BIOGRAPHICAL SKETCH

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NAME: Sara Campbell

eRA COMMONS USER NAME (credential, e.g., agency login): SACAMPBELL

POSITION TITLE: Associate Profession, Director Graduate Program in Kinesiology and Applied Physiology

EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)

| INSTITUTION AND LOCATION | DEGREE(if applicable) | Completion DateMM/YYYY | FIELD OF STUDY |
| --- | --- | --- | --- |
| Bloomsburg University of PA, Bloomsburg, PA | BS |  6/1999 | Exercise Science/Biology |
| Bloomsburg University of PA, Bloomsburg, PA | MS | 6/2001 | Exercise Science |
| Florida State University, Tallahassee, FL | PhD | 6/2007 | Exercise Science |
| Florida State University, Tallahassee, FL | Postdoc | 6/2010 | Nutrition/Physiology |
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**A. Personal Statement**I am an exercise physiologist who specializes in the gut microbiota. Humans live in symbiosis with clusters of microbes in various parts of the body ranging from the skin, gut, oral cavity, vagina, and other areas exposed to the environment. These bacterial communities are primary constituents of the microbiome which encompasses the complete genetic potential of a bacterial population as well the products of the microbiota (microbial taxa) and host environment. Balance in the gut regulates dietary energy harvest as well as the metabolism of microbial and host derived chemicals. Thus, any perturbations in the microbiota may interrupt intestinal homeostasis. The most common contributor to microbial changes is human behavior, through diet and exercise, which are also important factors for healthful aging. Exercise is effective at reducing the risk of many chronic conditions like obesity, diabetes, and heart disease. Exercise training enhances antioxidant capacity and reduced inflammation. Exercise is also known to exert a role in energy homeostasis and regulation and has been shown to manipulate gut bacterial populations. However, little is known about the forces/factors that drive microbial diversity resulting from exercise training. There are several significant scientific questions that remain to be elucidated that our lab investigates including: 1- What is the bidirectional link between the host exercise response and the gut microbial communities?; 2- What metabolites do the gut microbes produce in response to exercise training?; 3- How do these metabolites influence exercise capacity and tolerance?; 4- Can we elucidate which particular microbial guilds facilitate exercise capacity?; and 5- Does the activity of particular microbes change in response to exercise and does this improve intestinal health?

Ongoing and recently completed projects that I would like to highlight include:

**DoD-ONR N00014-19-1-2443**

Linking brown fat to the microbiome to enhance warfighter health

Role: Principal Investigator

03/2019 – 02/2023

Our proposed studies seek to identify the key active gut microbial species involved in the gut of RGS-14-KO mice and link these measures to BAT. In addition, our research is focused on assessing active bacteria in the gut and get at the underlying mechanisms impacting the development of BAT for the purpose of enhancing warfighter health.

**Busch Biomedical Grant Program**

The role of brown adipose tissue and microbiota in mediating healthful aging and improved exercise performance

Role: MPI (PI: Vatner DE)

11/2021 – 10/2023

The goal of this project is to obtain enough data for an NIH R01 application on the unique microbiota of the RGS14 KO brown adipose tissue mediating improved exercise performance and healthful longevity.

**Core Grant Program**

Metabolomic analysis

Role: Principal Investigator

12/2020 – 12/2021

The goal of this project is to supplement existing funds to analyze skeletal muscle tissue samples from RGS 14KO and WT mice for polar/non-polar positive and negative metabolites.

**DoD-ONR N00014-21-1-2276**

**Mirabegron and Physiological Function in Cold Environments**

Role: Co-I (PI: Johnson, BD)

05/2021 – 04/2023

Goals: The overall goals of this project are to determine the efficacy of acute mirabegron administration to improve cold tolerance and determine if mirabegron can accentuate thermogenesis during sympathetic activation.

**NIH-NIA 1R21AG071888-01**

**The Role of the Gut Microbiome in the Etiology of Sarcopenia**

Role: Collaborator (PI: McCarthy, JJ)

07/2021 – 06/2023

Goals: Identify the role the gut microbiota plays in skeletal muscle structure and function in sarcopenia and healthy states to elucidate potential microbiota-based treatments

**B. Positions, Scientific Appointments, and Honors**

**Positions:**

2019-present **Director**, Graduate Program in Kinesiology and Applied Physiology

2018- present **Associate Professor**, Department of Kinesiology and Health,
School of Arts and Sciences, Rutgers University, New Brunswick, New Jersey

2010 – 2018 **Assistant Professor**, Department of Kinesiology and Health,
School of Arts and Sciences, Rutgers University, New Brunswick, New Jersey

2007 - 2010 **Postdoctoral Fellow**, Department of Nutrition, Food & Exercise Sciences,
College of Human Sciences, Florida State University, Tallahassee, Florida

2005 – 2007 **Adjunct Faculty Member**, Department of Allied Health Education, Southwest Georgia Technical College, Thomasville, Georgia

2001- 2007 **Graduate Assistant**, Department of Nutrition, Food and Exercise Sciences College of Human Sciences, Florida State University, Tallahassee, Florida

2001 **Research Intern**, United States Olympic Committee, United States Olympic Training Center, Lake Placid, New York

1999 - 2001 **Graduate Assistant**, Department of Exercise Science and Athletics, College of Liberal Arts, Bloomsburg University of Pennsylvania, Bloomsburg, Pennsylvania

**Scientific Appointments**

* Editorial Board Member – Journal of Nutrition and Food Sciences (2010 - present)
* Editorial Board Member – Journal of Nutritional Disorders & Therapies (2012-present)
* Editorial Board Member – Journal of the International Society for Sports Nutrition (2014-present)
* Editorial Board Member – Journal of Clinical Nutrition and Gastroenterology (2014-present)
* Editorial Board Member - Journal of Nutrition (2021-present)
* Steering Committee – Genetic and Biological determinants of Physical Activity (GenBioPAC) (2022- present)

**Honors:**

* Regional Representative Mid-Atlantic ASCM 2018-present
* President, Mid-Atlantic ACSM, 2016-2017
* Fellow, American College of Sports Medicine, 2016-present

**C. Contributions to Science
1. Exercise mediates intestinal inflammation and improves microbial community structure**

Intellectual Merit: The major findings of these studies indicate that: (1) high-fat diets altered intestinal morphology particularly of the duodenum; (2) exercise protected duodenal morphology in the presence of a high-fat diet; (3) high-fat diets increased intestinal inflammation in all intestinal segments (duodenum, ileum and colon) and exercise reduced it; (4) exercise manifested a unique microbiome independent of diet; (5) exercise reduced blood levels of IL-6, insulin and ghrelin and increased levels of satiety related hormones. We observed that high fat diets accompanied with sedentary behavior increased the width of duodenal villi. We are the first using IHC to substantiate in situ inflammation and loss of intestinal integrity due to high fat diet and sedentary lifestyle in mice.

1. **Campbell S.C.**, PJ Wisniewski, M. Noji, L McGuiness, MM Häggblom, LB Joseph, SA Lightfoot, LJ Kerkhof. (2016). Exercise protects intestinal morphology and integrity while reducing inflammation in animals fed a high-fat diet. PLoS One.*).* 2016 Mar 8;11(3):e0150502. PMCID: PMC4783017.

2. **Campbell, S.C.**, Wisniewski, P.J. (Jan 2017). Exercise is a novel promoter of intestinal health and microbial diversity. Invited Review. Exercise and Sport Sciences Reviews (IF - 4.259) 45(1); 41-47. PMID: 27782912.

3. Wisniewski, P.J., Joseph, L.B., Composto, G., Gardner, C., Lightfoot, S.A., **Campbell, S.C.** (2019) Voluntary Wheel Running Reduces Colon Inflammation in Female but not Male Mice Fed a High-fat Diet. Comparative Exercise Physiology. 15(1):35-47. DOI: 10.3920/cep180032

**2. Bacterial communities in the small intestine respond differently to those in the cecum and colon in mice fed low and high fat diets.**

Intellectual merit: We used 16S rRNA gene sequencing to compare microbiota in the small intestine, cecum and colon in mice fed a low or high fat diet. The relative abundance of major phyla in the small intestine, Bacteriodetes, Firmicutes, and Proteobacteria, was like that in the cecum and colon; the relative abundance of Verrucomicrobia was significantly reduced in the small intestine compared to the large intestine. Several genera were uniquely detected in the small intestine and included the aerotolerant anaerobe, Lactobacillus spp. A high fat diet was associated with significant weight gain and adiposity and with changes in the bacterial communities throughout the intestine, prominent Gram-negative bacteria including genera of the Bacteroidetes and a genus of Proteobacteria significantly changed in the large intestine.

1. Onishi, J., **Campbell, S.C**., Moreau, M., Flashruit, P., Brooks, A., Zhao, X.Y., Häggblom, MM, Storch, J., (2017). Weight gain in the mouse diet induced obesity model is not dependent on shifts in the gut microbiome involving endotoxin-producing Gram-negative bacteria. Microbiology. Aug;163(8):1189-1197. PMCID: PMC5775896.

**3. Adenylyl cyclase 5 knock out mice have enhanced exercise tolerance which is supported by a unique microbiota and metabolic profile.**

Intellectual merit: AC5 mice AC5KO mice display enhanced lifespan, protection against obesity/type 2 diabetes, improved antioxidant defenses, and enhanced exercise capacity. Since the AC5KO mouse model demonstrates several unique features associated with improved health and longevity it is not surprising that these mice have a unique microbiota, that when abolished removes the enhanced exercise capacity suggesting adaptations are unable to occur without a microbiota.

1. Guers, J.J., Zhang, J., **Campbell, S.C**., Oydanich, M., Vatner, D.E., Vatner, S.F. (2017). Disruption of adenylyl cyclase type 5 mimics exercise training. Basic Res Cardiol. Sep 8;112(6):59. PMCID: PMC5833297
2. Dowden, R.A, McGuinness, L.R., Wisniewski, P.J., **Campbell, S.C.**, Guers, J.J., Oydanich, M., Vatner, S.F., Häggblom, M.M., Kerkhof, L.J. (2020). Host genotype and exercise exhibit species-level selection for members of the gut bacterial communities in the mouse digestive system. Nature Scientific Reports.10:8984. PMCID: PMC7265280.
3. Dowden, R.A, McGuinness, L.R., Wisniewski, P.J., Guers, J.J., Oydanich, M., Vatner, S.F., **Campbell, S.C.** (2020). Gut microbiota contribute to exercise capacity and metabolic profile in a wildtype and longevity model mouse. Med Sci Sport Ex. In Review.