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## Amazonian Maize: Diversity, Spatial Distribution and Historical-Cultural Diffusion

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## Amazonian Maize: Diversity, Spatial Distribution and Historical-Cultural Diffusion

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### Abstract

Subsistence is one of the factors that determined the presence or migration of prehistoric human populations. At the same time, humans were largely responsible for the dissemination of important crop plants such as maize (*Zea mays*). Maize is the major domesticated species in the New World, with thousands of landraces that were shaped by environment and human culture. Genetic analyses of archaeological and indigenous maize samples were used to verify the occurrence in South America of at least two major introductory waves of distinct races of maize from its center of origin in Mexico. The first occurred around 5000 years ago and spread primarily through the Andean region. The second one, 2000 years ago, spread through the lowlands of South America. These two distributions may reflect cultural isolation between the regions. In terms of subsistence, the present study found that the maize used by indigenous Brazilian populations, including those in Amazonia, is genetically closer to samples from Mexico than to samples from the Andes. This applies to both the contemporary and the archaeological samples indicating that the inhabitants of Brazil, including those from Amazonia, had a stronger relationship with populations from Central America and northern South America than from the Andean region. An exception can be seen in the region of northern Chile through Paraguay to southern Brazil, where the mixture of the three genetic groups indicates possible cultural contact between highland and lowland peoples. Additionally, the greatest diversity in maize was observed in samples from Roraima state, in northern Amazonia, and this may reflect the fact that human populations of the region had intense contact with different cultural groups, including the Andean groups.

## **Introduction**

The initial colonization of the Americas by humans is still a source of controversy, particularly with respect to the dates of migration from Asia (Neves et al. 1989; Pena et al. 1989; Prous 1989; Roosevelt 1996; Meltzer 2009). Regardless of when humans arrived in the Americas, they began to migrate and colonize regions from the far north to the south. Populations, groups with their own ethnic traditions, flourished and began to diffuse through time and space. Tracing these "internal" migrations depends on evidence from the remaining indigenous populations, historical data produced in the last 500 years, and archaeological evidence (Harlan 1975).

Over the course of human settlement in the Americas, a number of species became domesticated or semi-domesticated in a process that began about 10,000 years ago. These species were the basis for many of the crops that we eat today. Through the influence of humans, species such as maize, tomato, beans, groundnuts, and cassava, among many others, began to become domesticated from their wild ancestors (Harlan 1971, 1975; Gepts & Debouck 1991).

These domesticated plants were then spread by humans from their respective centers of origin and, upon the arrival of Europeans in the fifteenth century, major domesticated species of the New World were already widespread across the continents. For example, maize was being planted in all three Americas, its range reaching high latitudes in both hemispheres and from sea level to high altitudes. This range reflects the genetic diversity and plasticity of maize that allows it to occupy a range of diverse environments.

All this diversity is explained in part by the importance, past and present, of maize as a basic food for the majority of America's inhabitants. Along its evolutionary path and geographic dispersal, maize has been selected, in part, by the environmental characteristics of each place it was planted. It was also selected by people and cultures, according to their traditions and its uses, including use in the preparation of foods, beverages, and ornaments. This natural and human crop selection generated a number of varieties/landraces, often linked to specific human groups.

Thus, by analyzing different landraces of a given cultivated species, it is possible to determine those that have greater affinity and those that are more genetically distant. Adding geographical information to the relationships between these different varieties, we can analyze their spatial relationships. Additionally, if we include archaeological samples in the analysis, we can add a temporal dimension, indicating when different characteristics of a given landrace were present (Freitas et al. 2003). In this paper, we present possible routes for the spread of maize prehistorically and, in parallel, the possible routes of migration and cultural contact between human populations.

## **Materials and Methods**

This study analyzed 45 maize samples collected from traditional and indigenous populations from different parts of Brazil and Paraguay. Another seven archaeological samples of maize came from human inhabited rock shelters located in the Peruaçu River valley, Minas Gerais state, Brazil, and dated to between 1100 and 560 BP. Analysis also included data from the literature: samples collected in the center of origin for maize in Mexico and Guatemala, and samples from the Andes (three of them archaeological, dates ranging between 4500 and 400 years BP) (Table 1).

SAMPLE	SITE	ORIGIN	AGE (A.P)
A2	Boquete	Januaria-MG	570±60
A3	Boquete	Januaria-MG	890±50
A5	Lapa Hora	Januaria-MG	630±60
A6	Lapa Hora	Januaria-MG	630±60
A8	Boquete	Januaria-MG	570±60
A23	Boquete	Januaria-MG	940±60
A34	Caboclo	Januaria-MG	-
G6	Hastorf	Montanhas – Peru	440±40
G7	Tenney	Norte do Chile	1500±50
G8	Bonavia	Costa do Peru	4500±500

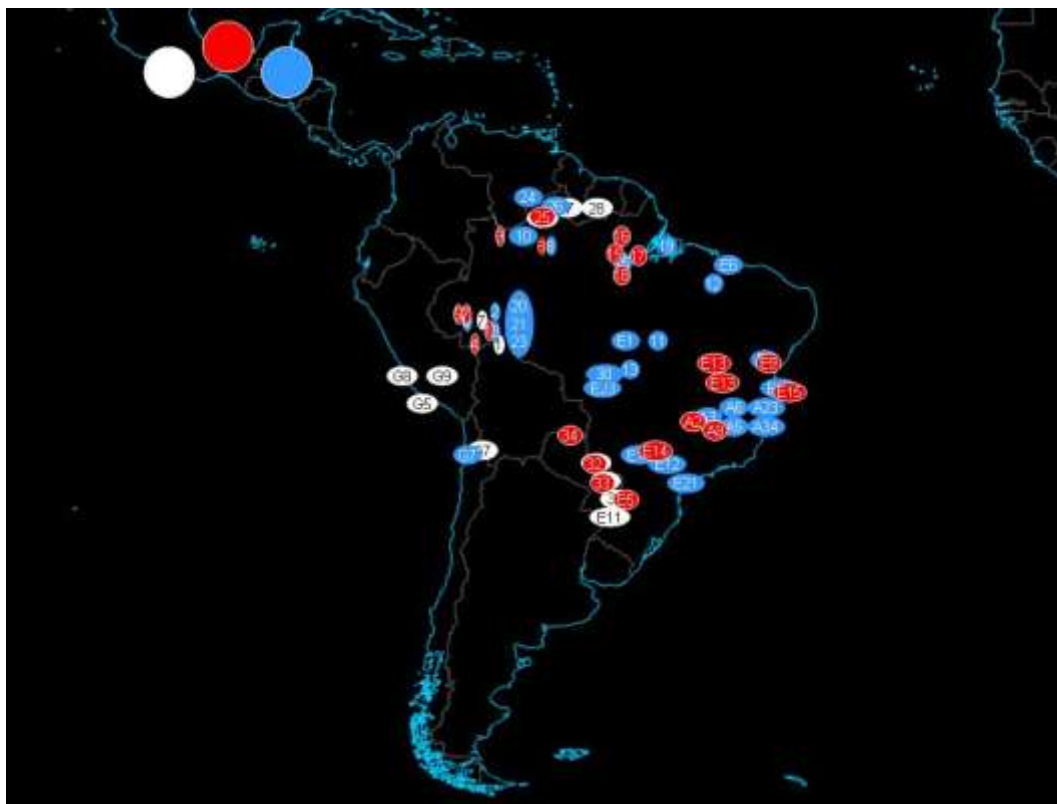
**Table 1** – Archaeological samples used in the analyses (A – archaeological samples direct used; G – archaeological samples from literature (Goloubinoff *et al.* 1993).

Fragments of genetic material (DNA) were extracted from each sample. The methodology used was the technique of extraction by CTAB, with a secondary purification, as reported by Allaby *et al.* (1997), where the target was a sequence in the *Adh2* gene (Freitas *et al.* 2003; Bustamante 2005). The DNA fragments obtained were then sequenced and compared by Network, to identify the mutations occurring in each sequence during the evolution of maize (Allabi & Brown 2000; Freitas 2001; Bustamante 2005).

## Results and Discussion

Analysis showed that maize has high genetic diversity in the target gene, showing many genetic patterns permitting a greater depth of study. Overall, it was noted that the sequences of all the samples could be grouped in three main genetic groups. One group, called "simple", genetically older, and the other two identified as "complex" are evolutionary more recent. These names are given to the genetic groups because of the genetic characteristics of the component sequences.

Interestingly, these genetic groups showed a specific geographic distribution in South America (Figure 1). Samples from one of the groups, the most primitive one (white icons in the figure), were concentrated in the Andean highlands, while the other two groups (blue and red icons in the figure) predominated in the lowlands (Figure 1). This distribution suggests that the introduction of different groups of maize into South America followed different routes of plant diffusion from Central America.



**Figure 1** - Map showing the locations of maize samples used in this study (samples were provided by traditional and indigenous farmers, and extracted from archaeological materials). Three major genetic groups were observed, identified by the colors: white – the simple group, oldest; red and blue – the complex groups, later chronologically. Samples that begin with the letter "G" were gathered from the literature (Note that the samples G7, G8 and G9, are archaeological). Samples beginning with the letter "A" are also archaeological and were directly analyzed in this study.

The first group of maize to enter South America was the simple group, as indicated by the study of archaeological samples. This genetic pattern is present exclusively in archaeological samples found in highland Peru, with dates of 4500 BP, Coastal Peru from 440 BP and northern Chile from 1500 years BP (Goloubinoff et al. 1993). This group was not found in the Brazilian archaeological samples. Apparently, this simple group was widespread along the Andes and just reached the border of the lowlands, with the exception of the southern part of South America.

Subsequently, new distinct groups of maize spread into South America., However, these groups followed new routes, spreading through the lowlands of the South America. It is interesting to note that apparently the "highland" and "lowland" genetic groups did not mix, remaining generally confined to their original areas of distribution. This genetic isolation appears to be more a consequence of cultural isolation between human groups (friendly or not), rather than due to environmental restrictions imposed by the genetic material (environment adaptation).

Four specific observations from the analysis of these maize samples can be made: (1) The southern region of South America, between the northern part of Chile and Argentina to Paraguay, is a region where East-West contact was effective, as samples belonging to the "highland" genetic group can be found in the lowlands (sample E11) and vice versa (G7). It is interesting to note that historical documents and archaeological work indicate that this was the region of the famous Peabiru's route, which connected the two coasts of southern South America. In this case the genetic data helps to corroborate other evidence. (2) The Amazon region has maize basically belonging to the two lowland complex groups. This is important, especially when there are divergent ideas about how humans influenced the Amazon region. Some researchers say that the Amazon was influenced by Andean populations, while others suggest

otherwise. Based on this study, in terms of subsistence and, more specifically in the case of maize, the inhabitants of the Amazon region were not influenced by the Andes. (3) The presence of a single “highland” group sample in the state of Acre, in western Amazonia (7), may indicate a small degree of Andean influence. However, this influence may have occurred in more recent times. In the late nineteenth and early twentieth century, the region was influenced by the rubber boom. The migrants moving into the region eventually displaced many indigenous peoples from their native lands, and some of these moved to the west into the Andean foothills in Peru. With the end of the rubber boom, many indigenous groups returned to their homelands. Some of them may have brought newly acquired agricultural materials, including maize. (4) The region where the greatest diversity of genetic groups and sub-patterns was found is in Roraima state, northern Amazonia, near southern Venezuela (samples 8, 9, 10, 24, 25, 26, 27, 28). Nine of 13 haplotypes documented in this study and in the literature occurred in this region. This indicates that the region could have been an important route of contact among different prehistoric human groups. Possible reasons for this could be: geography - the northern part of the continent is geographically closer to the center of origin for maize in Mexico; rivers - the rivers from the north served as natural routes for diffusion of human populations together with their cultures and crops; hybridization—it is the only place that one genetic hybrid pattern was found, showing the antiquity of maize in the region. Furthermore, northern Amazonia’s low and high altitudes present different environments for cultural adaptation. It is a region where colonization by non-indigenous populations was very recent, so a large percentage of the population is still indigenous. Most of the indigenous people live in consolidated territorial reserves that “soften” the impact of non-indigenous peoples, allowing for the survival not only of their cultures, but also their crops.

### **Final considerations**

Maize was found to have genetic characteristics that are widely distributed geographically in South America, both in terms of modern samples and in terms of archaeological samples. Since human action can explain the genetic-geographic patterns in maize from South America, the pattern can also serve as an indicator of where humans went or the preferred routes of migration of cultures that inhabited South America. Thus, the data presented for maize support the theory that two major human cultures occupied the continent, one related to highlands and the other in the lowlands (Piperno, 1978; McClintock et al., 1981). Apparently, in terms of subsistence, these two cultures were relatively isolated from each other, except for some regions where contact may have occurred. In terms of the Amazon, a region that has been the subject of discussions of cultural affinity, we can say that in terms of subsistence, specifically for maize, that the cultures that inhabited the Amazonian region were influenced to a greater degree by other lowland cultures than by Andean cultures. Finally, this study reinforces the importance of studies that focus on plants managed by humans. We suggest that archaeological excavations should pay special attention to these kinds of samples, as they may complement data from other fields of study.

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