

# Gut microflora and estrogens: a new paradigm for breast cancer risk reduction

**Dr. Kathleen Egan (Moffitt)**

**Dr. Lusine Yaghjian (UF)**



# Background



- Approximately 100 trillion microorganisms live in our bodies and most are found in our intestines;
- The dynamic gut microbiota has myriad influences linked to breast cancer:
  - host immunity
  - metabolism and absorption of a wide range of compounds (steroid hormones, phytochemicals, nitrates, and xenobiotics)
  - integrity of the epithelial barrier and absorption
  - host energy balance and nutritional status
  - host susceptibility to oncogenic factors

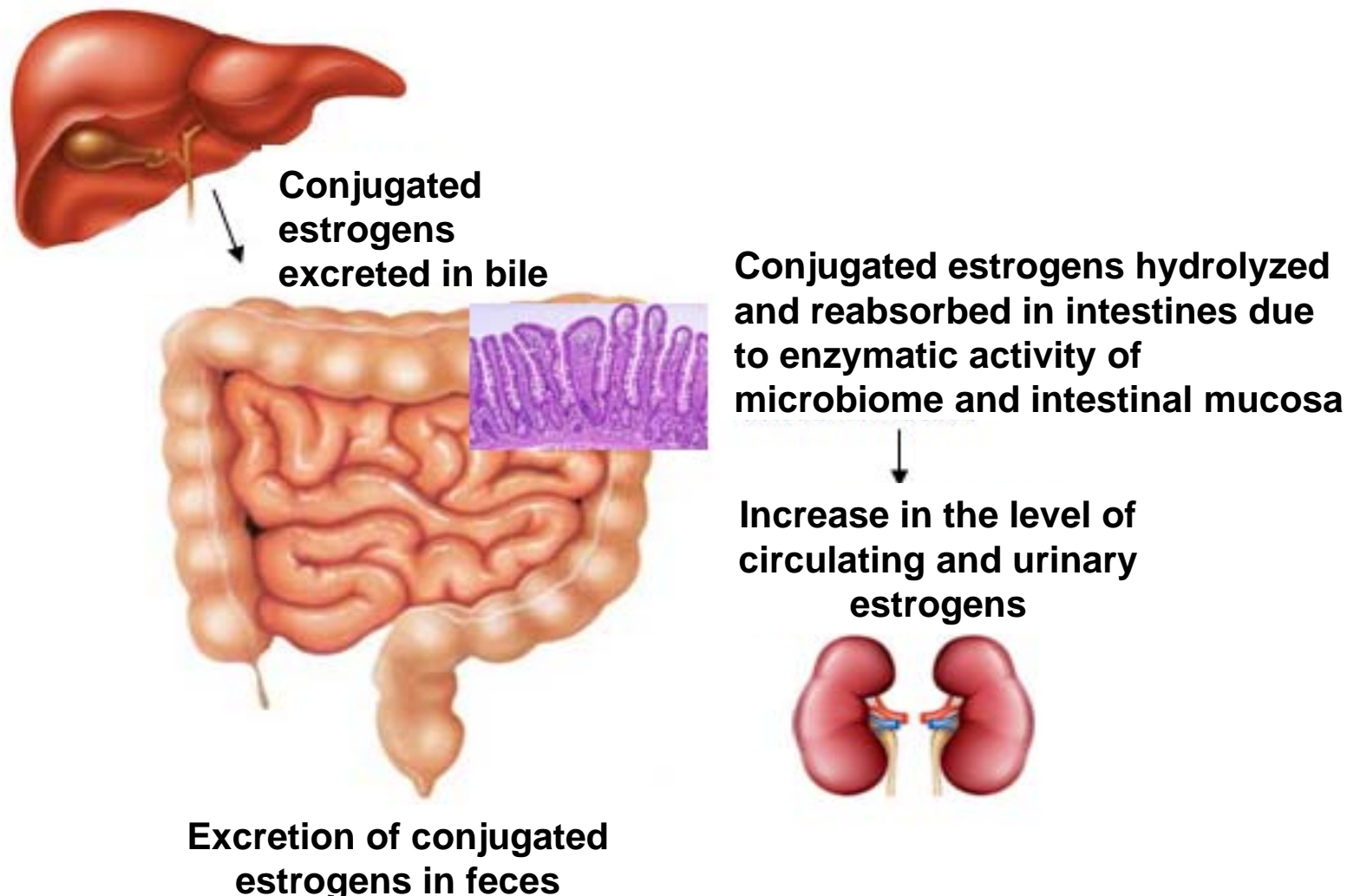
# Background (continued)

- Evidence that the gut microbiome contributes to cancer risk in human populations is limited:
  - In **retrospective case-control studies** observed microbial profiles in cancer patients could reflect changes that occurred *as a result* of cancer diagnosis or treatment
  - In **prospective cohort studies** large numbers of subjects must be studied, long follow-up is required, and repeat sampling may be necessary over many years
- An alternative is to study intermediate risk biomarkers as a proxy, such as endogenous estrogen levels, which are linked to breast cancer.

## Background (continued)

- Two recent studies provided the first evidence that the intestinal microbiome may influence circulating estrogen levels in postmenopausal women;
- Studies are small (n=17 and n=60), however, and findings require confirmation in a large and well characterized study population.

# Role of intestinal microbiota in estrogen metabolism



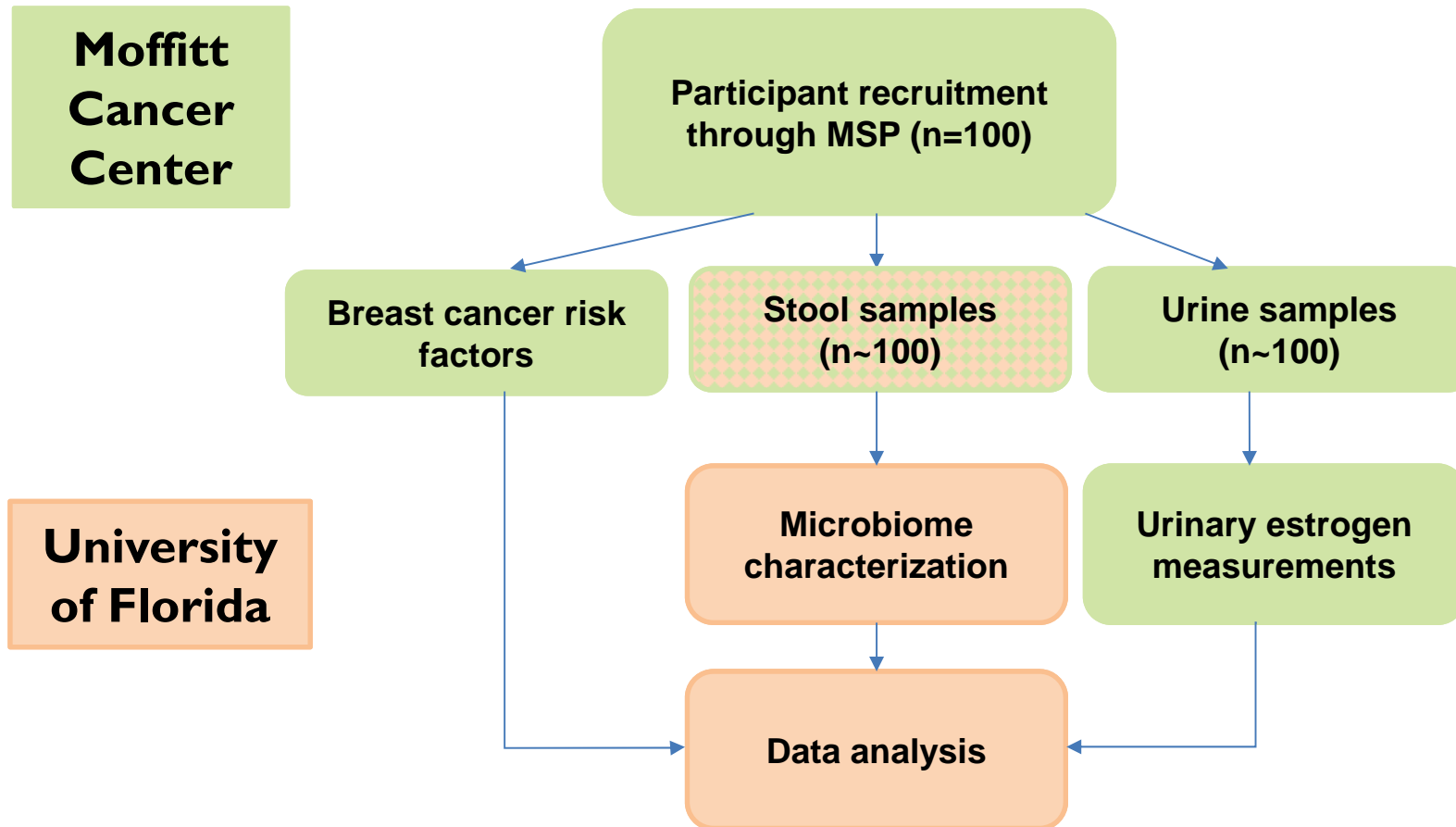
# FACCA Investigation

- **Hypothesis:** Specific microbiome profiles are associated with endogenous hormone levels as measured in urine
- **Specific Aim:** To examine associations of the fecal microbiome with individual urinary metabolites, total urinary estrogens, and metabolite to parent compound (estrone and estradiol) ratios that are reflective of the estrogen conversion rate

# Significance ...

- The project will provide new insights on the role of intestinal microbiome in endogenous estrogen metabolism;
- Findings will assist in planning large-scale investigations testing the hypothesis that the gut microbiome represents an important contributor to breast cancer via modulation of endogenous estrogen metabolism;
- As the gut microbiome is a potentially modifiable risk factor, the research may ultimately lead to specific dietary guidelines or even bio-therapeutic interventions to reduce breast cancer risk.

# Study design





# Project Team ...

- **Cancer epidemiology:** Dr. Lusine Yaghjian (*UF*) and Dr. Kathleen Egan (*Moffitt*), Co-Principal Investigators
- **Gut microbial ecology:** Dr. Volker Mai (*UF*) and Dr. Christine Pierce-Campbell (*Moffitt*)
- **Mass spectrometry:** Dr. John Koomen (*Moffitt*)
- **Statistics and “big data” analysis:** Dr. Mattia Prospero (*UF*)

# Study Population ...

- Eligibility criteria:
  - postmenopausal status
  - no history of hormone use within the prior 6 months
  - no history of breast cancer, metabolic or hepatic disorders, or chronic intestinal problems
  - BMI  $\leq 30$  kg/m<sup>2</sup>
- Exclusion criteria:
  - any oral/IV antibiotics within 30 days and/or more than two separate antibiotic regimens within the previous three months

# Recruitment and data/sample collection (Moffitt)



- Patients are recruited under the ‘Lifetime’ protocol, a long-running effort to enroll healthy persons for pilot- and prospective cancer-themed investigations;
- Survey data, body measurements, blood sample and breast density;
- FACCA grant – spot urine (estrogen measures) and stool samples (gut microbiome)

# Microbiota Profiling (UF)



- Bacterial genomic DNA is isolated and amplified according to standard methods;
- Sequence reads are generated using the Illumina MiSeq platform and processed through Dr. Mai's in-house pipeline for gut microbial classification;
- Each stool sample is processed to derive quantitative microbial signatures using an integrated suite of computational and statistical algorithms;
- Microbiome diversity and overall microbiome structure can be evaluated.

# Quantification of urinary estrogens (Moffitt)



- Proteomics Core at Moffitt under Dr. John Koomen;
- Urine samples are processed in parallel for extraction of estrogens;
- Liquid chromatography-selected reaction monitoring mass spectrometry (LC-SRM) is used to quantify each target molecule, using a published methods;
- Creatinine levels in urine will be measured in to adjust for hydration and inter-individual differences in kidney function.

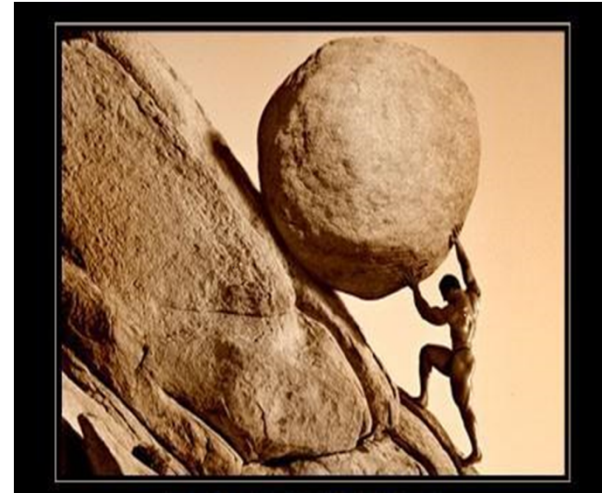
# Statistical Analysis (UF)



- Microbiome profiling will yield categorical variable (high/low) based on the proportions in different taxonomic units (Firmicutes, etc) and also the dominant bacterial signature;
- Associations with:
  - total urinary estrogens
  - Individual estrogen metabolites
  - metabolites to parent compound ratios
- GLM adjusting for potential confounders (BMI, parity, alcohol use, smoking, etc)



# Challenges ...



- EPI studies are complex!
- IRB approval took ~3mos;
- Vagaries of recruitment/ staffing;
- No-cost extension period will be needed to complete scientific aims of the investigation;
- Two-year project (or option for 2<sup>nd</sup> year) recommended for EPI projects.







Questions?