

**Steve Zegura**

September 25, 2010

## **Key Developments in Peopling of the Americas Studies (2007-2010)**

- I. Unanswered Questions (2004)**
- II. Chronological Framework (Calendar Years)**
- III. Beringia Colonization (Early Models)**
- IV. Hammer Lab Migration Models Based on the Y Chromosome (1997, 1999, 2004, 2006)**
- V. Ancient DNA Breakthroughs**
- VI. Major Caveats :**
  - A. Extinction (LOST DATA Problem and Climatic Warming)**
  - B. Confidence Intervals for Dates**
  - C. Need Autosomal Data**
  - D. Need Better Sampling to Test Hypotheses**
  - E. Some Recent mtDNA Genome Sequence-Based Models**
  - F. The Gene Flow / Admixture Problem**
  - G. Where (How) Does Language Fit with Non-linguistic Data?**
- VII. Candidates for Separate Migration Status (A Possible Discussion Topic)**

**I concluded my talk here in 2004 with a series of unanswered questions and caveats. The questions were the following:**

- **Did people continuously occupy Beringia from its latest inception 30,000 - 25,000 years ago to its demise nearly 10,000 years ago?**
- **Did people preferentially use the southern edge of Beringia as a coastal route to the Americas?**
- **Will we ever be able to differentiate clearly among:**
  - 1) **Multiple expansions or re-expansions from a single polymorphic source population or population system**
  - 2) **Multiple expansions from multiple “independent” sources (that may have been related in the past)**
  - 3) **A single expansion with ancient and/or subsequent gene flow solely by analyzing contemporary genetic data?**
- **Will ancient DNA studies provide heretofore unexpected answers, as well as lead to new questions and hypotheses about the early peopling of the Americas?**

TABLE I Approximate equivalence of radiocarbon and calibrated ages, from the Last Glacial Maximum to the Early Holocene.

Radiocarbon age	Median calibrated age
<i>(<sup>14</sup>C years before present or BP)</i>	<i>(calibrated years before present)</i>
18,000	21,285
17,500	20,635
17,000	20,120
16,500	19,665
16,000	19,170
15,500	18,815
15,000	18,320
14,500	17,475
14,000	16,690
13,500	16,040
13,000	15,350
12,500	14,625
12,000	13,865
11,500	13,340
11,000	12,945
10,500	12,465
10,000	11,485
9,500	10,840
9,000	10,085
8,500	9,440
8,000	8,860
7,400	8,200

NOTE: As derived by OxCal 3.10 (<http://c14.arch.ox.ac.uk/oxcal.php>).

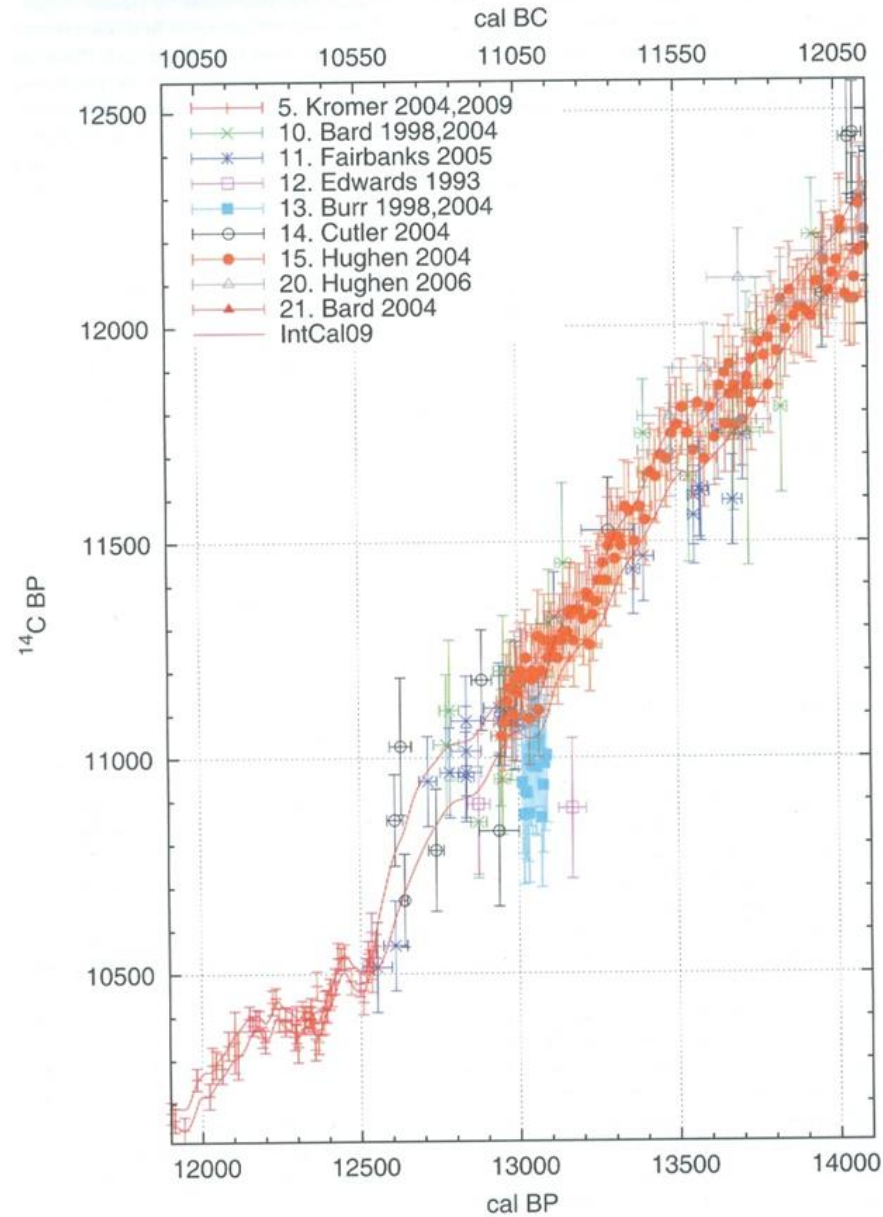
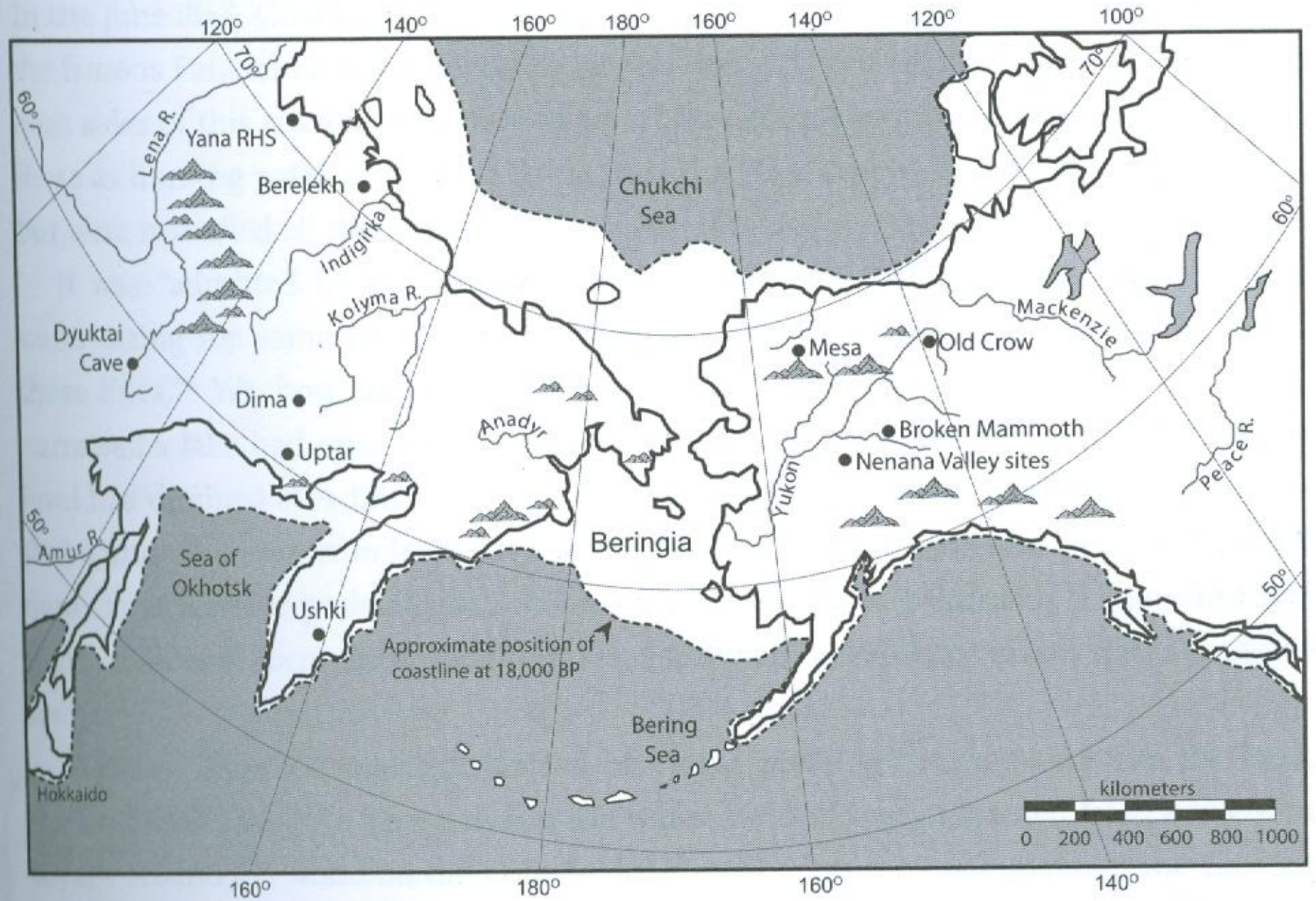


Figure 2 IntCal09 terrestrial calibration curve (1-standard deviation envelope) and data with 1-standard deviation uncertainty in the  $^{14}\text{C}$  and calendar ages. Complete references to the data sets are given in the Appendix.

Today		Holocene Epoch	Atlantic Period Optimum (7.8K →5.7K) ↑3.5° F
11.5 K yrs. ago* (11,485) 12.9	<b>M I S 2</b>	Pleistocene Epoch ends Younger Dryas	Cooling (↓9° F) End of Clovis Black Mat (No « Badaboom »)
14.7		Bølling-Allerød Interstadial	Warming (↑~13° F) Americas populated
17.5/18.0		Heinrich Stadial	Possible Colonization (Coast Route Open ~ 16.5K) Meadowcroft ? Cool
26.5 30/27		Last Glacial Maximum (LGM) (temporal and spatial variability) 18/19K→26.5K (~33K)  Beringia Maximum Extent ~30K→20K 4000 km E-W 1000 km N-S But glaciation only in mountains	Cold (↓~30° F)
60 K yrs. ago	<b>M I S 3</b>	Kargin Interstade Boutellier Interglacial/Stadial Middle Wisconsin Middle Weichselian Middle Pleniglacial	Yana River site (~30 K)  Regional and Temporal climatic variability  Warm and cool oscillations  Insolation peak at 35 K  Dansgaard-Oeschger (D-O) Warming Events  Warm period in Yana lowlands ~29-33K  Heinrich Events ~30K, 38K, 45K In North Atlantic

\*All dates in calendar years.



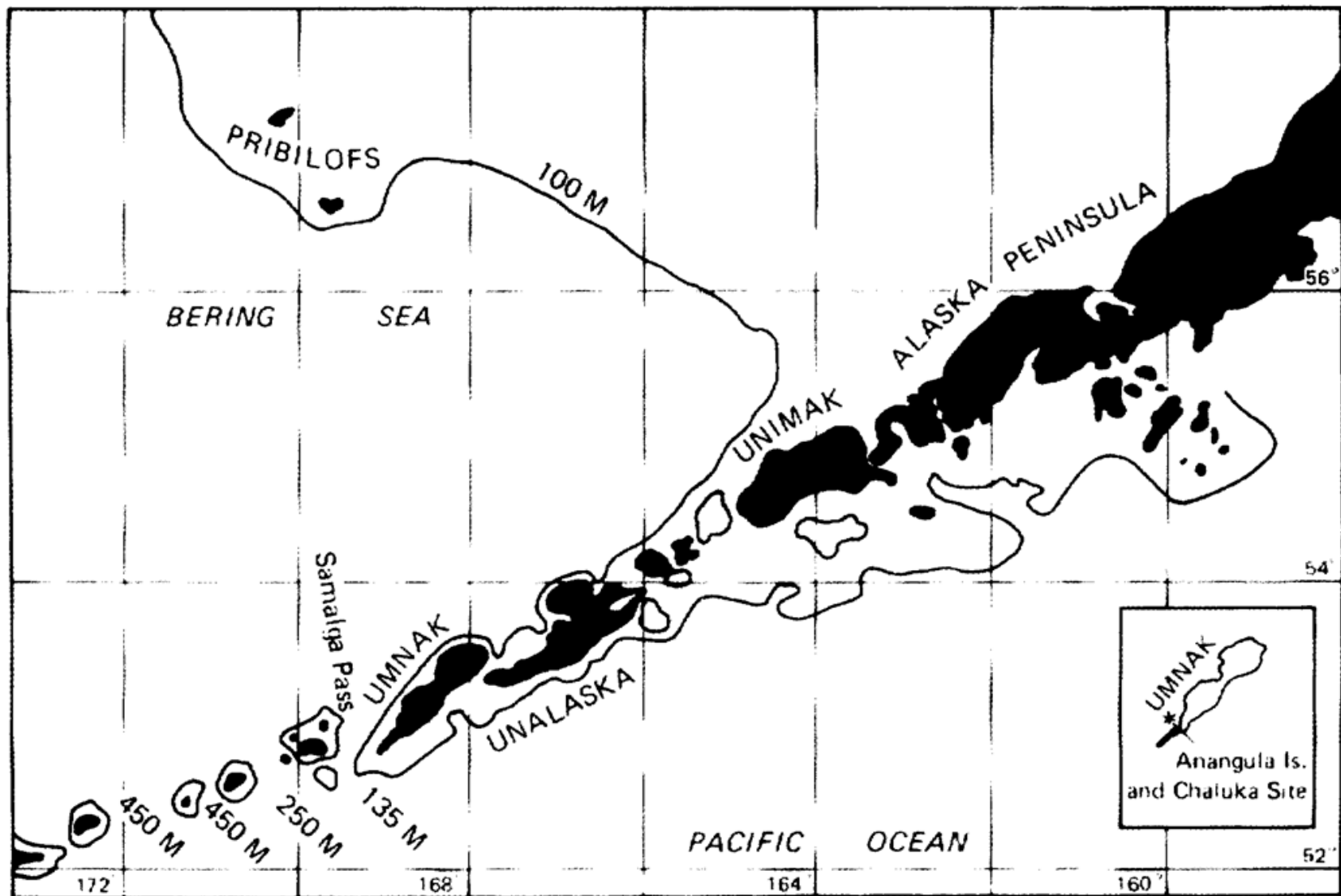


Fig. 32. Earlier coastline of the Bering Land Bridge 11–12,000 years ago. Umnak Island was then the terminus of the Alaska Peninsula. Samalga Pass, between Kagamil and Umnak Islands, was then the easternmost pass channeling whales, fur seals, and fish from the Pacific Ocean into the Bering Sea (courtesy of R. F. Black).

# SCIENCE

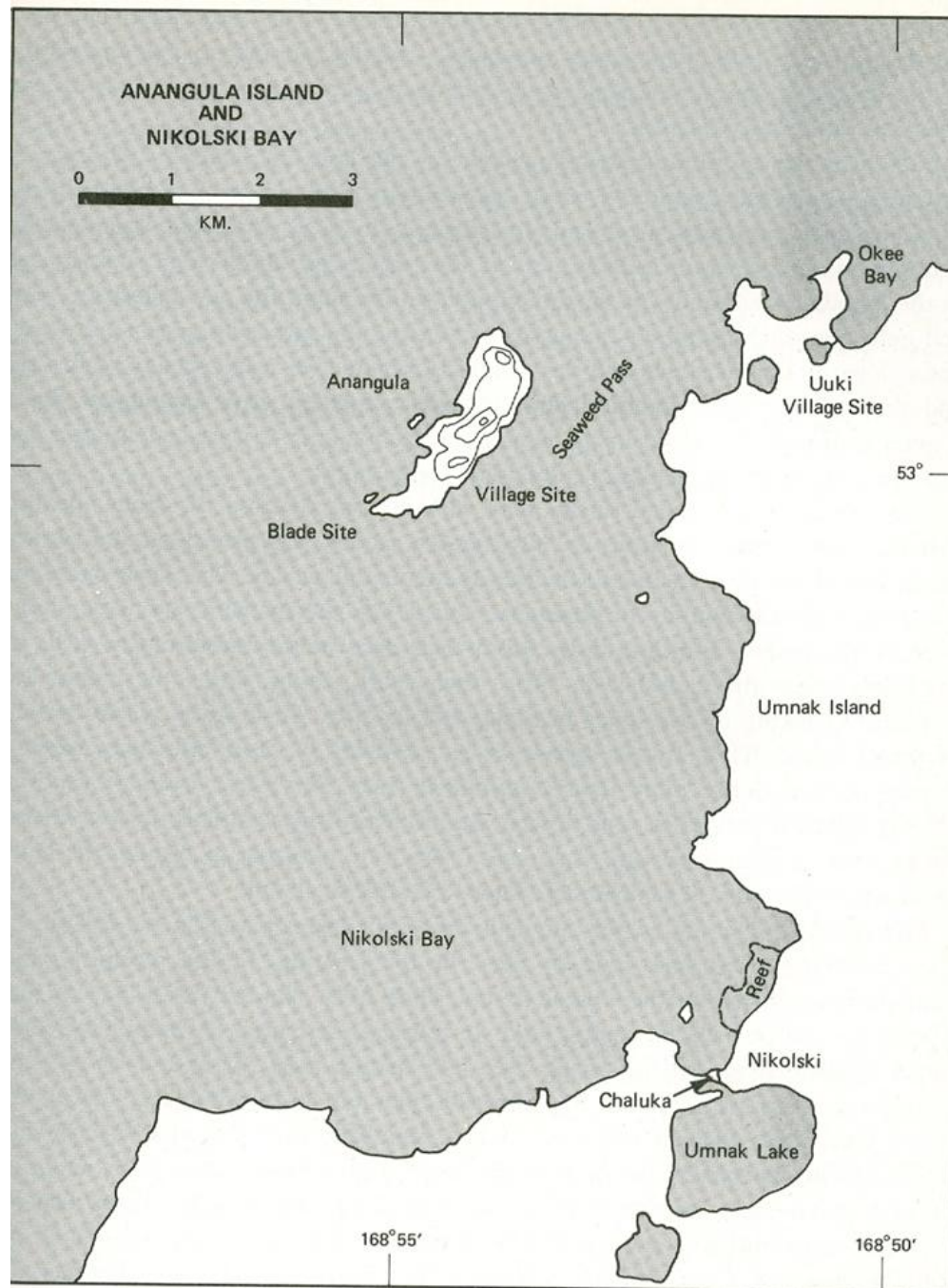
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*Fig. 18. Anangula Island and Nikolski Bay.*

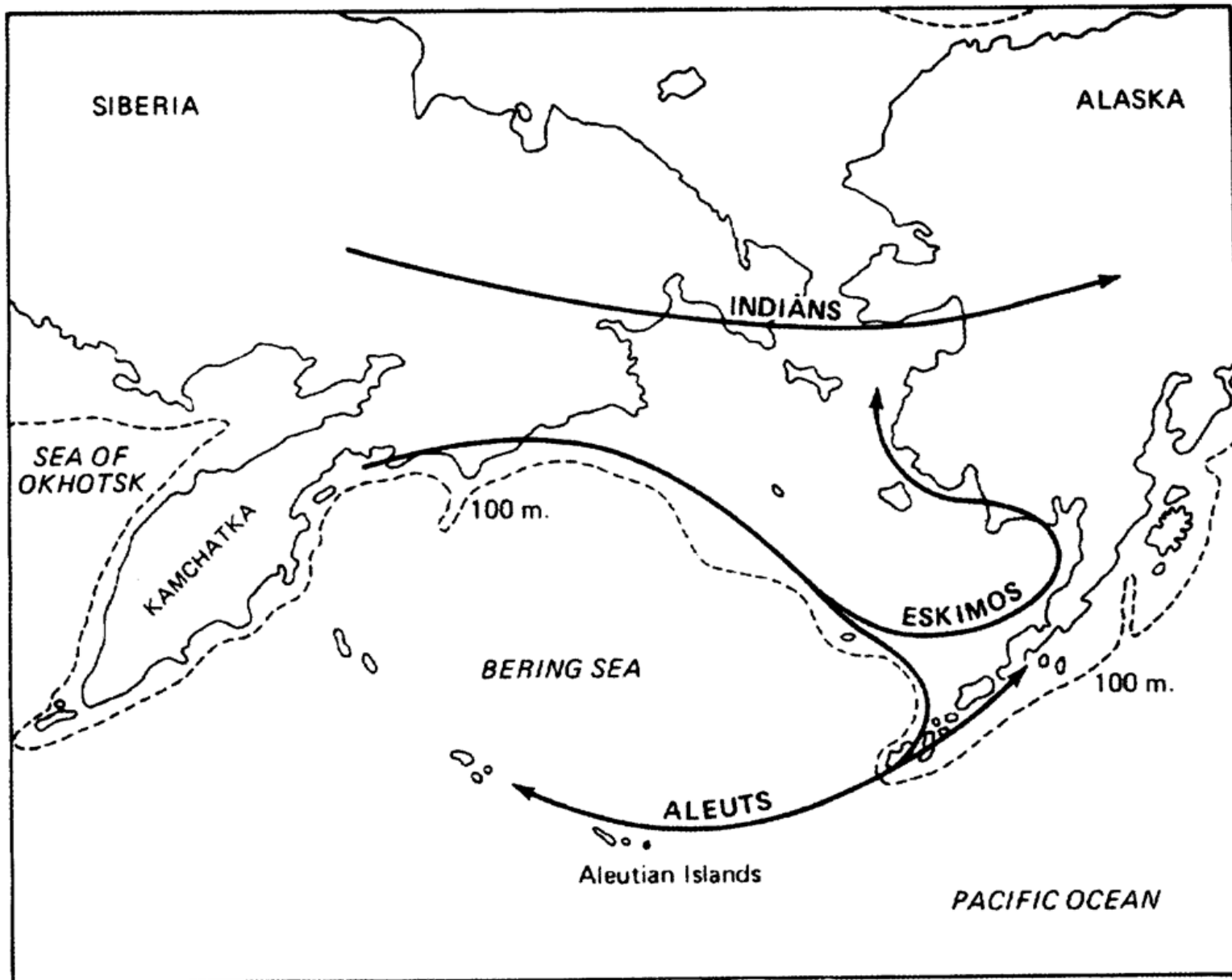
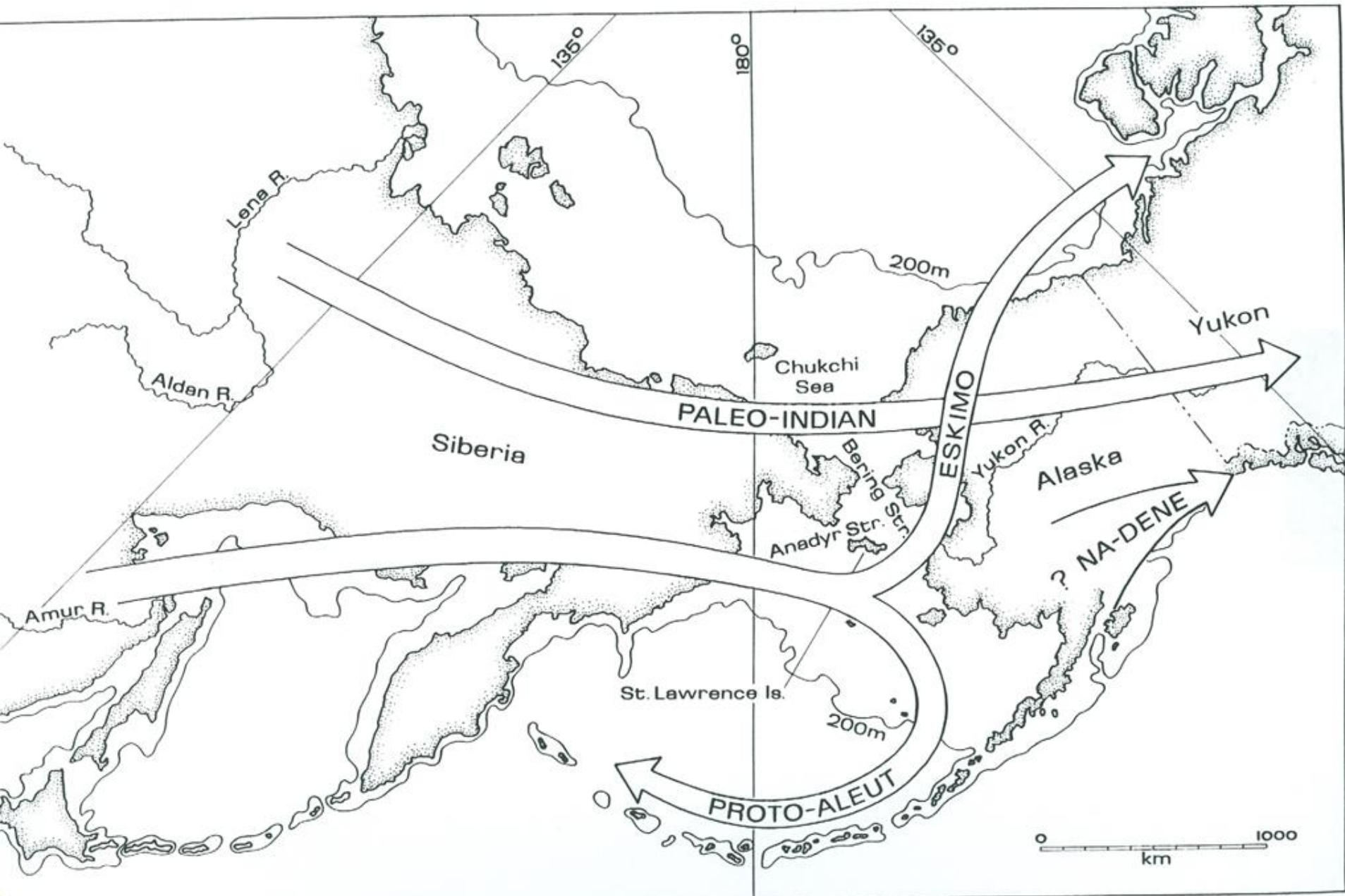
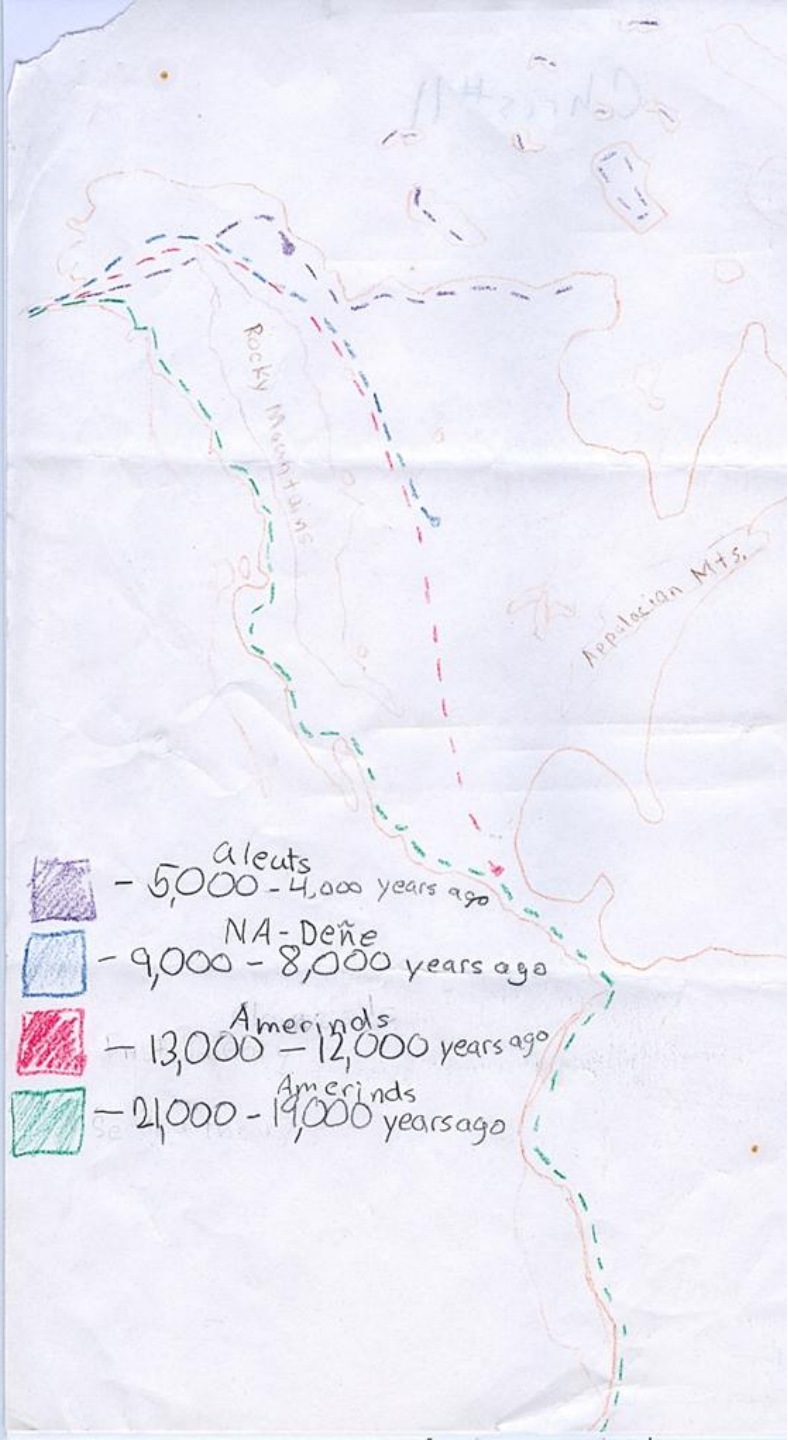
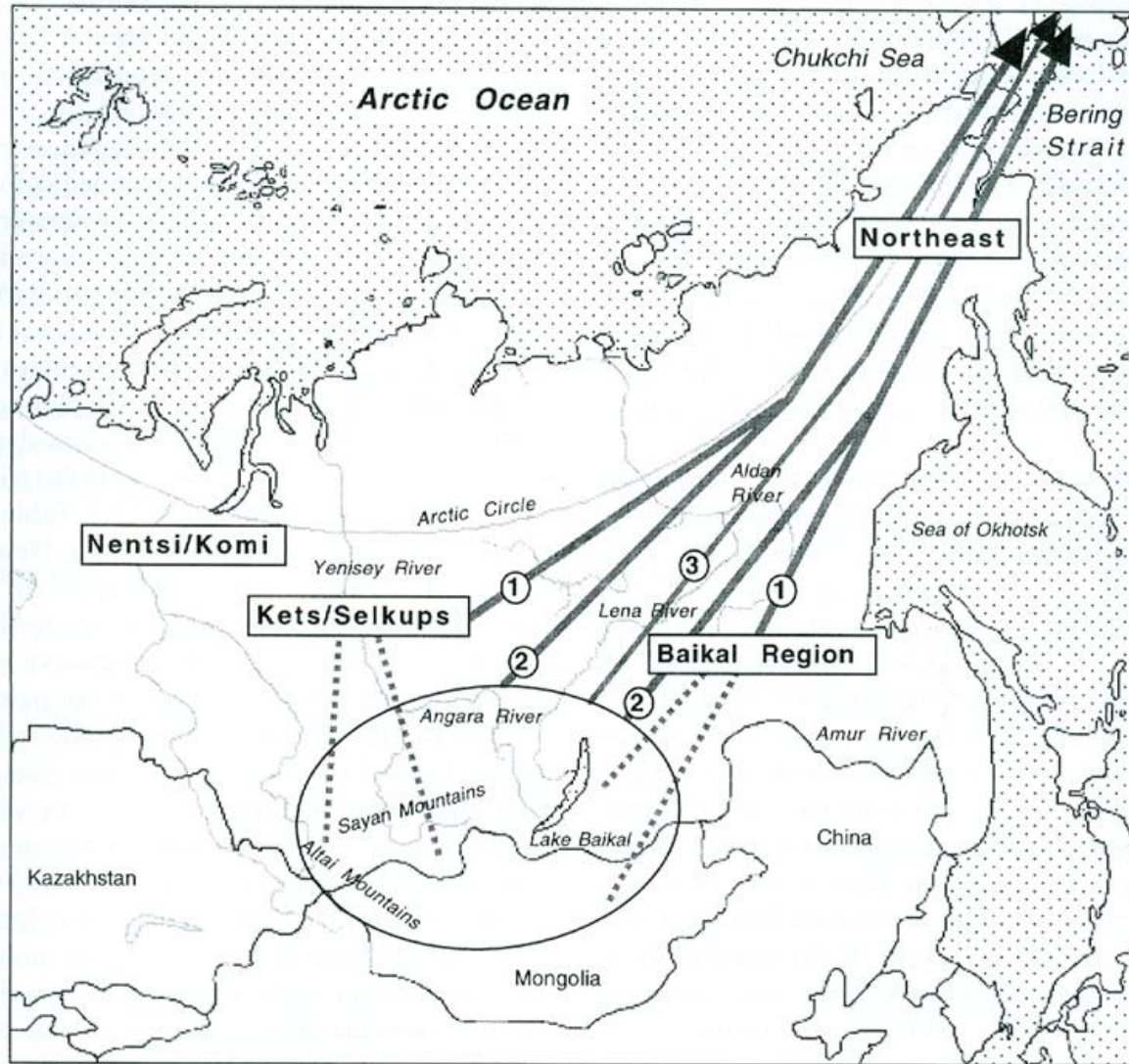


Fig. 31. Ancestors of the American Indians migrated through the interior of the Bering Land Bridge. Ancestors of the Aleuts and Eskimos followed the southern coast and diverged from each other in southwestern Alaska.

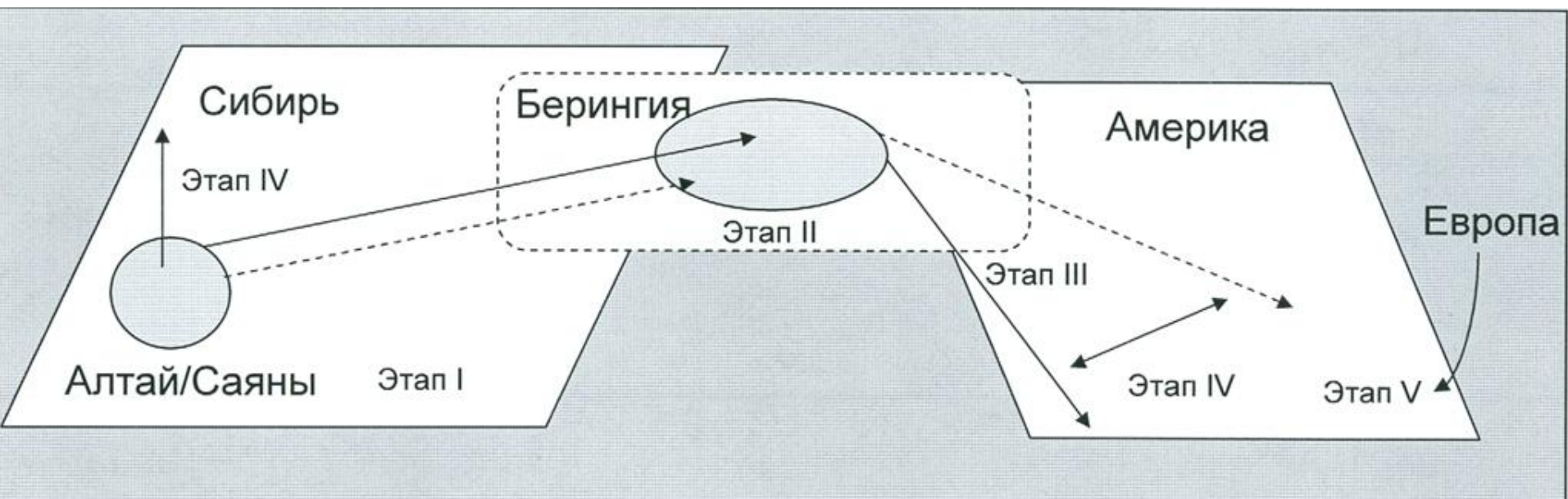






**Figure 6** Alternative models for the origin of New World founder haplotypes. Numbers in circles on the solid-lined arrows refer to models 1–3 as defined in the text. These illustrative arrows do not denote precisely defined geographic routes. The dotted lines extending into the large circle indicate the possible ancestral homeland of the Kets/Selkups (haplotype 1C-12A) and of the Baikal Region populations (haplotype 1F-11C).





# New Views From the Y Chromosome

## Three Models

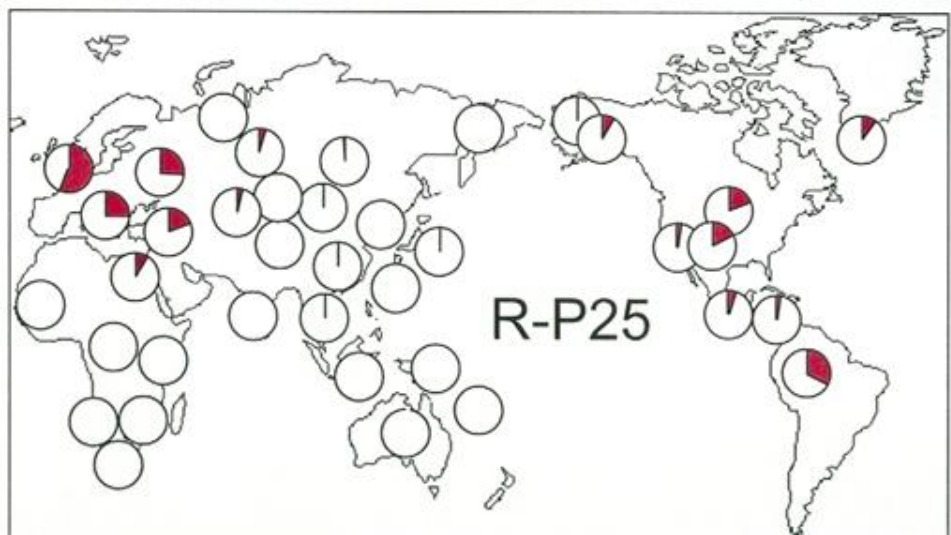
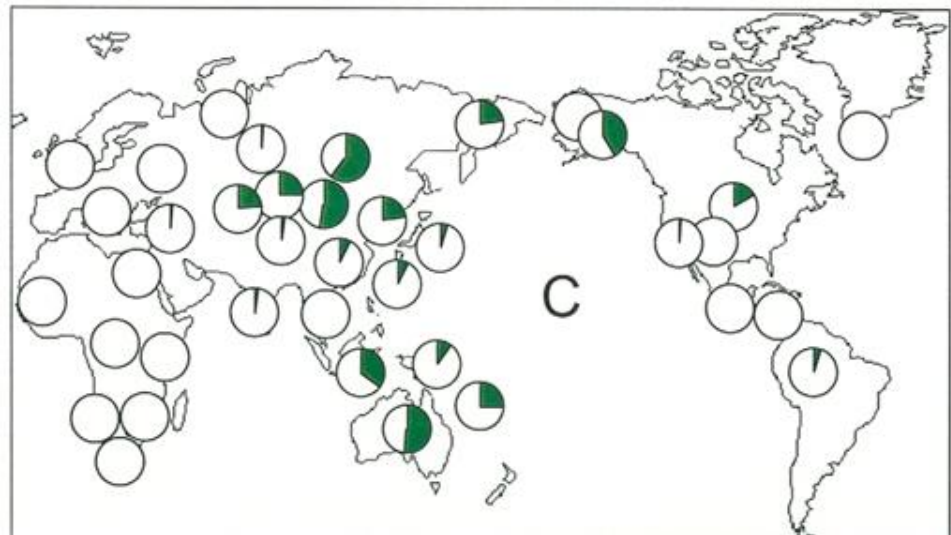
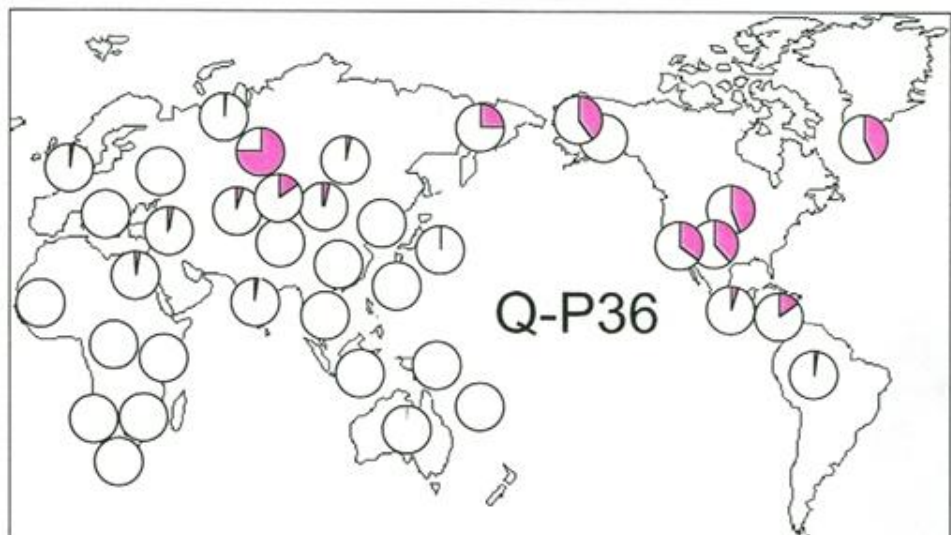
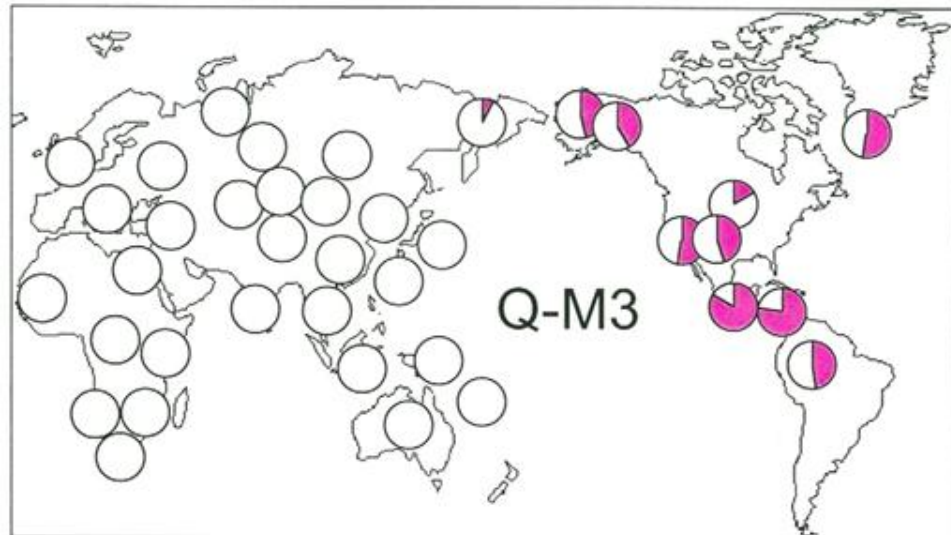
I. Colonization before LGM  
Interior and/or Coastal Route

**II. Colonization After LGM**  
A. One Wave of Migration  
Coastal Route Necessary

B. Two Waves of Migration  
Coastal Route First  
Interior Route Second





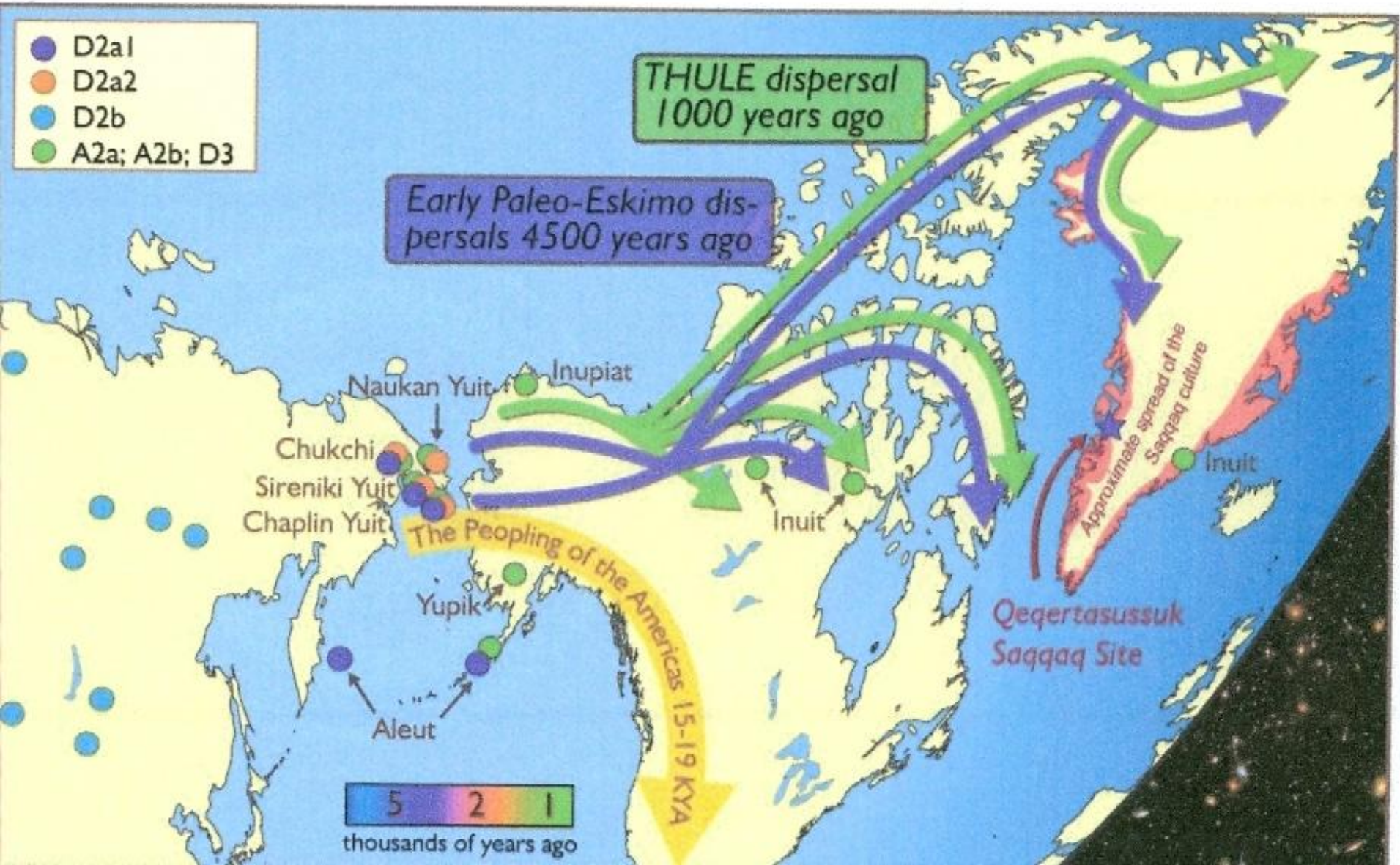


## Recent Ancient DNA Studies:

- Kemp *et al.* (2007):** On Your Knees Cave, Prince of Wales Island, SW Alaska  
Y: Q-M3; mtDNA New founder subhaplogroup D  
10,300 BP
- Kuch *et al.* (2007):** Beothuk, Newfoundland  
Y: Q-M3; mtDNA Hg X, HG C  
N=2 (died in 1819)
- Malhi *et al.* (2007):** mt DNA Hg M found at China Lake, BC  
~ 5000 BP
- Gilbert *et al.* (2008)** Paisley Cave, Oregon  
6 Human Coprolites  
mtDNA Hg A2, B2  
14,000 + BP
- Gilbert *et al.* (2008):** mtDNA Hg D2a1 (Hair)  
Saqqaaq Culture, Disko Bay, W. Greenland  
~4,000 BP
- Rasmussen *et al.* (2010):** Nuclear Genome of same Disko Bay Specimen  
Y = Q1a (Q-MEH2)

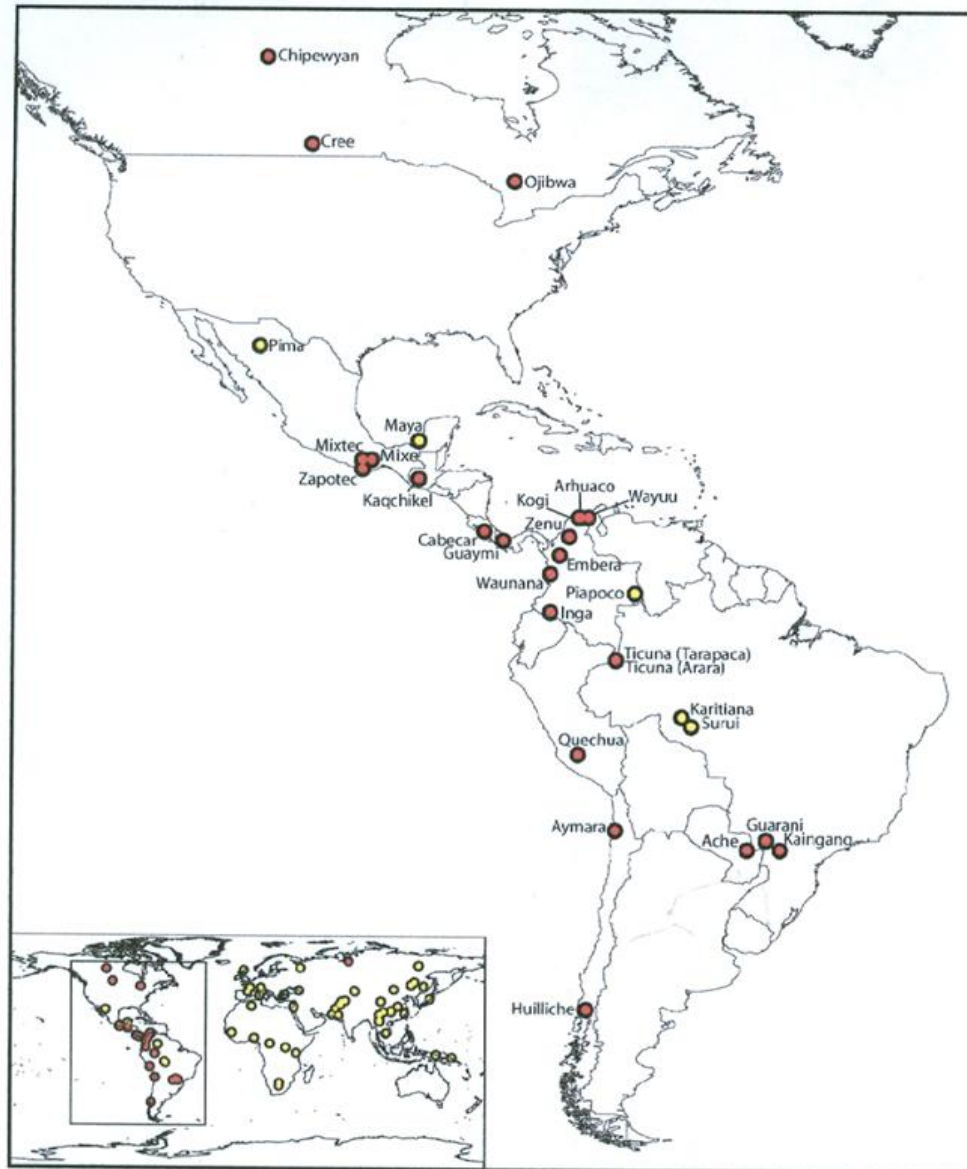






## Autosomal Data:

- Wang *et al.* (2007)** Only 3 of 29 populations North of Mexico, 678 STR's, N=422 (530), single coastal migration
- Wang *et al.* (2009)** 7 STR's on Xq13, only 1 of 6 populations from N. America, N=249, Americas colonized by a differentiated E. Asian population
- Bourgeois *et al.* (2009)** Exon 44 of dystrophin gene at Xp21, 9 geographically well-sampled populations, N=205, big N vs C+S American difference reflecting Beringian population structure (but no A-E samples)
- Ray *et al.* (2009)** Used Wang *et al.* (2007) data, 1 wave + gene flow model preferred; however, no test of 3 wave model done and no post-Columbus gene flow allowed, use Approximate Bayesian Computation (ABC) methods
- CAVEAT:** See Templeton (2010) *PNAS* article for a potentially devastating critique of the ABC methodology (“Coherent and incoherent inference in phylogeography and human evolution.”)
- Lewis (2010)** Used Wang *et al.* (2007) data to conclude that there was a major bottleneck or founder effect in N. America!



**Figure 1.** Populations Included in This Study

The world map shows the 78 populations investigated in the combined dataset, with the locations of the 29 populations studied in the Americas shown in detail in the larger map. The 25 newly examined populations, including the Siberian Tundra Nentsi, are marked in red, and the previously genotyped HGDP-CEPH populations are marked in yellow.

doi:10.1371/journal.pgen.0030185.g001

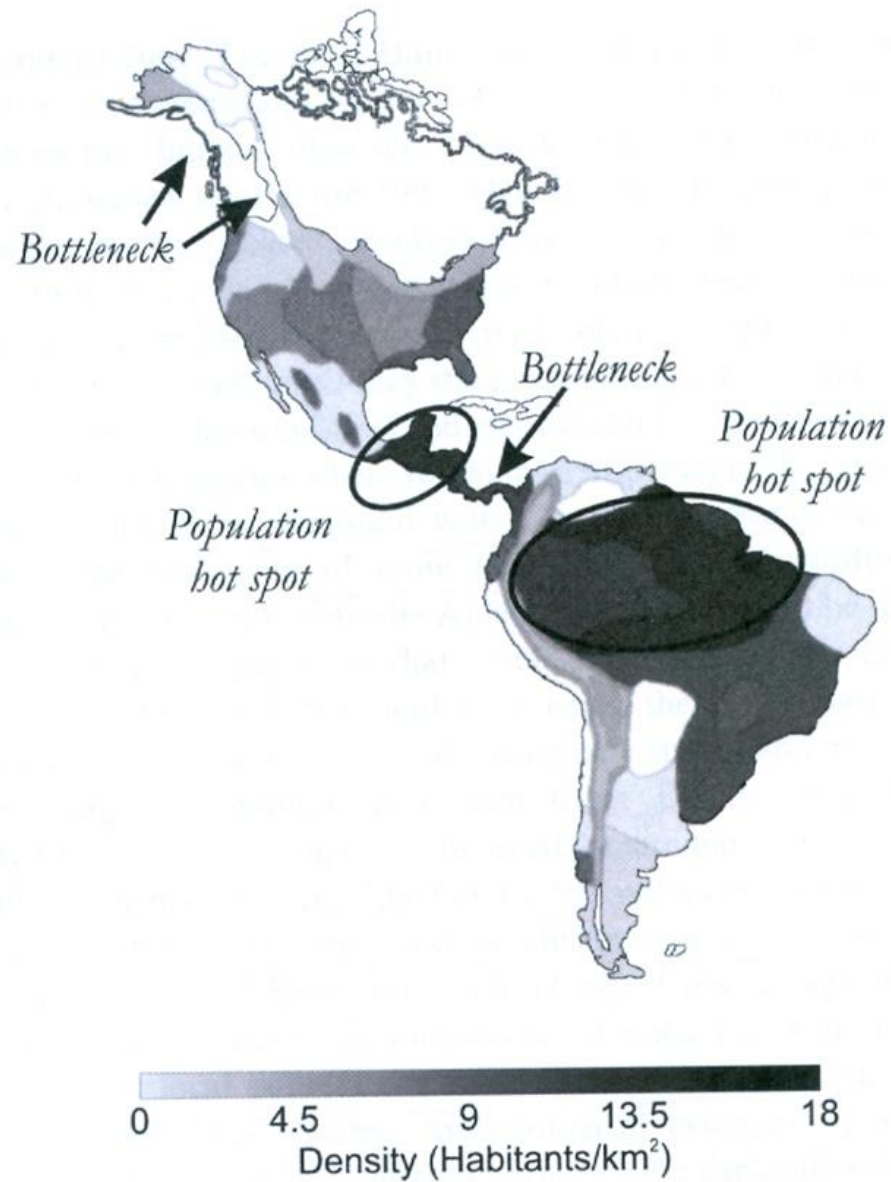
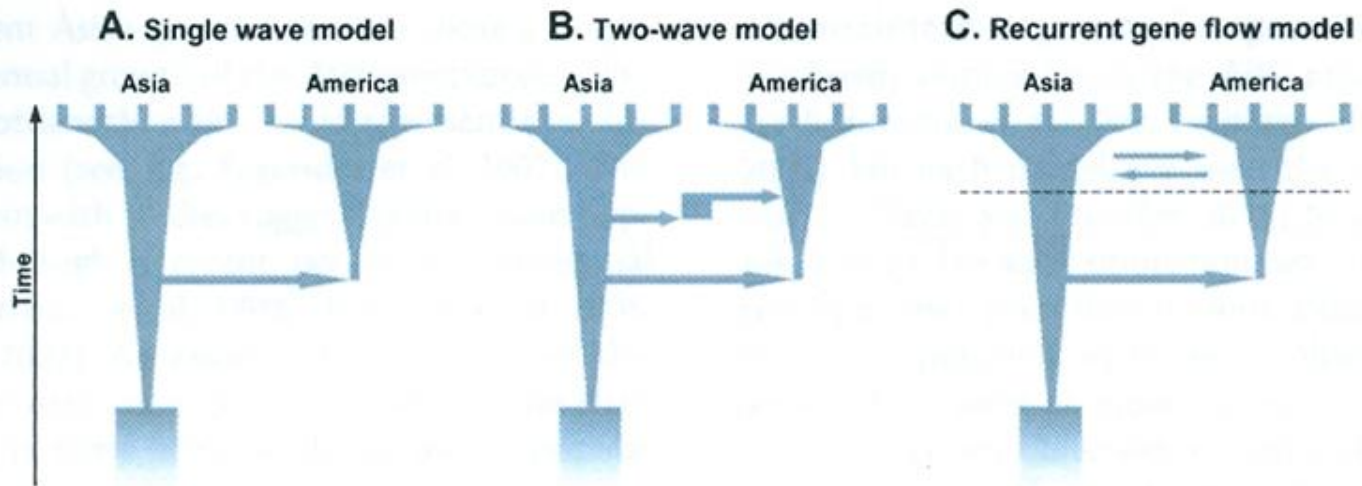


Figure 10 Spatial scheme of the dynamic of the human dispersal in the Americas, showing population distribution at *c.* 13,000 rcy BP, in a simulation with  $\alpha = 5$  per cent, as an example.

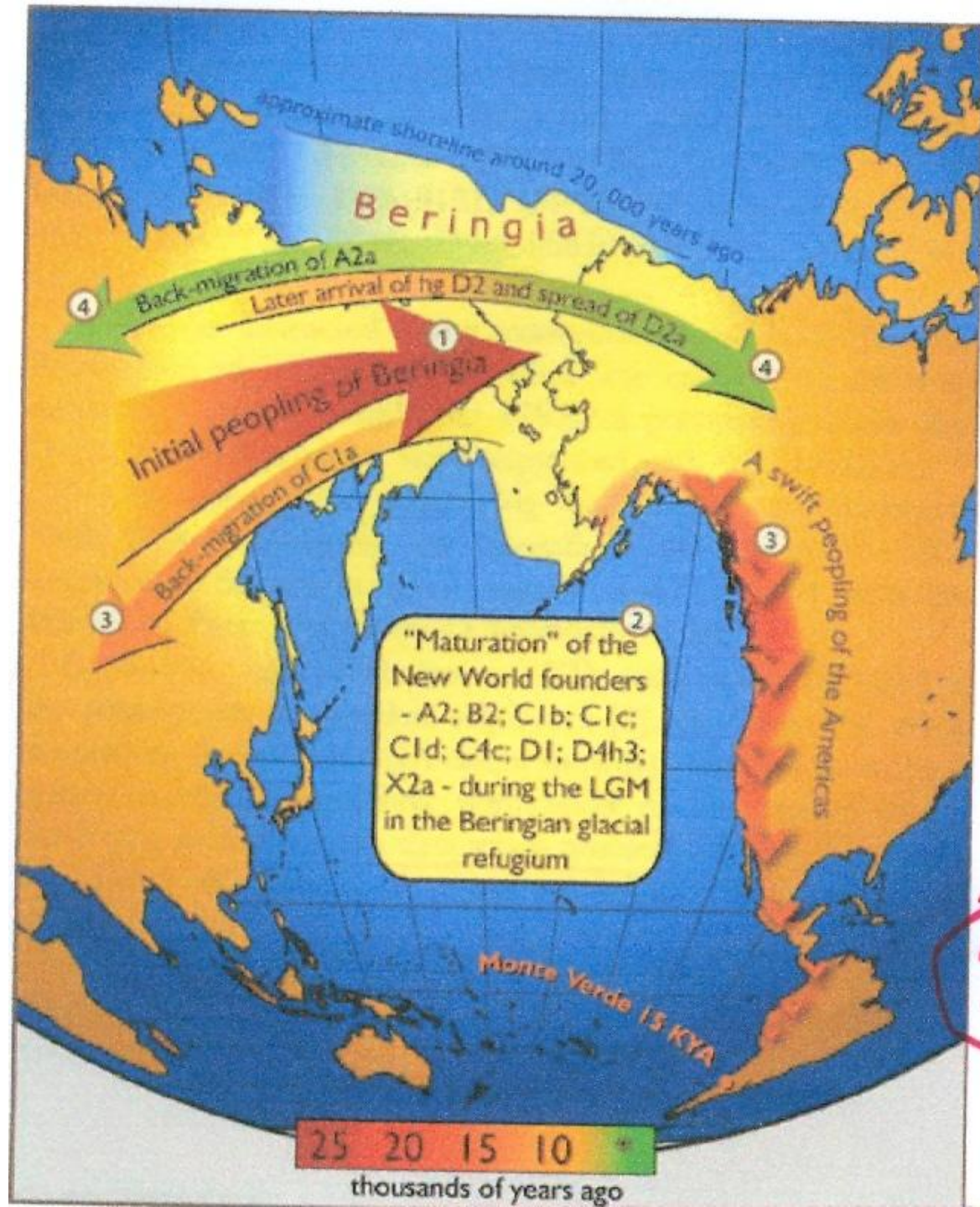


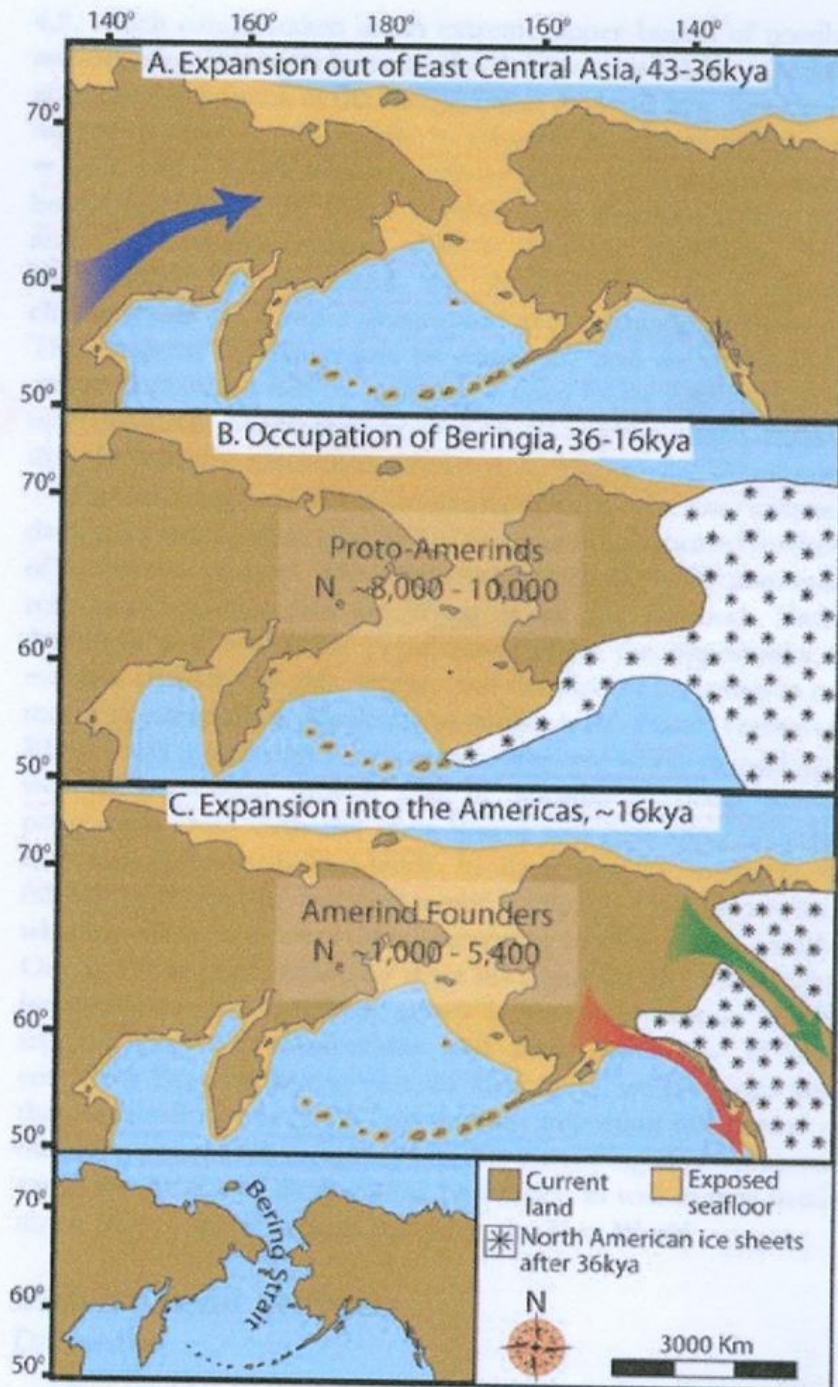


**FIG. 1.** Alternative models for the colonization of the Americas tested in this study.

## Recent mtDNA Genome Sequencing Papers:

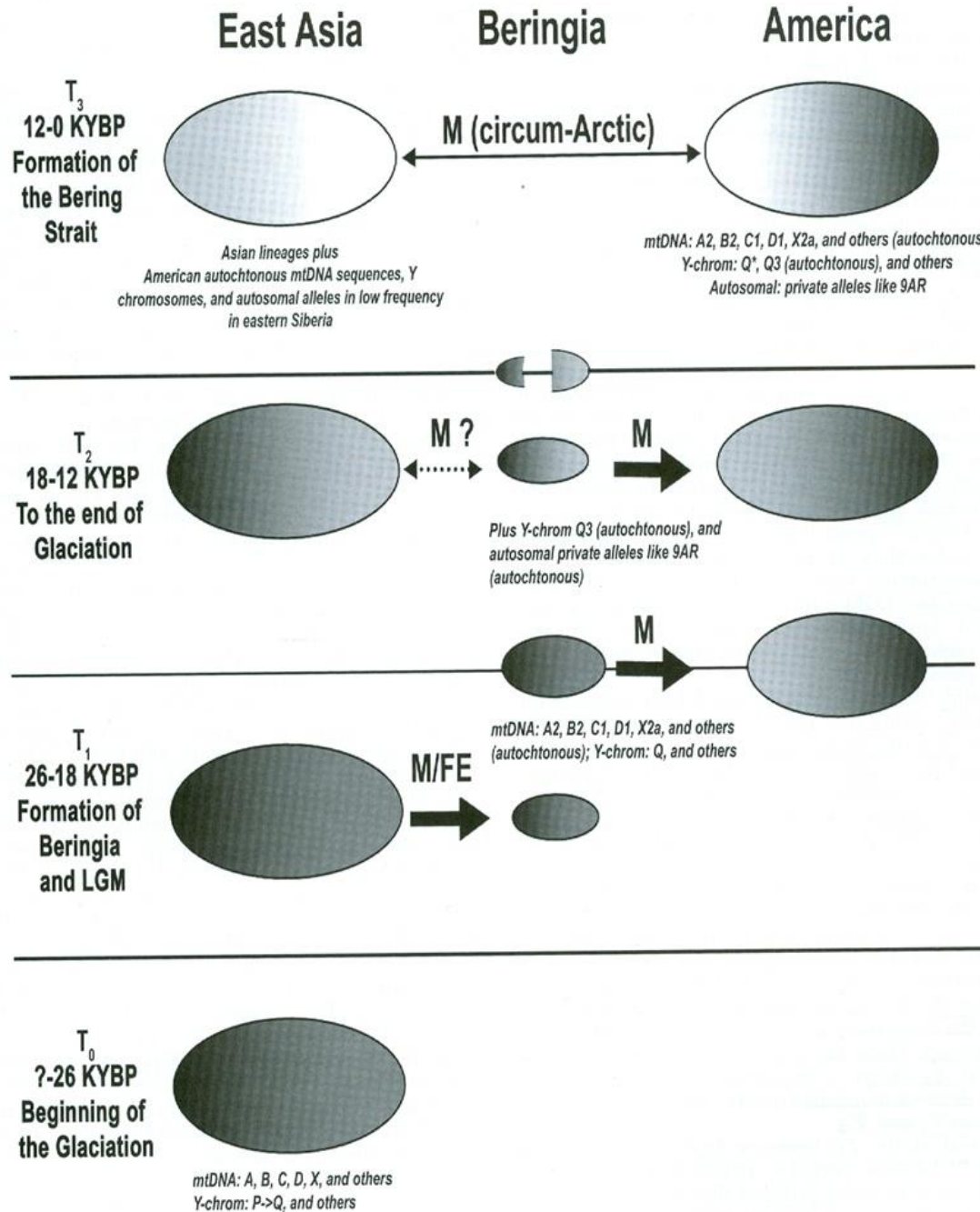
- Tamm *et al.* (2007) All mtDNA haplogroup dates between 10.3 K and 16.5 K, NOTE: all our Y-chromosome dates are between 10.1 K and 17.2 K; Beringian Standstill Model followed by swift migration throughout Americas with recent bidirectional gene flow involving Siberia
- Achilli *et al.* (2008) mtDNA haplogroup dates earlier (ave. ~ 19K), early dates support coastal route
- Perego *et al.* (2008) mtDNA Hg D4h3a via coast mt DNA Hg X2a via ice-free corridor  
Both migrations 15-17 K (Problem!), “A dual origin for the first Americans is a striking novelty from the genetic point of view” (A REAL PROBLEM!) cf. C. Turner (2005) for a summary of 45 papers discussing the number of migrations to the Americas, separate Beringian or Alaskan stocks for the Na-Dene + Aleut/Eskimo vs PaleoIndians
- Kitchen *et al.* (2008) Combination of nuclear and mtDNA, 3-step Colonization Model with  $N_e=1000 \rightarrow 5400$  people ( $N_e$  vs  $N_T$  problem)
- Fagundes *et al.* (2008) Deliberately left out E-A and Na-Dene samples and then concluded that there was a single Pre-Clovis colonization along the Pacific Coast! 15K  $\rightarrow$  18K population expansion

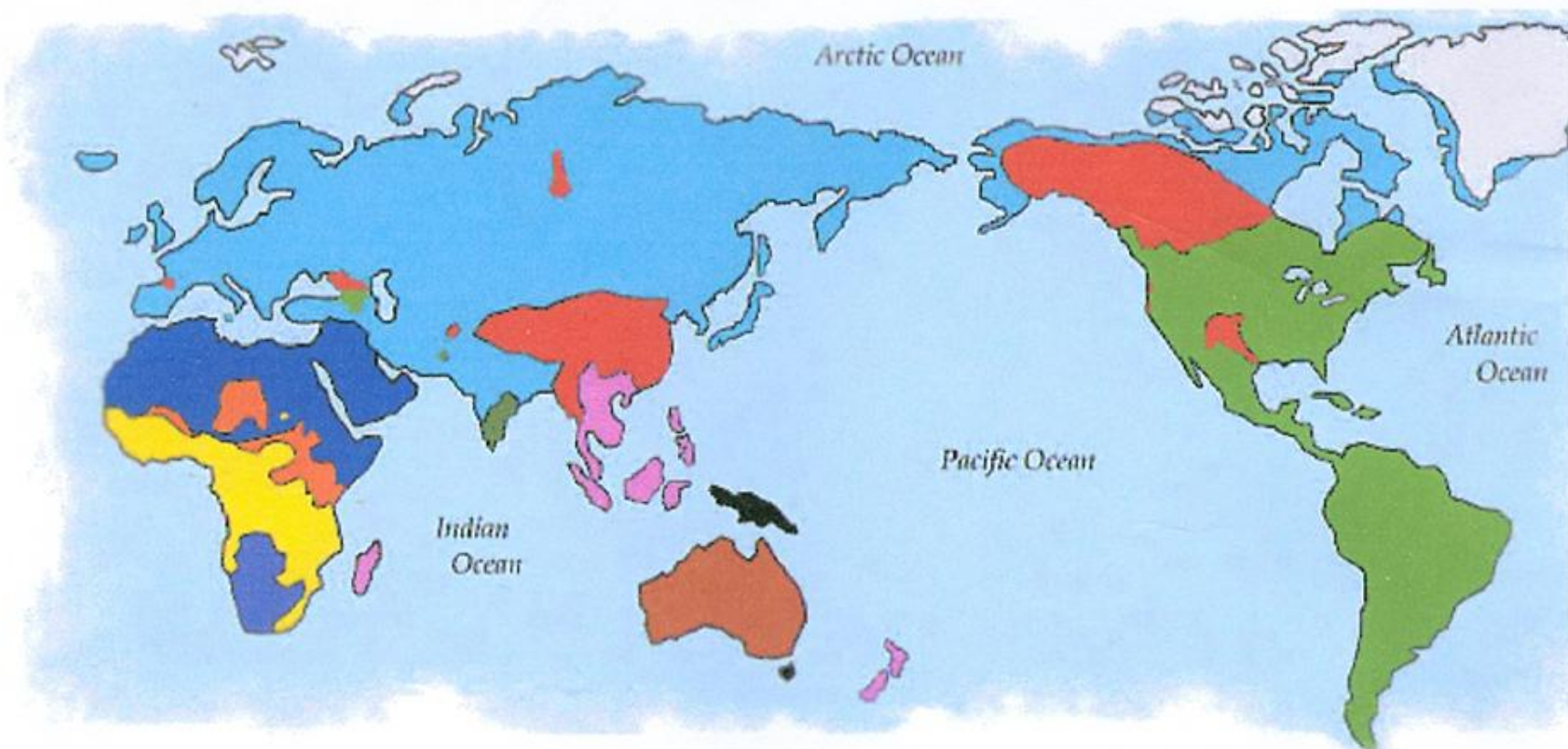




**Some Studies with Evidence of Admixture:  
Is the Gene Flow Ancient, Recent or Both?**

- Bosch *et al.* (2003)** 58% European admixture in Greenland Inuit males (Post-Columbus)
- Zegura *et al.* (2004)** 17% admixture in 588 male Native Americans, preponderance is from European males (Post-Columbus)
- Ray *et al.* (2009)** Recurrent Pre-Columbus gene flow between Asia and America using Wang *et al.*'s (2007) autosomal data (excluded last 200 generations in model)
- Hunley (April 2010)** AAPA Meetings Paper (Albuquerque), Wang *et al.*'s (2007) data showed that pervasive European admixture caused these autosomal data to fail the TREENESS test (Post-Columbus)
- Gonzalez-Jose *et al.* (2008)** Used craniometric data to underscore the role of "recent" admixture between Asian and American Circumarctic populations throughout the Holocene, bidirectional, proposed single-wave and gene flow model (similar to Ray *et al.* 2009) and unlike most skeletal-based papers which favor a two-wave model (older "Pre-Mongoloid" stratum followed by Sinodont "Mongoloid" morphology stratum)
- Malhi *et al.* (2008)** Significant paternal admixture in North American Native populations with European gene flow especially prevalent in the Northeast
- Zhadanov *et al.* (2010)** Genographic Consortium Project, Seaconke Wampanoag, S. Mass., N=28, incredibly high amount of Post-Columbian gene flow documented, NO Native American mt DNA haplogroups found and only 2 /17 males had Native American Y-chromosomes (Q-M3)
- Note:** Pelješac Peninsula near Dubrovnik, Croatia, Pavao Rudan's Lab in 1988 & 1990, our conclusion based on serogenetic markers + genealogical and demographic data: no one presently on Peljesac had ancestors there 500 years ago
- Rubicz *et al.* (2010)** ~70% Russian admixture for Bering Island Aleut males, ~85% for all available Aleut Y-chromosome data with mostly Russian source in West and Scandanavian/West European source in East; mtDNA showed very low levels of female-mediated gene flow





- |   |  |   |
|---|--|---|
| <span style="color: blue;">■</span> Khoisan             | <span style="color: green;">■</span> Dravidian       | <span style="color: pink;">■</span> Austric       |
| <span style="color: yellow;">■</span> Niger-Kordofanian | <span style="color: lightgreen;">■</span> Kartvelian | <span style="color: black;">■</span> Indo-Pacific |
| <span style="color: orange;">■</span> Nilo-Saharan      | <span style="color: lightblue;">■</span> Eurasiatic  | <span style="color: brown;">■</span> Australian   |
| <span style="color: darkblue;">■</span> Afro-Asiatic    | <span style="color: red;">■</span> Dene-Caucasian    | <span style="color: green;">■</span> Amerind      |

Language Families of the World (after Greenberg)

**Global Perspectives on Human Language**

## Some Candidates for Separate Migration Status:

GTZ (1986): Amerinds, Na-Dene, and Aleut-Eskimos

12 mtDNA "Founding" Haplogroups (Major vs. Minor; Early vs. Late): More than one migration implied by these data

Pacific Coast (mtDNA Hg D4h3a) Migration

Ice-Free Corridor (mtDNA Hg X2a) Migration

Y-chromosome Hg Q

Y-chromosome Hg C

Pre-Clovis People (Coastal)

Clovis People (Inland)

Anangula Aleuts

Later Aleuts

Saqqaq Greenland Paleo-Eskimos

Later Dorset Greenland Paleo-Eskimos

Alaskan Eskimo Ancestors of Canadian Inuit and Greenland Thule Eskimos

Early "Non-Mongoloid" Skeletal Populations

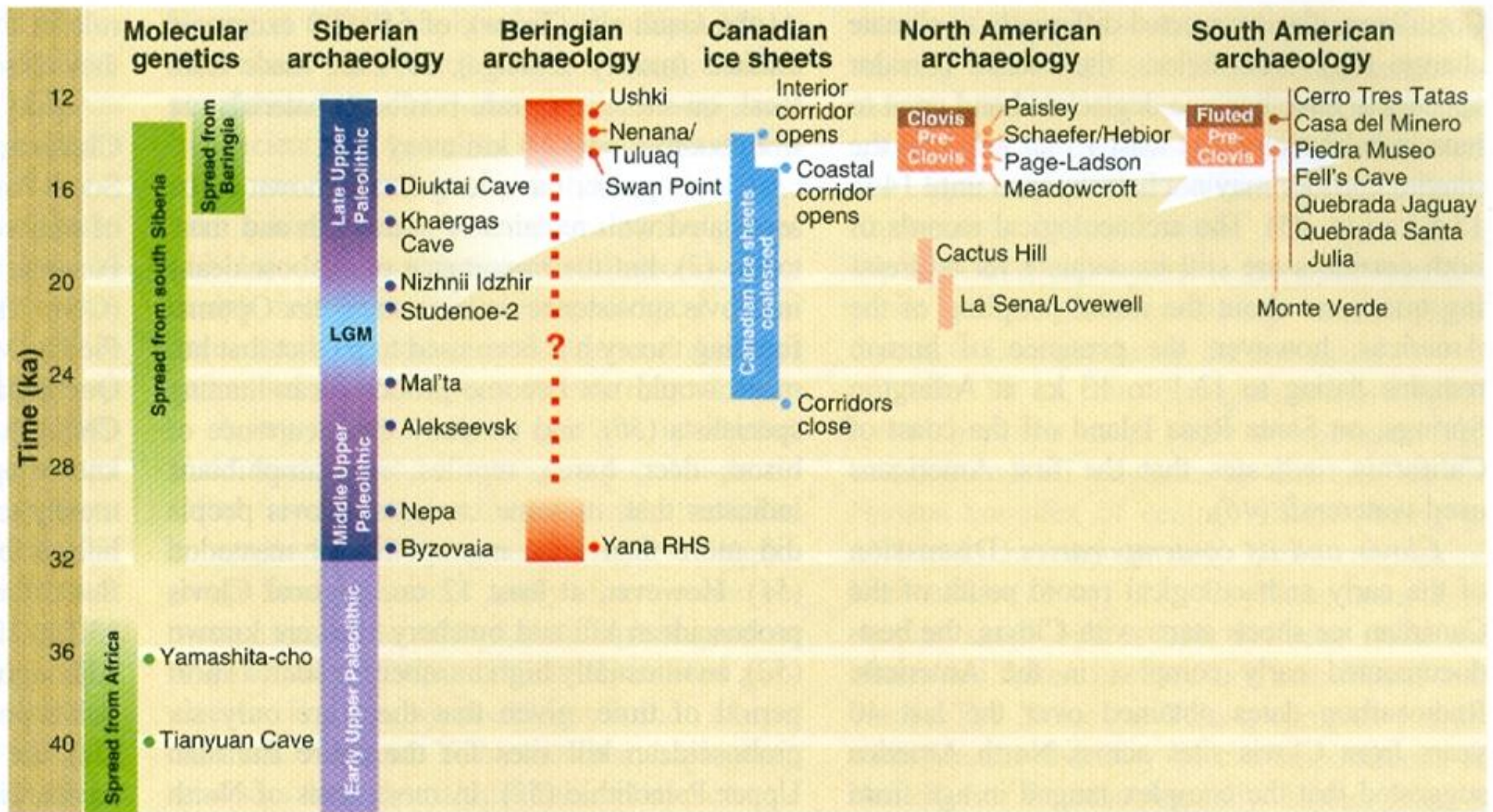
Later "Mongoloid" Skeletal Populations

Single Polymorphic Population from Beringia

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**Do I think there was only one early migration to the Americas? Of course not, even though our largest Y-chromosome database could only detect one migration statistically! Do I think there were exactly three as in the classic GTZ (1986) model? Probably not! I do know there had to be only one FIRST migration by definition, but after that, the field is still wide open (place your bets!)**





**Fig. 3.** Combined, the molecular genetic and archaeological records from Siberia, Beringia, and North and South America suggest humans dispersed from southern Siberia shortly after the last glacial maximum (LGM), arriving in the Americas as the Canadian ice sheets receded and the Pacific coastal corridor opened, 15 ka.