Chagas disease is one of the most devastating infectious diseases in Latin America. Due to its generally asymptomatic acute phase, Chagas disease often progresses into the incurable chronic stage that claims tens of thousands of lives each year. Chagas disease is a parasitic infection caused by the trypanosome, *Trypanosoma cruzi,* which is transmitted by triatomine "vinchuca" bugs. *Triatoma infestans* is the most common triatomine vector in Bolivia. Infection rates are higher in Bolivia than in any other part of the world. This vector prefers to nest in thatch roofs and mud walls which present considerable risks for poor, rural populations. Controlling the spread of Chagas disease can best be achieved through preventing the insect vectors from occupying households. By analyzing ten DNA microsatellite loci, *T. infestans* can be grouped into epidemiologically relevant genetic sub-populations using Bayesian model based clustering algorithms. The objective of this project was to determine if sub-populations of *T. infestans* are present. A sample of approximately 400 bugs previously collected from several communities in Chuquisaca, Bolivia was examined. The DNA was extracted and amplified via polymerase chain reaction. Once amplified, fragment analysis was preformed at an off-site laboratory. Different allele frequencies were observed within each town at each locus, and moderate population structure was observed. Nine clusters were determined to be the ideal number, with representation of each cluster present in multiple towns. Evidence if migration was also observed. Based on this trend, it was determined that insecticidal spraying must be implemented on a regional level rather than spraying individual households or towns in order to be effective.