

**Grant Number:** CN-15-1476

**Co-Principal Investigator (UC Campus):**

Dr Jeffrey Ross-Ibarra; Department: Department of Plant Sciences; Institution: UC Davis

**Co-Principal Investigator (Mexico):**

Dr Ruairidh Sawers; Department: LANGEBIO; Institution: CINVESTAV

**Academic Participants 1:**

Dr Stefan de Folter; Department: LANGEBIO; Institution: CINVESTAV

**Project Title:**

ADAPTIVE GENEFLOW FROM TEOSINTE TO HIGHLAND MAIZE IN CENTRAL MEXICO

**Título del Proyecto:**

FLUJO GENETICO ADAPTATIVO DE TEOCINTLE HACIA MAIZ EN LAS TIERRAS ALTAS DEL CENTRO DE MEXICO

**Amount Requested:** \$24,897.00

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**Abstract (English):**

Since domestication in south-western Mexico, cultivated maize has spread to become one of the world's most important crops. A key step in this story was the colonization of the central Mexican highlands, driving the subsequent rise of major pre-Hispanic cultures. Mexico's highland maize remains a genetically unique group largely untapped by conventional breeding. How did maize expand beyond its ancestral ecological range and adapt to the challenges of the highland environment? One intriguing possibility is that adaptation was facilitated by acquiring beneficial genes through inbreeding with the endemic wild grass Chalco teosinte. In collaboration between the group of Jeffrey Ross-Ibarra at UC Davis and Mexico's National Laboratory of Genomics for Biodiversity, we have used genomics-assisted techniques to identify and introduce candidate Chalco variation into lowland maize varieties. In this project, we will characterize these plants in field experiments conducted from sea-level to an elevation of greater than 2,500m in the Mexican highlands. Our work will provide insight both into the mechanism of past adaptation and the future conservation and responsible use of natural diversity for crop improvement.

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**Abstract (Spanish):**

El maíz desde su domesticación en el suroeste de México, se dispersó y actualmente es uno de los cultivos más importantes a nivel mundial. Un paso relevante fue la colonización de las tierras altas del centro de México, que impulsó el desarrollo de culturas prehispánicas importantes. Actualmente, los maíces de tierras altas son un grupo genético único que hasta ahora permanecen sin ser aprovechados en los programas de mejoramiento. Pero ¿Cómo es que el maíz se dispersó más allá de su

área ecológica y se adaptó a los retos presentados por las tierras altas? Se piensa que esta adaptación fue facilitada mediante la adquisición de genes por entrecruzamiento con el teocintle endémico Chalco. En colaboración entre el grupo de Jeffrey Ross-Ibarra de UC Davis y el Laboratorio Nacional de Genómica para la Biodiversidad, hemos identificado e introducido regiones candidatas de Chalco en líneas puras de maíz de tierras bajas. Pretendemos caracterizar estas plantas en campo desde el nivel del mar hasta por encima de los 2,500m en los valles altos. Así, nuestro trabajo proveerá información sobre los mecanismos de adaptación, que su vez son importantes para la conservación y uso responsable de la diversidad natural para el mejoramiento de cultivos.

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**Co-Principal Investigator (UC Campus)**

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**Co-Principal Investigator (Mexican Institution)**

**Title:** Dr  
**Name:** Ruairidh Sawers  
**Payroll** Profesor-Investigador  
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**Additional academic participant**

**Title:** Dr  
**Name:** Stefan de Folter

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**Abbreviated Curriculum Vitae (Uploaded File):** [Download](#)  
**Letters of Intent to Participate:** [Download](#)

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**Project Plan (Uploaded File):** [Download](#)  
**Bibliography (Uploaded File):** [Download](#)

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Attachment (Uploaded File):  
 DE\_FOLTER LETTER [Download](#)  
 MORENO\_LETTER [Download](#)  
 UNISEM\_LETTER [Download](#)  
 RNA\_QUOTE [Download](#)

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**Budget Summary:**

	Total	UC Campus	Mexican Institution
Salary	\$0.00	\$0.00	\$0.00
Employee Benefits	\$0.00	\$0.00	\$0.00
Supplies & Services	\$0.00	\$19,897.00	\$19,897.00
Travel	\$0.00	\$5,000.00	\$5,000.00
Other Costs	\$0.00	\$0.00	\$0.00
<b>Total Request</b>	<b>\$24,897.00</b>	<b>\$0.00</b>	<b>\$24,897.00</b>

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**Budget Detail:**

**UC Campus**

Salaries: \$0.00

Employee Benefits: \$0.00

Supplies & Services: \$0.00

Travel: \$0.00

Other: \$0.00

### Mexican Institution

Salaries: \$0.00

Employee Benefits: \$0.00

Supplies & Services: \$19,897.00

#### \$7,360USD Genotyping-by-sequencing.

2x 96-sample plates, extraction (QIAGEN DNA) and Illumina HiSeq run; 1 plate B73 x PT BC<sub>1</sub>S<sub>5</sub> population; 1 plate polymorphic *Inv4m* F<sub>2</sub> mapping population. Work will be divided between Cornell Genomic Diversity Facility, UC Davis and LANGEBIO Genomics Services (See Letter of Support, Andres Moreno). Budget estimate based on current Cornell rates.

#### \$4,287USD Transcriptome sequencing.

Preparation of 9x transcriptome libraries. Analysis of libraries on a lane of Illumina Hi-Seq (see Quote RNAseq).

#### \$8,250USD Field charges.

Three cycles (winter, highland and summer). Charges will cover shipping (as required), plant growth and management, and harvest. Additional labor/accommodation costs associated with pollination and phenotypic characterisation will be covered separately by Sawers.

Travel: \$5,000.00

#### \$5,000USD Student study stays.

Subsistence to support 2 Mexican student stays of 2 months in the US (\$1,250 student/month). Support will be used to supplement that available through CONACYT student scholarships to cover the stay in Davis. Travel costs to be covered separately.

Other: \$0.00