My personal interests are in germline development from a small RNA perspective. A unique feature of egg cells is an extensive program of post-ranscriptional gene regulation; various RNA-binding proteins are known to control the timing and spatial expression patterns of maternal proteins. In the last decade, newly discovered families of small RNAs have emerged as important regulators of gene expression and development in eukaryotes. microRNAs (miRNAs) are a widely conserved class of small (~22 nt) regulatory RNAs that repress the translation of target mRNAs through partially complementary base pairing. The first miRNAs were identified in *C. elegans* for their role in developmental timing. Subsequent studies in flies and mammals established roles for miRNAs in regulating diverse processes such as developmental patterning, cell growth, and metabolism.

I am currently investigating the activities of miRNAs that may control the timely translation of maternal mRNAs during oogenesis. Using genetics, molecular biology, and imagine techniques, my goal is to identify important miRNAs and their targets in both somatic and germline cells of the ovary, and characterize their roles in progression through oogenesis. Complementary studies on early development in other animal models indicate that this may be a conserved strategy for transitioning from maternal to zygotic control of gene expression.

In addition to the small regulatory RNAs (miRNAs, siRNAs, etc.) that regulate gene expression in most tissue types, animals have evolved a complex regulatory RNA pathway that is unique to germ cells. Piwi-interacting RNAs (piRNAs) maintain genomic stability by suppressing the mobilization of germline transposable elements, which otherwise cause DNA damage and sterility. piRNAs are bound by Piwi family proteins and guided to transposon RNA transcripts, which are then cleaved. This pathway has been described as a “small RNA” based immune system. I have recently become interested in visualizing transposon transcripts at their sites of processing by Piwi proteins, something that is critical for understanding this complicated

pathway. We are using the paradigm of P-M hybrid dysgenesis to mobilize endogenous P-elements in the germline, in order to visualize their mRNA transcripts at sites of piRNA processing. I am also using genetics and imaging to visualize transposons in the somatic cells of the ovary. The different functions of the somatic and germline piRNA pathways can be uncovered using these techniques. Elucidating the functions of these small RNA pathways will yield a better understanding of the processes animals use to control the gene expression and development of their germ cells.