A NOVEL HOST AND MICROBIAL BIOMARKER PANEL FOR EARLY DETECTION OF OVARIAN CANCER

Subina Mehta, Kristin Boylan, Amy Skubitz, Ashley Petersen, Pratik Jagtap and Timothy J. Griffin

Department of Biochemistry, Molecular Biology and Biophysics

University of Minnesota

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pjagtap@umn.edu

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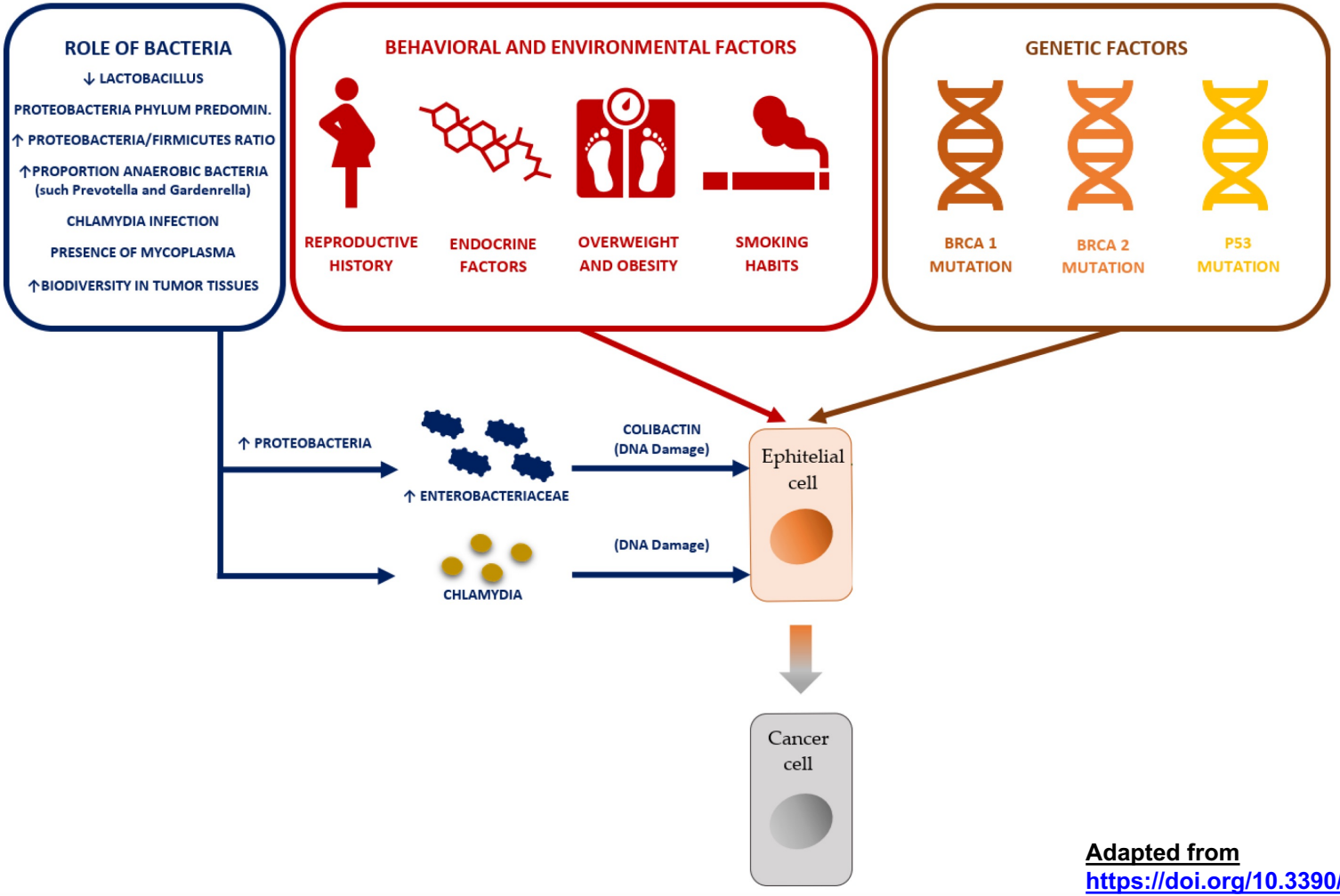


Adapted from
https://doi.org/10.3390/ijms232416019

INPUT: CLINICAL DATASETS

Pap test fluid samples

20 non-cancer controls (Benign and healthy)

....

20 HGSOC patients

....

11-way multiplexed labeling (TMT11)

4 data sets

Quantitative proteomics data

Amy Skubitz

THE PROCESS: DATA ANALYSIS WORKFLOW

4 data sets

Quantitative proteomics data

Database generation

UniProt

FASTA DATABASE

Comprehensive Protein Database

MetaNovo

Reduced Database

Discovery workflow

MS Datasets

Search GUI Peptide Shaker

FragPipe

MaxQuant

Identification of Microbial Peptides

Verification

Unipept

PepQuery

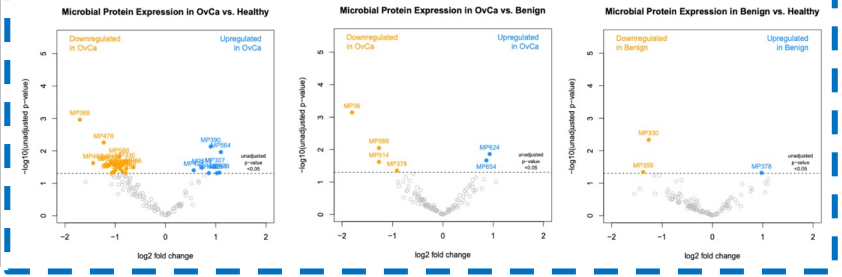
Protein Database of PepQuery verified organisms

Quantitation

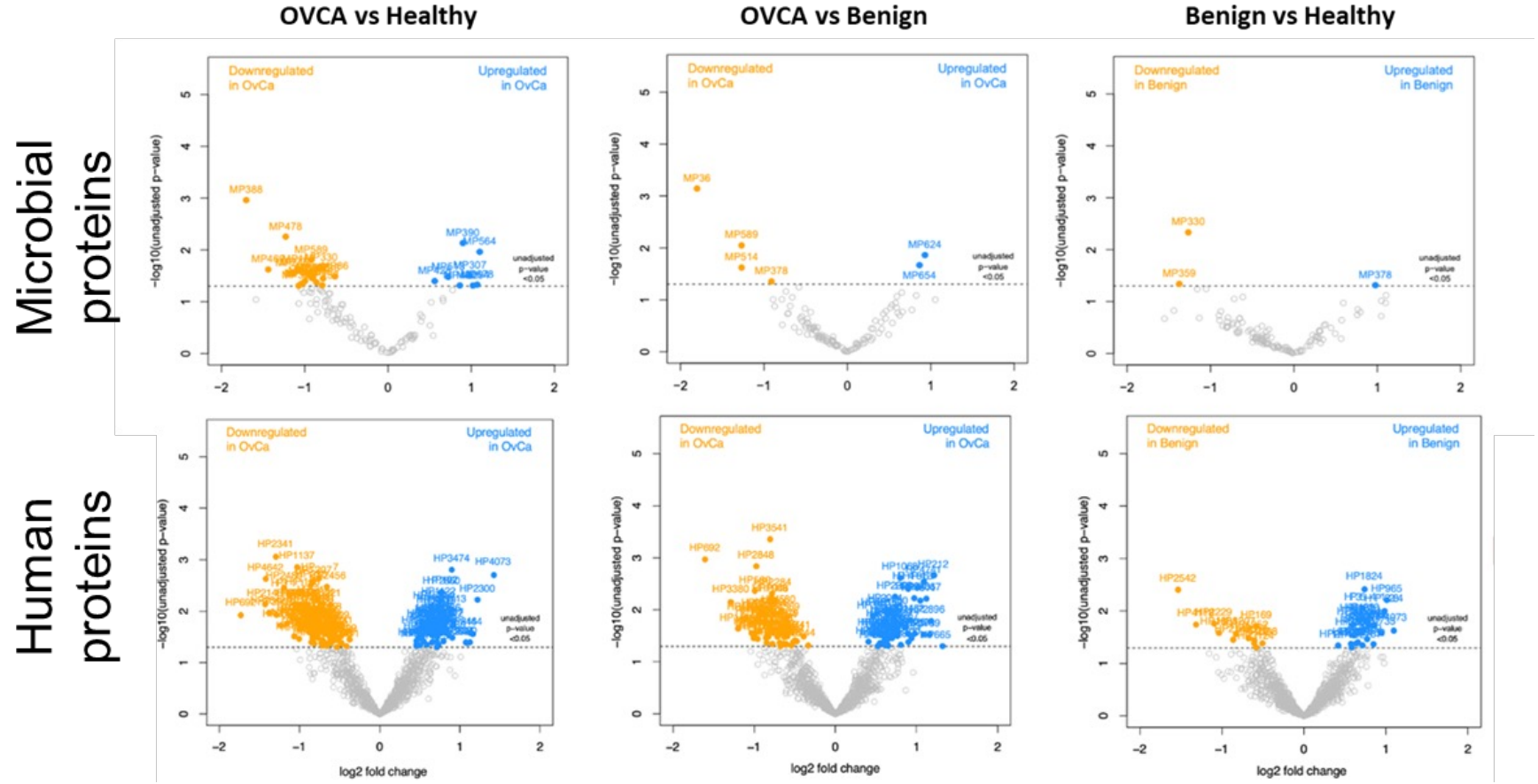
MS Datasets

Data Analysis

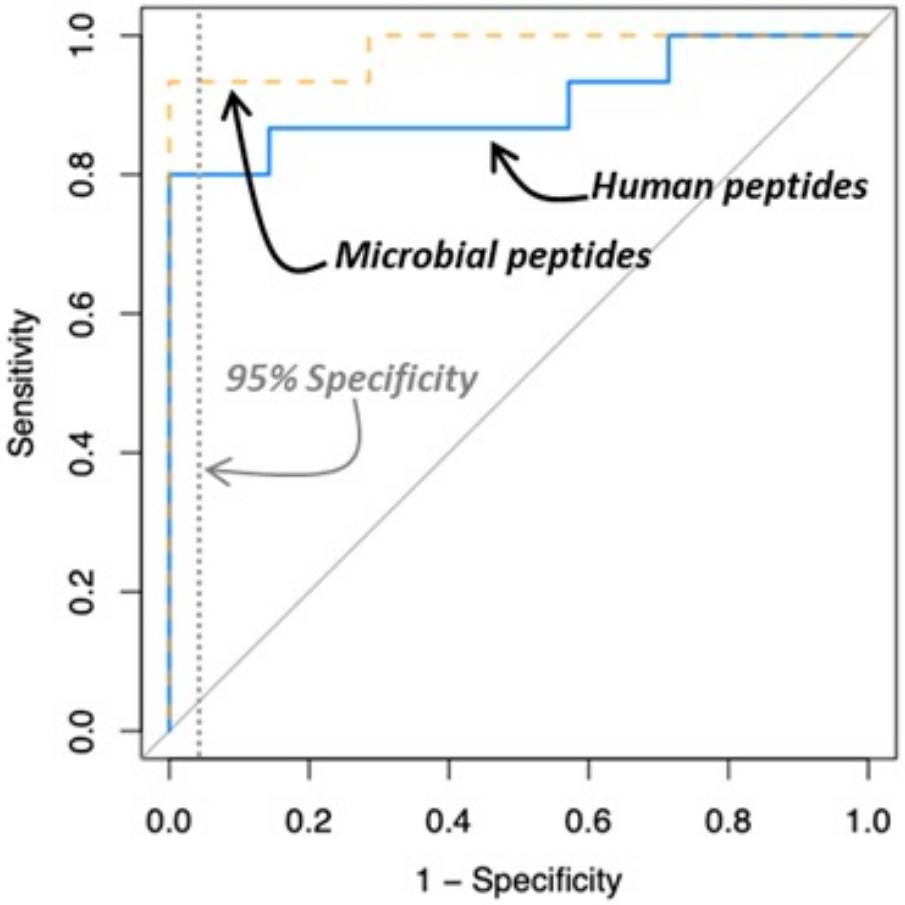
Statistical Analysis



OUTPUT: DIFFERENTIALLY ABUNDANT MICROBIAL AND HUMAN PROTEINS



RESULT: MICROBIAL PEPTIDES OFFER IMPROVED DETECTION OF OVCA



VALIDATION OF A NOVEL HOST-MICROBE PEPTIDE PANEL FOR OVARIAN CANCER EARLY DETECTION FROM ROUTINELY COLLECTED CLINICAL SAMPLES.

Aim 1. Verify promising PTF microbe-human peptide markers for OvCa detection in an expanded MS-based proteomics dataset.

Aim 2. Validate verified differentially abundant microbe-human peptide markers via targeted MS-based assays.

Aim 3. Evaluate the performance of validated microbe-human peptides to detect OvCa.

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