Research Abstract
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Embryonic exposure to endocrine disrupting chemicals (EDCs) that mimic estrogens and androgens elicit permanent effects on the developing gonad. These exogenous compounds are particularly concerning because of their suspected role in rising reproductive disorders, infertility, and cancers. A significant gap in our knowledge is that exact pathophysiological mechanisms of toxicity and endocrine disruption by EDCs remain largely unknown. To begin filling this gap, I will use the Japanese medaka (Oryzias latipes), a freshwater teleost fish that shares molecular and cellular mechanisms with humans and is an established model for reproductive and developmental toxicity testing. To this end, I will use single-cell RNA sequencing (scRNA-seq) to compare transcriptional profiles of gonadal cells isolated from normal male and female gonads to those isolated from exposure to exogenous sex hormones (17ß-estradiol and 11-ketotestosterone, respectively) during sensitive developmental windows. The short-term goal is to identify altered cell types and expression patterns in hormone-treated fish, allowing us to further identify candidate targets and mechanisms of endocrine disruption in the developing gonad. Characterizing molecular mechanisms of sex-specific gonadal differentiation and alterations induced by EDCs is necessary due to their ubiquitous environmental presence, human exposure concerns, and known or suspected roles across a spectrum of endocrine-related disease.