Overview

Villages of Khmu shifting cultivators living in the mountains of northern Laos recognize and name approximately 20 different landraces of rice, and they appear to allocate them differentially according to varying microenvironmental conditions. Since rice is wind-pollinated and undergoes >3% cross-pollination every year, these landraces must be maintained by active, ongoing human selection for long-term varietal identity. Thus, Khmu farmers appear to be consciously selecting their primary caloric staple for genetic diversity, and for variation in agronomic performance. An interdisciplinary study is underway to characterize this selection process, and to investigate its local effects on rice genetic diversity and ultimately on crop yield and nutritional adequacy. Collaborators will work with informants in the field to identify all locally recognized landraces and examine cultural salience and consensus with respect to the phenotypic traits used by the Khmu to distinguish those landraces. In addition, differential spatial allocation of seeds from the various landraces by soil quality, slope and aspect of hillsides, elevation, companion crops, distance from homestead and other aspects of the agricultural landscape will be fully investigated.

An important aspect of the study, and the focus here, is to characterize genomic variation and selection within and among all local rice landraces using DNA capture methods and massively parallel sequencing. Goals are to study aspects of population structure and natural history of Khmu landraces, and to identify major regions and specific targets of genetic selection related to the observable phenotypes upon which decisions regarding landrace cultivation are made.

Methodology:

This component of the broader study first seeks to determine i) age and level of genomic differentiation among landraces, ii) levels of inter-varietal admixture that are allowed to occur without disrupting landrace identity, and iii) lineage history of the landraces, with respect to common ancestry or multiple cultural/phylogenetic origins. This will be accomplished through highly multiplexed SNP capture using custom, genome-wide RNA probes, massively parallel high-throughput Illumina sequencing, and computational population genomic methods. Next, the genomic data will be analyzed for signals of selection, and landrace-specific candidate genes will be identified. Annotated and predicted functions of these genes from public databases will be compared with the phenotypic targets of selection identified by collaborators working with Khmu informants to analyze the level of concordance between the explicitly identified targets of selection at the decision-making level and genes influencing agronomically important performance traits.

Training and skills:

CENTA students will attend 45 days training throughout their PhD including a 10 day placement. In the first year, students will be trained as a single cohort on environmental science, research methods and core skills. Throughout the PhD, training will progress from core skills sets to master classes specific to the student's projects and themes. The candidate will already possess a background in molecular biology and/or population genetics from his/her prior education. He/she will receive comprehensive training in molecular biology methods pertinent to next-generation sequencing and target enrichment. The candidate will also receive initial and continuing...
training in programming, scripting, bioinformatics, and statistical skills needed for handling and analyzing large volumes of next-generation sequence data.

**Partners and collaboration (including CASE):**
Collaborators comprise an interdisciplinary group studying biological, cultural, and demographic aspects of traditional rice-based agriculture in Laos: Prof. James Wood (Biological Anthropology, The Pennsylvania State University), Dr. Shinsuke Tomita (Center for Southeast Asian Studies, Kyoto University), Dr. Daniel Parker (Shoklo Malaria Research Institute, Thailand, Oxford University).

**Possible timeline:**
**Year 1:** Training in relevant lab methods and computational skills. Computational development of a rice SNP panel appropriate for the target populations. DNA extraction and library prep.
**Year 2:** Genotyping and population genomic analyses, publication of population structure and natural history results.
**Year 3:** Functional genomic comparisons of new genotype data and published resources, publication of results.

**Further reading:**


**Further details:**
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