Genetic Analysis of Human Coprolites from Southeastern Utah

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Evaluating the Farming/Language Dispersal Hypothesis with genetic variation exhibited by populations in the Southwest and Mesoamerica

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Edited by Francisco Mauro Salzano, Instituto de Biociencias, Porto Alegre, Rio Grande do Sul, Brazil, and approved February 25, 2010 (received for review June 23, 2009)

The Farming/Language Dispersal Hypothesis posits that prehistoric population expansions, precipitated by the innovation or early adoption of agriculture, played an important role in the uneven distribution of language families recorded across the world. In this case, the most widely spread language families today came to be distributed at the expense of those that have more restricted distributions. In the Americas, Uto-Aztecan is one such language family that may have been spread across Mesoamerica and the American Southwest by ancient farmers. We evaluated this hypothesis with a large-scale study of mitochondrial DNA (mtDNA) and Y-chromosomal DNA variation in indigenous populations from these regions. Partial correlation coefficients, determined with Mantel tests, show that Y-chromosomal variation in indigenous populations from the Americas occupied by populations that shared a suite of cultural characteristics, which was first defined by Kirchhoff (12). The northern limit of Mesoamerica has fluctuated throughout prehistory, both expanding opportunistically and contracting under the threats of nomadic tribes to the north, and at its peak, it overlapped the southern frontier of the Southwest (11, 12).

The earliest widely accepted evidence of maize comes from San Marcos Cave in the Tehuacán region of Oaxaca, accelerator mass spectrometry dated to ~5,600 years before present (YBP) (dates are presented as calibrated calendar years unless otherwise noted) (13). However, recent phytolith data have pointed to an origin in the lowland tropics of Tabasco more than 7,000 YBP (14).
Maize Agriculture

San Marcos Cave, Tehuacán Valley 5600 YBP
Bat Cave, New Mexico 4090 YBP
Three Fir Shelter, Arizona 3890 YBP
Tornillo Shelter, New Mexico 3460 YBP
San Marcos Cave, Tehuacán Valley 5600 YBP

Distribution of the Uto-Aztecan Language Family

Northern Origin

Southern Origin

Merrill et al (2009) *PNAS*

Hill (2001) *Am Anthropol*
Sampling in Mesoamerica and the Southwest

mtDNA variation in 13 populations (both UA and non-UA), N= 848

Combined with data from the literature, 17 populations, N= 960

Y-chromosome variation studied in 11 of these populations, N= 178 males from
Data from:
Carlyle et al. 2000
De la Cruz et al. 2008
Gonzalez-Oliver et al. 2001
Kemp et al. 2005
Kemp et al. 2010
Malhi et al. 2003
Schurr et al. 1990
Torrioni et al. 1992
Mantel Test*

* See Kemp et al (2010) *PNAS* for details
An Additional, Unexpected Discovery
Haplogroup B network, a reenactment
A Southwest Specific Sub-Haplogroup (B2a)
An in situ expansion
Data from:
Carlyle et al. 2000
De la Cruz et al. 2008
Gonzalez-Oliver et al. 2001
Kemp et al. 2005
Kemp et al. 2010
Malhi et al. 2003
Schurr et al. 1990
Torroni et al. 1992
When did the Secondary Expansion Occur?

2,105 YBP (99.5% CI 1,273-3,773 YBP)

Figure from Kemp et al (2010) PNAS
Maize Agriculture

San Marcos Cave, Tehuacán Valley 5600 YBP

Bat Cave, New Mexico 4090 YBP

Three Fir Shelter, Arizona 3890 YBP

Tornillo Shelter, New Mexico 3460 YBP

San Marcos Cave, Tehuacán Valley 5600 YBP
Neolithic Demographic Transition (NDT) in the Southwest
Independent archaeological evidence
Kohler et al. (2008) American Antiquity
Outstanding Questions about this Expansion

Could this expansion blurred our ability to make interpretations of the pre-farming gene pool?

Why only in haplogroup B?

And what about the guys?
Bayesian Coalescent Inference of Past Population Dynamics from Molecular Sequences

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Rise and Fall of the Beringian Steppe Bison

Beth Shapiro,1,2 Alexei J. Drummond,2 Andrew Rambaut,2 Michael C. Wilson,3 Paul E. Matheus,4 Andrei V. Sher,5 Oliver G. Pybus,2 M. Thomas P. Gilbert,1,2 Ian Barnes,6 Jonas Binladen,7 Eske Willerslev,1,7 Anders J. Hansen,7 Gennady F. Baryshnikov,8 James A. Burns,9 Sergei Davydov,11 Jonathan C. Driver,11 Duane G. Froese,12 C. Richard Harington,13 Grant Keddle,14 Pavel Kosintsev,15 Michael L. Kunz,16 Larry D. Martin,17 Robert O. Stephenson,18 John Storer,19

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Sequence Data
Phylogenies Contain Information about Past Population Dynamics

Probability of Coalescence is Inversely Related to Population Size

From Drummond et al. (2003) TREE
Southwest Demographic Profile
Bayesian Skyline Plot (Kitchen, Flanigan, and Kemp unpublished)

Years Ago

Nef
Ancient DNA is Archaeology
Literally Digging for Molecules
Turkey Pen Ruins
Basketmaker II Population
Members of the Green Expedition Excavating Turkey Pen Ruin, 1891

Image from Blackburn and Williamson (1997)
The results on the following two slides have not undergone peer review. In this case, consider them as preliminary and do not cite them without permission from the lead author (Brian M. Kemp)
Results

25/31 samples contained preserved ancient mtDNA

3/25 were of mixed Native American haplogroups

Data on map from:
Carlyle et al. 2000
De la Cruz et al. 2008
Gonzalez-Oliver et al. 2001
Kemp et al. 2005
Kemp et al. 2010
Malhi et al. 2003
Schurr et al. 1990
Torrioni et al. 1992
When did the Secondary Expansion Occur?

2,105 YBP (99.5% CI 1,273-3,773 YBP)

14/18 hg B exhibit the 16111 and 16483
Cowboy Cave, Walter’s Cave, and Old Man Cave
Archaic Populations
The results on the following two slides have not undergone peer review. In this case, consider them as preliminary and do not cite them without permission from the lead author (Brian M. Kemp)
Cowboy Cave, Walter’s Cave, and Old Man Cave
Archaeic Populations

N=45 Coprolites that date ~6,000-9,000 YBP

- **Cowboy Cave** = 0/3
  - Haplogroup B

- **Walter’s Cave** = 1/3
  - Haplogroup B

- **Old Man Cave** = 39
  - 1 Haplogroup A
  - 12 Haplogroup B
  - 3 Haplogroup C
  - 1 Haplogroup D
  - 4 No DNA, 18 still working on them
Results

BMII N= 22

Archaic Pooled N=17

Data on map from:
Carlyle et al. 2000
De la Cruz et al. 2008
Gonzalez-Oliver et al. 2001
Kemp et al. 2005
Kemp et al. 2010
Malhi et al. 2003
Schurr et al. 1990
Torroni et al. 1992
Conclusions/Take Home Messages

Early southwestern farmer populations have a high frequency of expansion form of hg B (with 16111 and 16483)

BSP analysis suggests the expansion to date around 4,000-ish years ago

Subhaplogroup B2a expansion is at least ~1,000-2,000 years old (BMII)

Regional expansion likely occurred on an Archaic baseline containing a high frequency of haplogroup B i.e. genetic continuity dating to this period

The Southwest is the ideal region in which to study the intersection between genetic and archaeological evidence for population demography
Acknowledgements

Funding provided by:

Social Sciences and Humanities Research Council of Canada Grant.

Grant awarded to Matson RG (PI), Lipe WD (Collaborator), and Kemp BM (Collaborator). “Cultural Transformations in Southwestern Prehistory: New Insights from Old Collections.”

Washington State University New Faculty Seed Grant

Department of Anthropology

Please visit my new lab website! www.wsu.edu/~bmkemp

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