

**Department of Anthropology  
COLLEGE OF Arts and Sciences**

**SUMMER RESEARCH OPPORTUNITIES  
FOR UNDERGRADUATE WOMEN**

**APPLICATION DEADLINE: March 1, 2012**

*The Department of Anthropology is pleased to offer the following research project for the summer of 2012. Interested students are urged to contact the faculty member(s) directing the project that most interests them. By contacting the faculty member, you can discover more about the project, learn what your responsibilities will be and, if possible, develop a timetable for the twelve-week research period.*

**PROJECT TITLE: Pigmentation candidate gene variation in African and Melanesian populations**

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**Project Description**

Skin pigmentation is a phenotypic trait that shows a striking amount of variation across the human species. This variation is strongly correlated with the intensity of ultra-violet radiation (UVR), suggesting that observed patterns of variation may reflect adaptation to different UVR environments. Genetic data indicates that similarities in pigmentation phenotype in low-UVR regions of Europe and East Asia are the result of evolutionary convergence—different genetic mutations have occurred in each region that lead to a similarly adaptive phenotype. However, much less is known about the potential role of convergent evolution in shaping pigmentation similarities across populations living in high-UVR environments (e.g. sub-Saharan Africa and Island Melanesia).

This summer project will take on the first steps to address this question through a combination of wet-lab and bioinformatic work. A sample of Island Melanesian individuals will be sequenced for pigmentation candidate loci. These sequences will be screened for mutations that may affect phenotype. Patterns of nucleotide variation and haplotype diversity will be investigated using standard population genetics methods to assess the potential role of natural selection. These Melanesian data will be compared to publically available sequences from the same loci in Nigerian individuals surveyed as part of the 1000 Genomes Project. In addition to measures of within-population diversity, levels of between-population divergence will be explored in an effort to identify loci that have been driven to high frequency by natural selection in each of the populations.