**VMSRTP Mentors**
**Biomedical Genomics and Bioinformatics**

## Brinkmeyer-Langford, Candice (VIBS)

My primary research focus is genomics. I am particularly interested in comparative genomics: learning about the dynamics underlying human diseases by studying their counterparts in animals. One of the goals of my research is to identify and characterize environmental and genetic interactions that contribute to neurological conditions resulting from antecedent viral infections. I am particularly interested in identifying how genetic background influences disease diversity following infection by a neurotropic virus. This research is expected to increase knowledge about virally-influenced complex neurological conditions in humans and ultimately lead to the development of novel predictive models. I am also involved in research using a model of the human disease Duchenne muscular dystrophy known as Golden Retriever muscular dystrophy (GRMD). In both humans and dogs, this disease is caused by a genetic defect in a single gene, yet the amount of variation seen in the clinical signs of the disease suggests that other elements contribute to its presentation, progression, and overall severity. I seek to understand these modifying factors in GRMD, knowing that the findings can be used in the future to develop targeted treatments for the human disease.

## Davis , Brian (VIBS)

## Porter, Weston (VIBS)

My laboratory is interested in determining the role of factors in normal development and how disruption of these pathways results in associated pathologies.

## Raudsepp, Terje (VIBS)

Comparative genomics and molecular cytogenetics of animals, birds and other vertebrates organization, function and evolution of sex chromosomes; equine genomics - genomics of genetic diseases and disorders of sexual development and reproduction; alpaca and camelid genomics.

## Rijnkels, Monique (VIBS)

We are studying transcriptional regulation and the genomics of the mammary gland and the role of epigenetic events during mammary gland development and lactation. We use various genomics approaches to mammary gland biology and my laboratory has been using ChIP-seq, DNase-seq, ATAC-seq and other epigenomic approaches to determine chromosomal states at different developmental time points to determine the role of epigenetic regulation in mammary gland development and understand gene regulation in the mammary gland in general. We use transgenic mouse models to study gene regulation in mammary gland development and lactation.

## Sitcheran, Raquel (MCMD)

A key feature of all aggressive tumors, such as high-grade gliomas, is their ability to invade healthy tissue. Indeed, the infiltrative growth of cancer cells is a major impediment to efficacious treatment. We study the role of NF-κB regulatory proteins in regulating cancer cell behavior, particularly how they acquire motility and invasive potential. NF-κB is a ubiquitously expressed, evolutionarily conserved transcription factor that responds to a variety of signals and regulates fundamental processes, including cell growth and proliferation, inflammation, invasion and angiogenesis. Aberrant NF-κB activity or expression is associated with many cancers, as it can promote tumorigenesis, tumor progression and resistance to therapy. We are taking interdisciplinary approaches in cell imaging, in vitro 3-D invasion assays, biochemistry and animal models to study how different signals regulate NF-κBNF-κB and how de-regulation of the NF-κB pathway impacts cancer cell growth, self-renewal and survival.

## Threadgill, David (VTPB)

My laboratory uses the mouse as an experimental genetic model to investigate factors that contribute to inter-individual differences in health and disease. Our current research activities include the identification and functional characterization of alleles contributing to cancer susceptibility, the function of the Erbb gene family in development and disease, and the role of genetic variation in response to environmental stimuli. To support these investigations, we also are developing new genetic tools to support mammalian systems genetic approaches to phenotypes with complex genetic and environmental etiologies. Cancer genetics: We are focusing on colorectal and breast cancer to identify environmental factors and genetic polymorphisms contributing to differential susceptibility to the development and progression of cancer. We are also developing approaches to exploit these factors to prevent or delay cancer as well as to identify new therapies. Epidermal growth factor receptor (Egfr): We are using mouse models with genetically engineered or spontaneous mutations to elucidate the biological role of Egfr and other member of the Erbb gene family in vivo. These studies have lead to new insights into the role of these genes in neuronal survival and behavior, obesity, cancer and cardiovascular disease. We are currently performing mechanistic studies to identify how the Erbb genes contribute to normal and abnormal phenotypes. Genetics of environmental response: Just as individuals differ in their genetic constitution and disease susceptibility, they also differ in their responses to exogenous stimuli. We are using mouse models to investigate responses to environmental factors like the enteric flora of the gastrointestinal tract and diet and toxicants like dioxin and trichloroethane. The goal of these studies is to identify how individual responses to environmental factors leads to differential disease susceptibilities. Systems genetics resources: We are leading a large international effort to develop and exploit a new mouse genetic resources that will support the integration of genetics into systems biological analyses at the whole animal level. These efforts are based upon the Collaborative Cross, which is a unique recombinant inbred population of mice that have randomly assorted the genetic polymorphisms present in the eight founder inbred strains.

## Turner, Nancy (NUTR)

Dr. Turner's research program focuses on determining the impact of dietary constituents on regulatory processes that may protect against carcinogenesis and inflammation in the colon. Her lab is evaluating the effects of fiber sources and the specific phytochemicals contained within them on aspects of cellular proliferation or apoptosis, and microbial/epithelial cell interactions. The goal is to determine how these normal processes are being perturbed by chemical carcinogens, radiation or pro-inflammatory compounds, and how diet may mitigate the damage caused by them. Work conducted in the laboratory is currently funded by the United Sorghum Checkoff Board, the California Dried Plum Board, and the National Space Biomedical Research Institute.

## Wang, Fen (IBT)

The laboratory focuses on understanding the molecular basis of cell signaling, and how aberrant cell signaling leads to birth defects and causes cancers. Using in vitro cell culture systems and in vivo mouse models, we study how the fibroblast growth factor (FGF) activates its receptor (FF) tyrosine kinase, and how the activated FF transmits the signals to downstream targets and regulates proliferation, differentiation, homeostasis, and function of the cells, as well as in organogenesis and development, including prostate and cardiovascular system development. The laboratory also employs molecular biology, cell biology, and mouse genetic technologies to study how aberrant FGF signals promote tumor initiation, progression, and metastasis. In addition, how environmental factors contribute to tumorigenesis and congenital birth defects by modulating FGF signal intensity and specificity is also under the scope of our research interests.