vs negative(n=3)

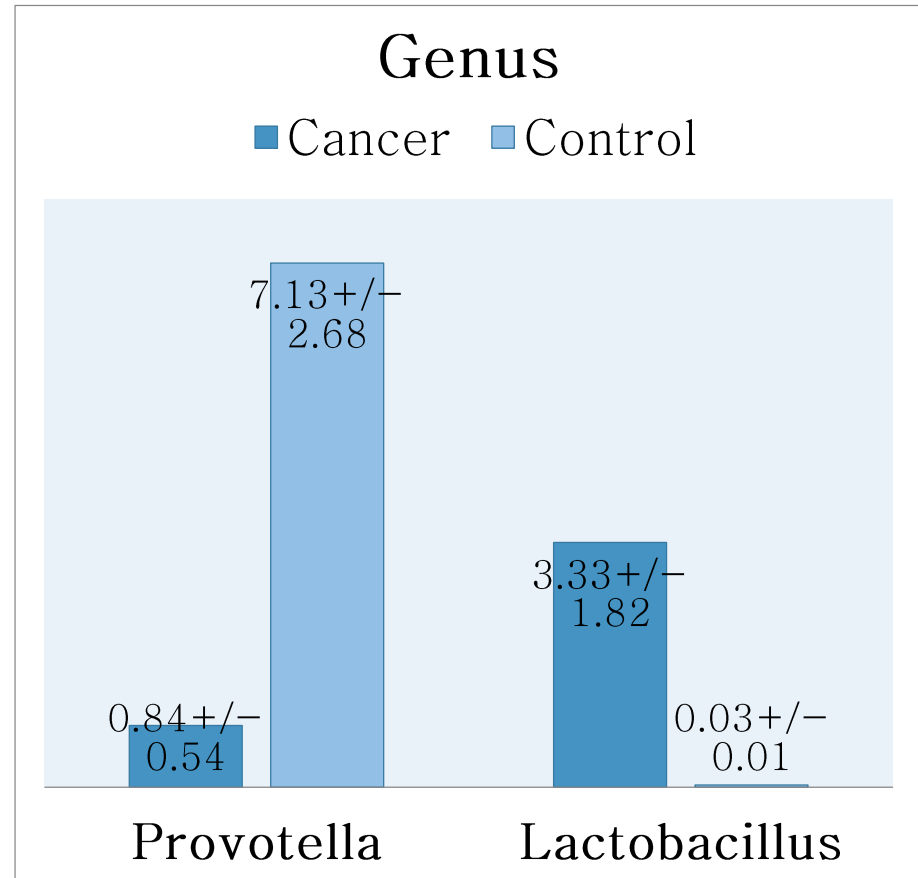
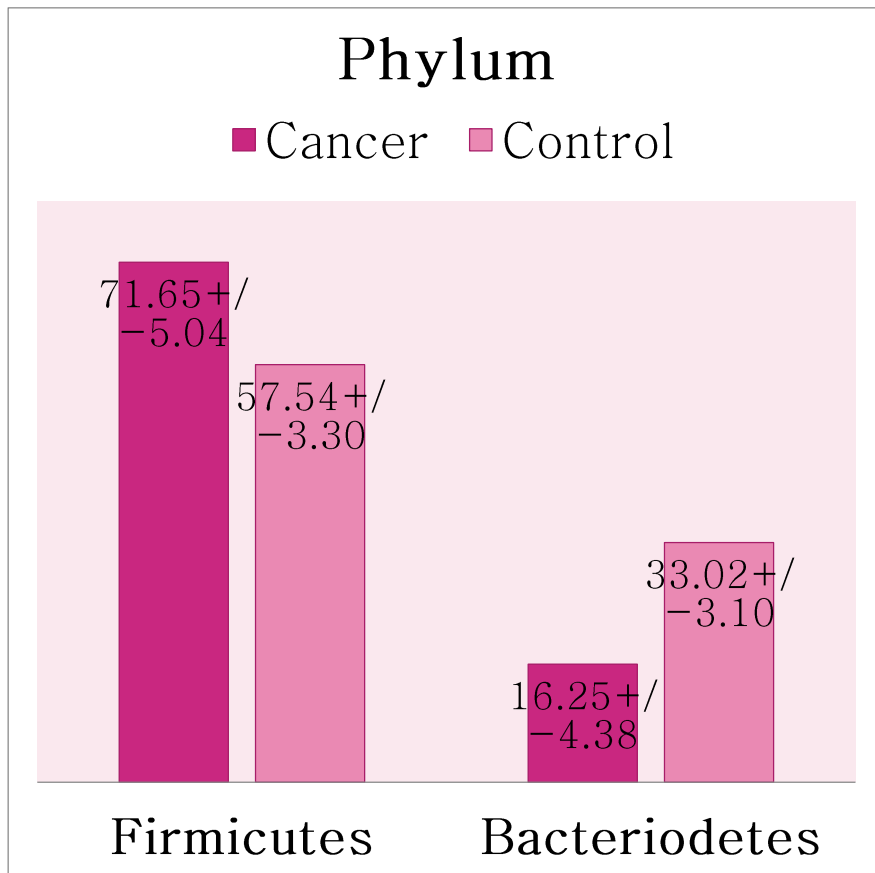


Gut microbiome analysis



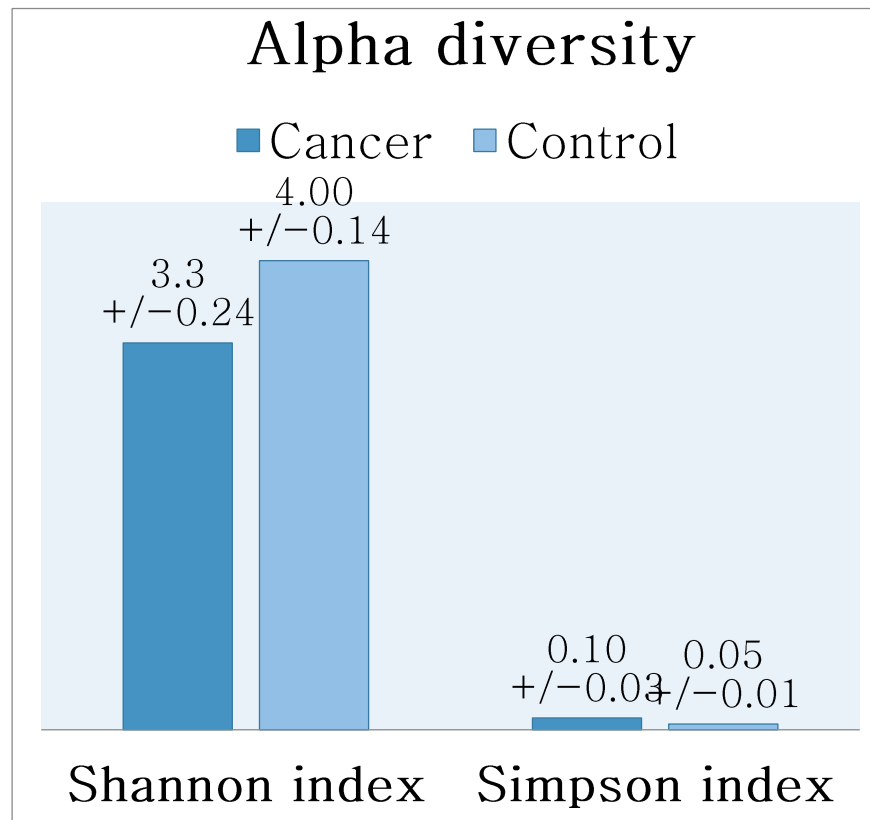
Gut microbiome analysis

Cancer vs Controls (Age, BMI matching)



Gut microbiome analysis

Cancer vs Controls (Age, BMI matching)



Summary and Conclusion

Summary and Conclusion

Breast

microbiome

- Dominant phylum were **Firmicutes** and **Proteobacteria**
- **Higher** prevalence of **Firmicutes** and **lower** prevalence of **Bacteroidetes** were related with **higher** stage of breast cancer.
- **Firmicutes** was higher prevalence in ER negative patients.

Prevalence of Firmicutes

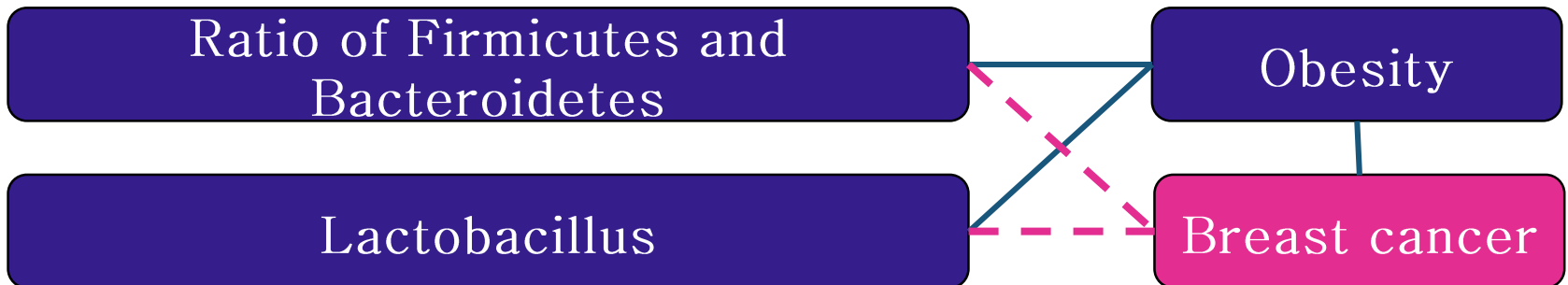


Prognosis or Progression

Summary and Conclusion

Gut microbiome

- Firmicutes and Lactobacillus levels were **higher** and Bacteroidetes and Prevotella levels were **lower** in breast cancer group.
- Bacterial groups of control group showed higher diversity.



Summary and Conclusion

- This study showed the characteristics of microbiome in breast tissue and gut of Korean female breast cancer patients. Who are they?
- Further large-scaled studies should be performed to elucidate the precise roles of microbiome in breast cancer.



What are they doing? (Functional profiling)
How do they work? (Mechanism investigation)

Thank you for listening