Kathryn began studying the Bactrocera model of species differences in the 1990s at the University of Sydney and more recently in the school of BEES at the University of NSW.

Genomes and transcriptomes for the study of species differences

Darwin’s mystery of mysteries, the origin of species, remains a subject of intensive research and debate. The modern synthesis emphasizes the importance of geographic isolation in the prevention of gene flow and the formation of reproductive isolation. Where closely related species exist in sympatry other mechanisms must be proposed to explain the maintenance of separate species. A pair of tephritid fruit flies, Bactrocera tryoni and Bactrocera neohumeralis, occur in overlapping ranges on the east coast of Australia and are proving to be an excellent model for the study of the genetics of species differences.

The species pair facilitates the search for the genetic basis of speciation because they are genetically extremely similar. However they are reproductively isolated by time of mating, a trait which is genetically controlled and sensitive to light intensity. Interspecies crosses in the lab produce fertile hybrids allowing genetic and molecular analyses. We have previously used microsatellites and a candidate gene approach to investigate the genetic differentiation of the species. Now the advent of next-generation sequencing allows exploration of the genome as a whole.

I will present recent results for this model system using these techniques which have enabled us to generate the complete genome sequence for B. tryoni, partially assembled genomes for related species, and replicated, quantitative transcriptomes. These are a new resource for studying all aspects of the biology of these species, including traits relevant to pest status, questions of genome evolution and the genetics of species formation.