Supplementary Documentation

Management Plan

Communication

All team members will communicate on a monthly basis via a scheduled conference call. UC Davis has a ReadyTalk license allowing inexpensive web-conference hosting; other institutions will call in and can share slides, video, their desktop, and audio. During these calls we will discuss progress, problems and solutions, as well as ways to more efficiently collaborate and coordinate among laboratories. One member from each of two labs will present an update of thier work. Postdocs and all students will be expected to participate.

Team members will hold an annual meeting in person each year as a satellite meeting to a conference (either Plant and Animal Genome or the annual Maize Genetics Conference). PIs not able to make the meeting will join via teleconference. Annual meetings will consist of PIs reporting progress during the past year and goals for the upcoming year.

Outreach

The exchange program will be coordinated between team members. Management of visa and travel costs will be done through UC Davis, as DR. Ross-Ibarra's program has experience with international exchange with Mexico.

Dr. Flint-Garcia will coordinate the annual phenotyping workshop, held each year in Columbia. The workshop will be timed to coincide with data collection at the end of the field season each year. The workshop will be advertised broadly (evoldir list-serv, maizegdb, etc.). Attendees will be expected to pay their own travel and purchase a handheld device

Research

Total research commitment to this grant for each PI will be:

- Angelica Cibrian Jaramillo: 5%

- Graham Coop: 5%

- Sherry Flint-Garcia: 10%

- Matthew Hufford: 15%

- Jeffrey Ross-Ibarra: 10%

- Ruairidh Sawers: 15%

Below are details of the responsibilities of each team member during each year of the grant, with initials as shown in summary Table 3. Although one group will take lead for writing publications, it is anticipated that several team members and members of their groups will be coauthors on many of these publications.

Year		1	2	3	4	5
Aim QTL mapping	1.1	SFG, RS, JRI	SFG, MBH, RS, JRI	SFG, MBH, JRI	SFG, JRI	SFG
Aim Admix mapping	1.2	MBH	MBH, GC	MBH, RS, GC	MBH, GC	–
Aim Population genetics	2	JRI, MBH, GC	JRI, MBH, GC	JRI, MBH, GC	JRI, MBH, GC	JRI, MBH, GC
Aim Functional analyses	3.1	RS	RS, SFG	RS, SFG, MBH	RS, SFG	RS, SFG
Aim RNA-seq	3.2	–	ACJ	JRI, ACJ, RS	JRI, ACJ	JRI, ACJ

Table 3: Proposed timeline of activities showing which team members will be responsible for each objective. Team member names are abbreviated: MBH, Matthew Hufford; JRI, Jeffrey Ross-Ibarra; SFG, Sherry Flint-Garcia; GC, Graham Coop; RS, Ruairidh Sawers; ACJ, Angelica Cibrian Jaramillo

Year 1

Aim 1.1 SFG will generate seed of F2:3 for Mexico and F2 for S. American cross. JRI will sequence parents of both crosses. RS will choose highland site.

Aim 1.2 MBH will collect seed from Ahuacatitlan. GC will focus on developing methods for admix mapping.

Aim 2 MBH will collect seed from additional admixed populations. JRI will genotype samples from highland Mexico maize. AJC and MBH will put together dataset of global highland maize. GC will work on methods for selection in admix populations.

Aim 3.1 RS will screen HIFs and advance the population. Initial crosses for allelic series will be performed.

Year 2

Aim 1.1 SFG and RS will grow mapping population at each of 3 locales. SFG, RS, and MBH will phenotype populations in field. SFG will genotype F2 plants. JRI will phenotype root chilling.

Aim 1.2 MBH will genotype samples. RS and MBH will grow samples at two locations. GC will begin data analysis.

Aim 2 JRI will genotype seed from additional admix populations. MBH will genotype global highland maize collection. JRI and GC will begin data analysis of introgressed highland maize.

Aim 3.1   RS will advance the HIF and NIL populations.

Aim 3.2   ACJ will choose NILs for RNAseq analysis

Year 3

Aim 1.1   SFG and RS will grow second replicate of mapping population at each of 3 locales. SFG, RS, and MBH will phenotype populations in field. SFG and JRI will build map and begin QTL analysis.

Aim 1.2   GC and MBH will complete data analysis and begin writing.

Aim 2   JRI and GC will work on data analysis of admixed teosinte and highland Mexico maize. MBH will begin data analysis of global highland maize.

Aim 3.1   RS, SFG, and MBH will grow and phenotype HIFs and NILs. RS will advance both populations.

Aim 3.2   ACJ and RS will grow NILs and donors in highland and lowland environment. ACJ will extract RNA. JRI will perform RNAseq library prep and sequencing.

Year 4

Aim 1.1   SFG and JRI will perform QTL analysis

Aim 1.2   GC and MBH will write paper.

Aim 2   JRI and GC will finish data analysis and begin papers for admixed teosinte and highland Mexico maize. MBH will finish analysis of global highland maize.

Aim 3.1   RS will advance both populations. SFG and RS will analyze data.

Aim 3.2   JRI and ACJ will analyze RNAseq data.

Year 5

Aim 1.1   SFG will write paper.

Aim 2   MBH, JRI, and GC will write papers.

Aim 3.1   RS will advance both populations. SFG and RS will write paper.

Aim 3.2   JRI and ACJ will write paper.