

## **David Green Smith University Webb Page and Credentials (as of July 2006)**

**Molecular Anthropologist, University of California, Davis**

### **Research Objectives:**

To gain an understanding of Native American biological origins and population history through the study of ancient and modern DNA.

### **Current Projects:**

#### *Paleo-American Genetic Research*

Haplogroup and Sequence the Control Region of mtDNA of Paleo-Americans (7,000 ybp and older) in North America.

#### *Distribution of Native American mtDNA markers Haplogroups A, B, C, D, and X in North America*

Lorenz and Smith (1996) found that Native American mtDNA haplogroups are non-randomly distributed throughout North America. This research continues in order to find tribal specific markers among Native American groups and learn more about possible migration routes during the peopling of North America and population movements after the initial peopling.

#### *Population Prehistory on the Columbia Plateau*

DNA sequence and RFLP analysis of modern and ancient Native American groups on the Columbia Plateau to address hypothesis of a proto-Algonquian migration to the Midwest U.S. from the Columbia Plateau approximately 4000-6000 ybp (Denny 1991). Also, issues of biological relationships to Great Basin and California populations will be addressed. Ancient samples are included from: the Memaloose Islands, the Dalles, the Congdon Site, the Braden Site, and the Demoss Site.

#### *Population Prehistory of the Great Lakes Region*

DNA sequence and RFLP analysis of modern and ancient Native American groups of the Great Lakes Region to infer regional population history. This research will also address the existence of a possible proto-Algonquian migration from the Columbia Plateau to the Midwest/Great Lakes Region and possible biological relationships of Native Americans of the Great Lakes Region to ancient Native Americans of the Columbia Plateau. Ancient samples included from sites of the Old Copper Culture and the Glacial Kame Culture.

#### *Population Prehistory of California*

DNA sequence and RFLP analysis of modern and ancient Native American groups of California to identify mtDNA markers for Penutian and Hokan speaking groups. Issues of California prehistory and a Penutian population intrusion from the Great Basin and/or the Southern Columbia Plateau will be addressed. Ancient samples included from sites of the Windmill and Berkeley Pattern.

## **Native American Research**

### **Research Objectives:**

To gain an understanding of Native American biological origins and population history through the study of ancient and modern DNA.

### **Ancient DNA Analysis:**

We extract DNA from ancient tissue (i.e. bone, teeth, other tissue) and use PCR based techniques to perform RFLP and DNA sequencing analysis. This analysis makes it possible to ascertain the sex of the individual and/ or identify the likely biological source population of the sample.

### **Primate Genetic Management and Parental Assessment:**

We develop and apply PCR-amplified STR markers to identify parentage, calculate kinship and inbreeding coefficients, estimate parameters of genetic diversity, genetic subdivision and founder representation within the colony, and collaborate with principal investigators on colony management strategies and on research involving those data.

### **For Collaborators:**

DNA samples (between 1 and 5 mls of whole blood or 1 mg of tissue) should be shipped overnight in dry ice to our laboratory. Pricing is negotiable, depending on resources. Acknowledgment should be given in all publications (including theses and dissertations) that result from our services, and two reprints should be donated to our laboratory.