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SANTA BARBARA • SANTA CRUZ

DEPARTMENT OF PLANT SCIENCES
MAIL STOP 4
UNIVERSITY OF CALIFORNIA
ONE SHIELDS AVE
DAVIS, CALIFORNIA 95616-8780
TELEPHONE: 530-752-1703
FAX: 530-752-4604

COLLEGE OF AGRICULTURAL AND
ENVIRONMENTAL SCIENCES
AGRICULTURAL EXPERIMENT STATION
COOPERATIVE EXTENSION

Diane Jofuku Okamuro
Plant Genome Research Program
The National Science Foundation
Room 685N
4201 Wilson Boulevard
Arlington, VA 22230

Dear Diane:

I am currently collaborating with a team of CoPIs from American (UC Davis, U. Missouri, Iowa State) and Mexican (LANGEBIO) institutions to write a proposal regarding the genomic basis of high elevation adaptation in maize. We plan to submit this to the Catalyzing New International Collaborations (CNIC) program at NSF, which offers initial support for international collaborations with the expectation that a subsequent proposal be submitted to an appropriate NSF Directorate. Prior to submission, applicants are strongly encouraged to contact and receive feedback from the Program Officer in the NSF Division to which the eventual proposal will be submitted. According to the CNIC Program Solicitation, the Program Officer will then "advise potential proposers if the proposed international collaboration activity should be submitted to CNIC or to other existing programs as a regular proposal, a supplement, or an EAGER." I am writing to you because our intended eventual funding target for this project is the Plant Genome Research Program. Please find below a brief description of the activities we are proposing for the CNIC grant and how we foresee these will provide essential preliminary data for a PGRP grant; we would be happy to send any additional information that might be helpful. We would greatly appreciate your feedback.

Sincerely,

A handwritten signature in black ink, appearing to read "Jeffrey Ross-Ibarra", with a long horizontal line extending to the right.

Jeffrey Ross-Ibarra

Proposal Title: The Genomic Basis of High Elevation Adaptation in Maize

Maize (*Zea mays* ssp. *mays*) was domesticated in southwest Mexico from teosinte (*Zea mays* ssp. *parviglumis*), a wild, lowland species with a narrow ecological distribution. Despite the limited environments inhabited by its progenitor, maize has spread to regions spanning a wide climatic range. During its global diffusion, maize has adapted to high elevation environments on multiple independent occasions. Reciprocal transplants of maize landraces across an elevation gradient have experimentally demonstrated this highland adaptation. Our previous work has suggested this adaptation has been obtained both through gene flow from highland-adapted wild relatives and through new mutations arising during the spread of maize. Recently developed sequencing resources present the opportunity to assess the genomic architecture of high elevation adaptation in great detail. While such studies will provide much information regarding the basic evolutionary history of maize, they will also generate valuable data for continued improvement of maize in the face of growing human populations and climate change, particularly in high elevation regions of the developing world where the maize yield gap is the greatest.

The international collaboration we are proposing would bring together researchers from the United States and Mexico who have the theoretical, computational, and field-based expertise necessary to effectively address local adaptation in maize:

- 1) Jeffrey Ross-Ibarra, Project PI, Associate Professor, UC Davis: Population genomics of maize
- 2) Graham Coop, Associate Professor, UC Davis: Theoretical population genetics
- 3) Matthew Hufford, Postdoctoral Scholar, UC Davis (current); Assistant Professor, Iowa State University (Fall 2013): Evolutionary genomics of wild maize
- 4) Sherry Flint-Garcia, USDA-ARS Research Geneticist and Adjunct Assistant Professor, University of Missouri: Quantitative genetics and maize breeding
- 5) Angelica Cibrian Jaramillo, Assistant Professor, LANGEBIO: Ecological genomics of plant species in Mexico
- 6) Ruairidh Sawers, Assistant Professor, LANGEBIO: Maize adaptations to abiotic stress

Over the course of one year, a CNIC grant would fund two meetings—one at LANGEBIO in Mexico and one at UC Davis—to report on generation of preliminary data for a PGRP grant and to discuss the grant's general scope. For preliminary data, the CNIC grant's budget would support two field seasons (summer and winter) for development of mapping populations used to investigate the genetic architecture of highland adaptation traits in maize landraces from Mexico and South America. Parents of the mapping populations will be lowland- and highland-adapted landraces from each of these regions. Additionally, a CNIC grant would include funds for full-genome resequencing and SNP discovery in the parents of the mapping populations we will develop. Our hope is these activities will strengthen a developing international collaboration and provide valuable resources for a long-term project on high elevation adaptation in maize.