Elizabeth Eisenhardt, Fordham University. Reevaluating the Taxonomic Validity of Two Eastern Chipmunk Species: *Tamias striatus lysteri* and *Tamias striatus fisheri*. Mentor: Dr. Evon Hekkala

Abstract: This study explores the validity of two eastern chipmunk subspecies, *Tamias striatus lysteri* and *Tamias striatus fisheri*. In 1929, A. Howell classified five subspecies of eastern chipmunk based on morphological characters and mapped their distributions. Howell found the boundary between *T. s. lysteri* and *T. s. fisheri* to be near Armonk, NY, the location of this study. Genetic techniques can aid in clarifying these original classifications. Prior research found a fixed difference in the mitochondrial 12S region which supports a possible species level distinction between the two subspecies (Miller & Bohls 2013). This study examines other gene regions including *CytochromeB*, *ZP*, and microsatellites using contemporary and historical samples. Contemporary samples were from three localities: Lagrange, NY, Armonk, NY, and Pleasantville, NY. Historical samples were collected from the American Museum of Natural History. DNA was extracted from each sample. Contemporary DNA extracts were used in amplifying *CytB*, and these PCR products were sequenced at Macrogen. Sequence data was used in constructing phylogeographical analyses. ZP amplification was insufficient. Historical 12S sufficiently amplified and is being prepared for sequencing. Additionally, eleven microsatellites were screened and the five most successful were used in population structuring and genetic diversity measures. Results of phylogeographical analysis found that there was one widespread haplotype with individuals from all three localities and that the Calder samples exhibited a private haplotype for *CytB*. Contemporary Microsatellites resulted in no structuring or variable genetic diversity in the Armonk and Pleasantville localities. Historic samples 12S sequence are to be added to Miller & Bohls data set.