

Possible PhD projects under ICRAF-Czech collaboration:

Pre-requisites:

1. Species selection based on priority listing from the 101 [African Orphan Crops Consortium](#) species
2. National partners contacts interested on the species
3. Existence of species diversity in natural or cultivated populations

Shortlisted species include:

1. *Faidherbia albida*
2. *Vitellaria paradoxa*
3. *Moringa oleifera*,
4. *Sclerocarya birrea*,
5. *Annona senegalensis*

Each candidate would focus on one of the priority species, with work packages inspired by areas I or II as specified below:

The proposed outline of projects would remain the same as proposed in Area I for any of the species short listed above. For Area II, species for which a mapping population is available can only be used. At present it is available for *Vitellaria paradoxa* (shea).

I. Area-1: Applied Ecological Genomics and nutritional characterization

Title of project: To understand genomic, nutritional and phenotypic diversity in species X and developing SNP markers associated with a few important environmental parameters

Objectives:

1. To understand and analyze genetic diversity in the natural and domestic stands of species X.
2. To understand and analyze nutritional diversity in the fruits of natural and domestic stands of species X.
3. To understand and analyze nutritional diversity in the fruits of natural and domestic stands of species X.
4. To find out genomics markers associated with environmental variables as quasi-adaptation markers

Expected outcome:

1. Understand natural variation in genetic, phenotypic and nutritional diversity of the species
2. A few SNP markers (~50) linked with environmental variables that are known to impact adaptation of the species to high temperature, low moisture, and other important contributors.
3. These markers help us to screen these populations and select 1/10th of them to go into pre-breeding orchards. This data will also be corroborated with nutritional and phenotypic data.

Tentative time-lines:

1. Species distribution modelling and mapping using ensemble suitability modelling approaches¹, mapping of environmental diversity within species distribution range, devising collection strategy based on collection gap analysis, establishing collection and logistics protocols, hands on lab work- **6 months**

¹ One of the co-supervisors at ICRAF is the developer and maintainer of the *BiodiversityR* package in which application the applicants will be trained (see <https://doi.org/10.1016/j.envsoft.2017.11.009> or <http://www.worldagroforestry.org/atlas-central-america>)

2. Collection of samples (each ecozone represents proportionate diversity to make a total of ~300-400 individuals with location mapping), sending/bringing leaves and fruits to relevant labs, DNA extraction- **8 months** (*caution- getting samples out of Ethiopia needs to be followed up within Ethiopian framework of law*)
3. Genotyping data generation- **4 months**
4. Genotyping data analysis- **4 months**
5. Nutritional data generation- **4 months**
6. Nutritional data analysis- **3 months**
7. Papers and thesis writing- **7 months**

Total time: 3 years

II. Area 2: Applied Genomics

Title of project: Development of genomics resources for species X and its application for developing a linkage map. Species X must have a mapping population-priority to be given *Vitellaria paradoxa* (shea).

Objectives:

1. To phenotype selected mapping population over 2-3 years
2. To develop sufficient number of SNP markers for shea linkage mapping (~5000).
3. Develop a SNP-marker based linkage map

Expected outcome:

1. Development of an array of SNP markers for shea
2. To understand phenotyping behavior of the mapping population
3. A SNP linkage map for shea.
4. Optional- to have QTL map of shea by fusing phenotype and genotype.
5. Propose best bi-parental mapping scheme for next level of breeding

Tentative time-lines:

1. Reconnaissance and understanding of the population to define proper achievable objectives- **4 months**
2. Phenotypic data collection- 4 months x 2 years= **8 months**
3. Genomics data screening to short list SNPs and designing SNP assays- **6 months**
4. Population screening using SNP markers- **6 months**
5. Genotype data analysis and linkage map construction- **6 months**
6. Papers and thesis- **6 months**

Total time: 3 years