There are mainly two aims of the project:

(a) A pattern of geographic variation of parasitoid virulence has been observed from previous studies. By transcriptome analysis we aimed to better understand the geographic mosaic of parasitoid virulence, specifically we were interested in performing differential expression analysis in two beetle species that had a common parastoid enemy.

(b) Using RAD seq to perform population genomics analysis of the parasitoid populations. By performing these studies in the same sites, we may be able to use the observed population structure in our interpretation of patterns in the transcriptome analysis.