Peopling of the Americas
Figure 13.1 Human Evolutionary Genetics, 2nd ed. (© Garland Science 2014)
Luzia: Brazil

Buhl Woman: Idaho

PoW: coastal Alaska

Spirit cave: Nevada

Kennewick: WA
Questions that archaeology hasn’t answered

- Pre-Clovis: shortly before? Or long before?
- Early (>8 KYA) Paleoindian skulls (e.g., Kennewick) look different from later skulls. Why? Did early settlers go extinct?
Kennewick man aDNA

Rasmussen et al. 2015
Controversial “three-migration” hypothesis: Three Native American language families indicate three waves of migrants into the New World.

Amerind (early migration): Contains all the hundreds of languages spoken by all other north and south Native Americans. Highly controversial.


Eskimo-Aluet (late migration): Spoken in far north America, Greenland and parts of Siberia. Not controversial.
Genetic evidence
Pairwise Fst values from classical polymorphisms
mtDNA evidence
Y chromosome data
Autosomal data
HEG model
2015 genetic analyses
Paleoamerican “relic” model

Fig. S38. Simplified schematic of the scenario proposed by (23) where the Americas are peopled by two waves of migration. Under this hypothesis, the first migration (1, indicated in green) consists of the “Paleoamericans”, a population that shares a recent common ancestor with Papuans. The second wave of migration (2, indicated in blue) occurs later by the morphologically different Amerindians that share recent common ancestry with East Asians. The Amerindians largely replaced the Paleoamericans, however, some populations (e.g. the Pericúes/Fuego-Patagonians) have been described as relict Paleoamericans on morphological grounds. The expected tree topology is given (centre) and key locations (including our sample sites) are labeled. Potential gene flow between the arrows is omitted.
Raghavan et al. 2015

Four questions:

1. Timing of divergence from ancestral population?

2. Number of migrations into the Americas?

3. 15K years of isolation in Berengia?

4. Post-Pleistocene survival of relic Australo-Melanesian population in Americas? (based on differences in cranial morphology)

Methods:

31 high coverage modern genomes from the Americas, Siberia, and Oceania

23 Ancient genomic sequences from the Americas, 0.2 to 6 ka.

SNP chip data from 79 individuals from 28 modern populations from the Americas and Siberia

Existing genetic data

Reanalysis of skull morphology
First estimated divergence times between Native Americans and the Koryak of Siberia, one of the genetically closest sampled East Asian populations to Native Americans (fig. S5), using demographic models that reflect a clean split between the populations (28). With both diCal2.0 and the IBS tract method, the split of Native Americans (including Amerindians and Athabascans) from the Koryak dates to ~20 ka (tables S11A and S12 and fig. S15) (28).

We further applied diCal2.0 to models with gene flow postdating the split between Native Americans and Koryak (Fig. 2A) and found that they provided a better fit to the data than did the models without gene flow (fig. S18) (28). Overall, simulated data based on the models inferred by using diCal2.0 and real data show very similar IBS tract length distributions (Fig. 2B) and relative cross coalescence rates (CCRs) between pairs of individuals estimated by using the Multiple Sequentially Markovian Coalescent (MSMC) method (method 3) (Fig. 2, C and D) (28, 44). This serves as a confirmation for the model estimates from diCal2.0. We evaluated all three methods using simulations under complex demographic models and additionally investigated the effects of switch-errors in haplotype phasing on the estimates (28).

We then applied the diCal2.0 model that allows for gene flow between populations after SCIENCE sciencemag.org 21 AUGUST 2015 • VOL 349 ISSUE 6250 aabb3884-3
The data presented here are consistent with initial migration of Native Americans and with later gene flow from sources related to East Asians and, more distantly, Australo-Melanesians. From that single migration, there was a diversification of ancestral Native Americans leading to the formation of northern and southern branches, which appears to have taken place ~13 ka within the Americas. This split is consistent with the patterns of uniparental genomic regions of mtDNA haplogroup X and some Y chromosome C haplotypes being present in

Fig. 5. The Paleoamerican model.

(A) Principal component analysis of 19 ancient samples combined with a worldwide reference panel, including 1823 individuals from (6). Our samples plot exclusively with American samples. Plots with other reference panels consisting of Native American populations are provided in fig. S32. (B) Population structure in the ancient Pericú, Mexican mummy, and Fuego-Patagonian individuals from this study. Ancestry proportions are shown when assuming six ancestral populations (K = 6). The top bar shows the ancestry proportions of the 19 ancient individuals, Anzick-1 (5), and two present-day Native American genomes from this study (Huichol and Aymara). The plot at the bottom illustrates the ancestry proportions for 1823 individuals from (6). Our samples show primarily Native American (ivory, >92%) and Siberian (red, ~5%) ancestry. The plot with K = 13 is provided in fig. S33.
Skoglund et al. 2015

One question:
• Were there one or two founding populations of Native Americans?

Methods:
• 63 individuals “without discernable evidence of European or African ancestry” from 21 Native American populations
• Genotyped at 600,000 SNPs
Skoglund et al. 2015

Figure 1 | South Americans share ancestry with Australasian populations that is not seen in Mesoamericans or North Americans. a, Quantile–quantile plot of the Z-scores for the D-statistic symmetry test for whether Mixe and Suruí share an equal rate of derived alleles with a candidate non-American population, X, compared to the expected ranked quantiles for the same number of normally distributed values. b, Z-scores for the $h_4$-statistic. c, Z-scores for the ChromoPainter statistic. d, Heatmap of ChromoPainter statistics. For non-Americans we display the symmetry statistic $S$(non-American; Mixe, Suruí and Karitiana) for donating as many haplotypes to Mixe as to Suruí and Karitiana. For the Americas we plot $S$(Onge; Mixe, American) for receiving as many haplotypes from the Onge as do the Mixe.
The population movements responsible for these findings should be occurred within the last few thousand years. Further insight into Amazonians as would be expected if the Population Y migration had more, we detect no long-range admixture linkage disequilibrium in that the source of Population Y in Eurasia no longer exists; further-itations, it is not particularly closely related to any of them, suggesting at least two streams of migration or alternatively a long drawn out ancestry of Native Americans from Central and South America cannot of the archaeological associations, our results suggest that the genetic Population Y ancestry may be found in non-Clovis sites. Regardless had entirely First American ancestry that are contemporary to or earlier than Clovis sites. The fact that the South America. There are several archaeological sites in the Americas morphology.

The Population Y we have reconstructed from the genetic data had this morphology and that date to younger than 10,000 years old have been of some early Native American skeletons, which some authors have This discovery is striking in light of interpretations of the morphology Native Americans from Amazonia and the Central Brazilian Plateau. sent-day East Asians and Siberians, likely contributed to the DNA of Amazonian ancestry that comes from an Australasian related population

Figure 2 | A model of population history that can explain the excess affinity to Oceanians observed in Amazonian populations. a, We fit an admixture graph model where a population related to the Andamanese Onge contributed a fraction $\alpha$ of the ancestry of 'Population Y', which later contributed a fraction $\gamma$ to the ancestry of Amazonian groups today (the remainder of which is related to Mesoamerican Mixe). b, Two-dimensional grid of combinations of the admixture proportions $\alpha$ and $\gamma$ which are compatible with the data in terms of how many predicted $f_4$-statistics deviate by $Z \geq 3.0$ from empirical values.