

# **Biology Seminar**

---

**Dr. Xiang Gao**

**University of North Texas, Dept. Biological  
Sciences**

## **Studying genome evolution with experimental and computational methods**

My research interest is to study genome structures and the underlying evolutionary mechanisms that have shaped the genomes. In this talk, I will discuss three projects in which I have applied molecular biology and/or bioinformatics techniques in this research area. The first project is to study how transposable elements, which are major components in genomes, have become integrated in host genome sequences. We have revealed a novel targeting mechanism of chromviruses, a type of retroelements that relies on its encoded chromodomain to recognize specific features of host chromosomes, e.g., histone code, for integration into heterochromatic regions of the host genome. In the second project, I will show that internal gene duplication is a widespread and powerful evolutionary force, which often leads to the creation of new gene features, e.g., new introns. Finally, I will discuss our ongoing effort to employ a maximal likelihood method to estimate nucleotide diversity and linkage disequilibrium from five complete sequenced individual human genomes, which allows us to infer the common and unique genomic features of different human populations.

**Nov 5, 2010**

**2:00 PM**

**ENV125 (EESAT)**