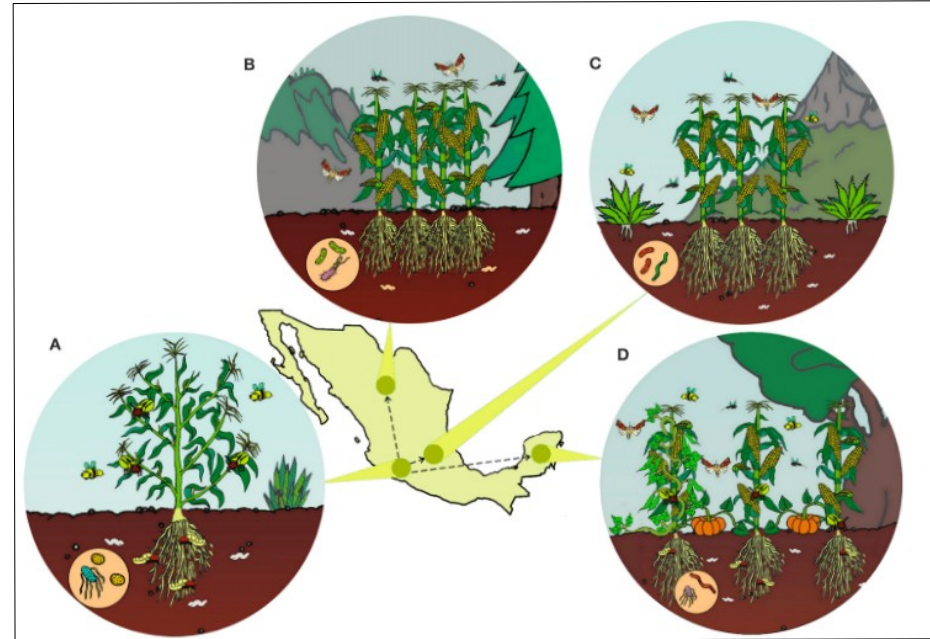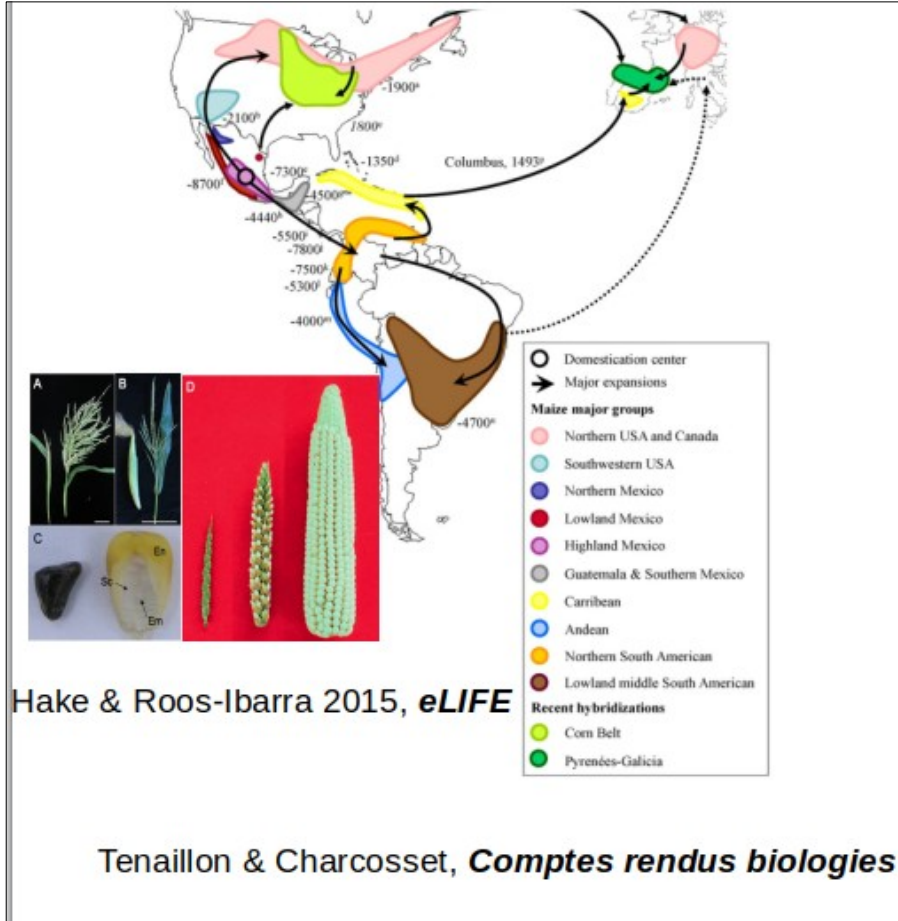# Establishment of evolutionary populations in the *Olotillo* race as an option to recover diversity and local adaptation

Duhyadi Oliva García

Mexico, center of origin and diversification of maize

Hake & Roos-Ibarra 2015, *eLIFE*

Tenaillon & Charcosset, *Comptes rendus biologies*

Chen *et al*. 2017, *Frontiers in Ecology and Evolution*

Maize landraces conservation

Chapalote

Arteaga *et al*. 2016, ***Genomics Data***

Recover diversity to promote local adaptation

We are currently in a vicious circle that includes loss of genetic diversity and yield

Dyer *et al*. 2014, ***PNAS***

How?
Evolutionary breeding

¿Evolutionary breeding?

Evolutionary populations, EP

It involves **mixing seeds** with different evolutionary origin

Suneson 1956, *Agronomy Journal*

Genetically diverse populations will be subjected to the force of **natural and artificial selection over several generations** at the planting site

Murphy 2005, *Renewable Agriculture and Food Systems*

Wheat-landraces

Maize-chapalote landraces

¿Why Olotillo?

- Currently Olotillo is planted in a smaller proportion. **Inbreeding**.

- Rescuing the diversity of *Olotillo* is relevant due to the cultural value it has as well as its resistance to drought.

- This project focuses on taking advantage of the genetic diversity of the landraces within *Olotillo*, with the aim of recovering genetic diversity and yield through a method known as evolutionary breeding (EB).

Objective

In this work we intend to determine the effectiveness of the different degrees of representation of local, regional and national diversity in the initial composition of evolutionary populations of the *Olotillo* maize race. We also want to take into account the adequacy, environmental conditions, increase or decrease of genetic diversity and its usefulness for farmers.

One of the questions to solve

What is the effect of building initial evolutionary populations of corn with varying degrees of diversity in the speed of adaptation to a locality and the purification of **deleterious alleles**?

Mix local

Mix local + Mix regional

Mix local + Mix National

30 m

30 m

5m

5m

Evolutionary populations

Mix local	R1	N1
Mix local	R2	N2
Mix local	R3	N3

Tool house

Establishment of evolutionary populations

Temporal
June

2 cycles for year

Irrigation cycle
January

Local   **Regional**   **National**

Phenotypic characterization

Length   Width   Number of rows   Grains per row

*Also features of the plant will be taken
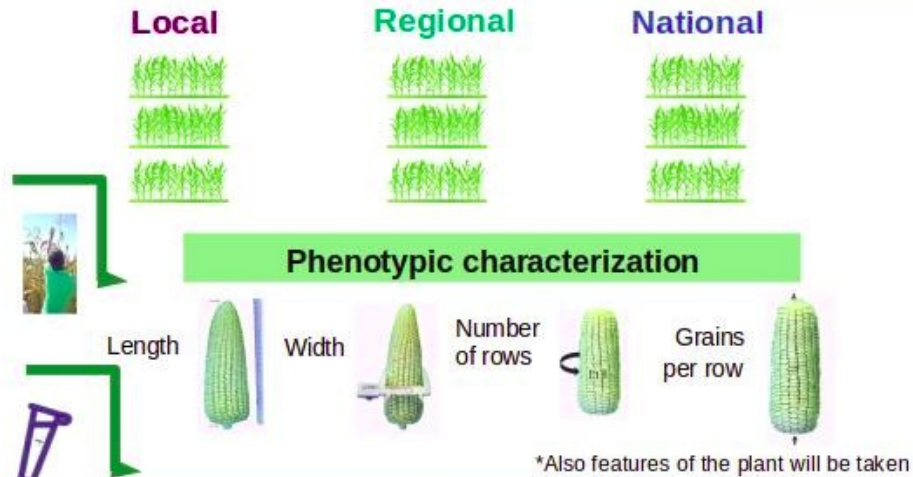
Kit DNA Extraction: 10 individuals x plot

Sequencing and identification of deleterious alleles

Whole Genome Sequencing (WGS)

Genomic DNA   Fragmentation of Genomic DNA   Sequencing   Data Analysis & Report

Sorting Intolerant From Tolerant

PROVEAN

BAD_Mutations
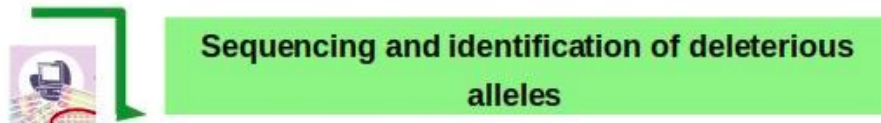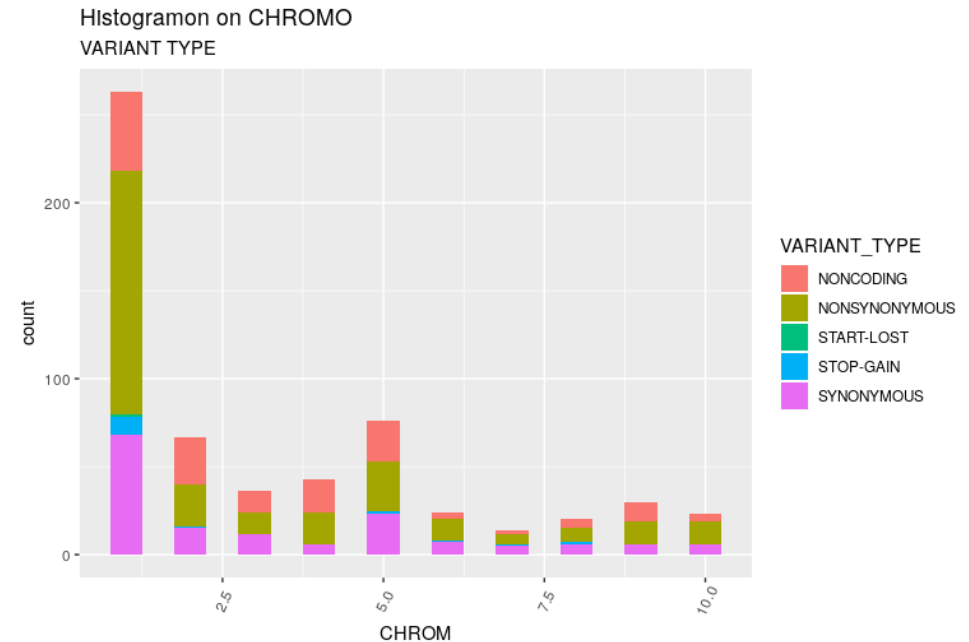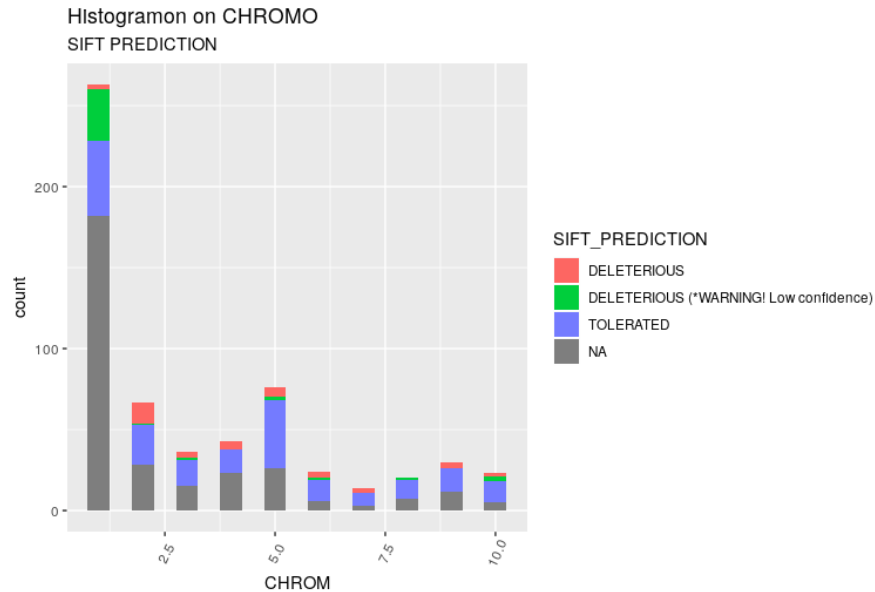
Preliminary results

Using the SIFT (Sorting Intolerant From Tolerant) software, the amount of deleterious alleles in different races of maize was predicted (including *Olotillo*) from Arteaga et al 2016

For your attention thanks