Estimating Admixture Graphs with *qpGraph*

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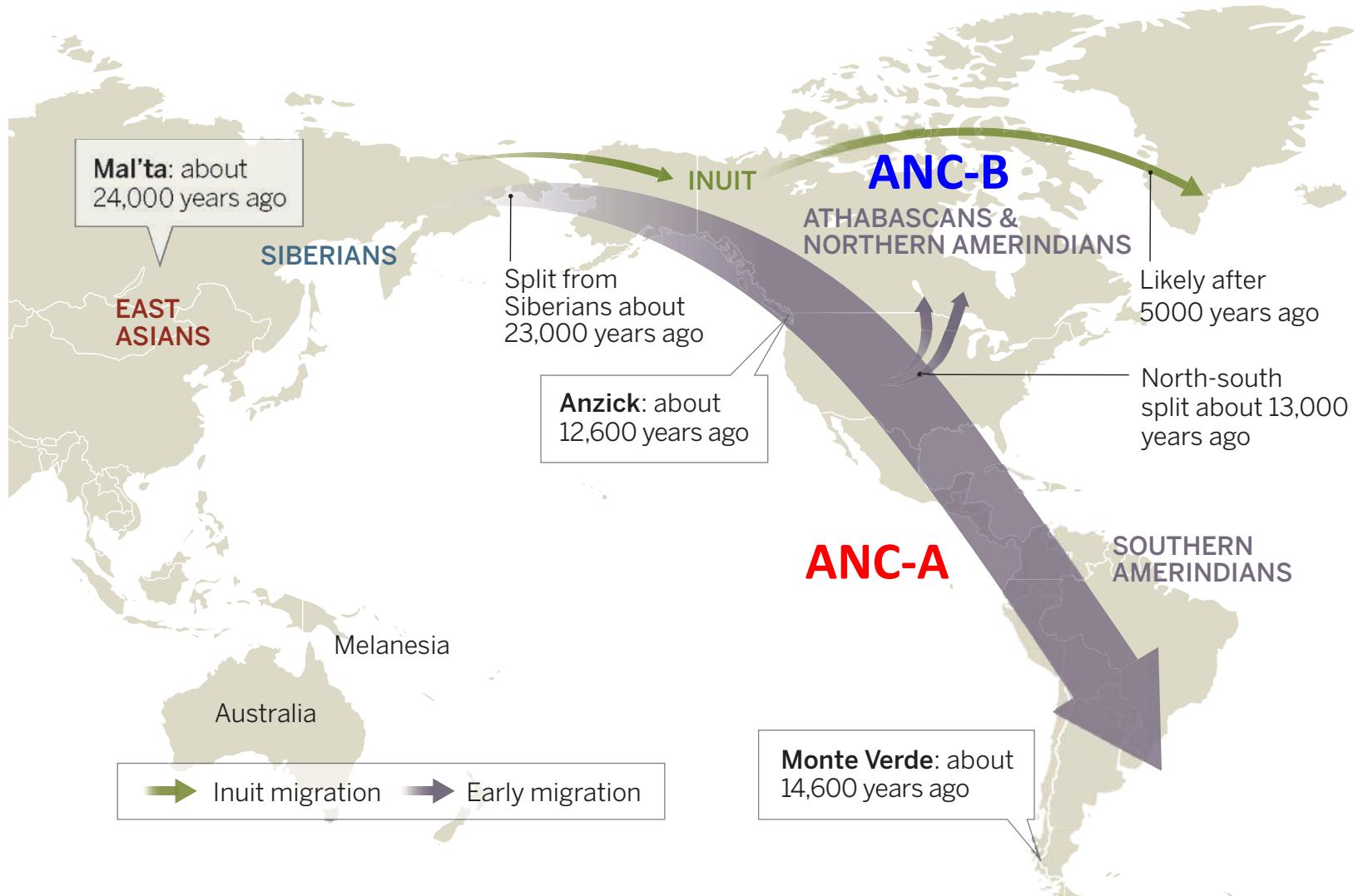
Workshop on Computational Population Genetics

Max Planck Institute for the Science of Human History, Jena

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Settlement of the Americas

Mal'ta: about 24,000 years ago

SIBERIANS

EAST ASIANS

Split from Siberians about 23,000 years ago

Anzick: about 12,600 years ago

INUIT

ANC-B

ATHABASCANS & NORTHERN AMERINDIANS

Likely after 5000 years ago

North-south split about 13,000 years ago

ANC-A

SOUTHERN AMERINDIANS

Melanesia

Australia

Inuit migration   Early migration

Monte Verde: about 14,600 years ago
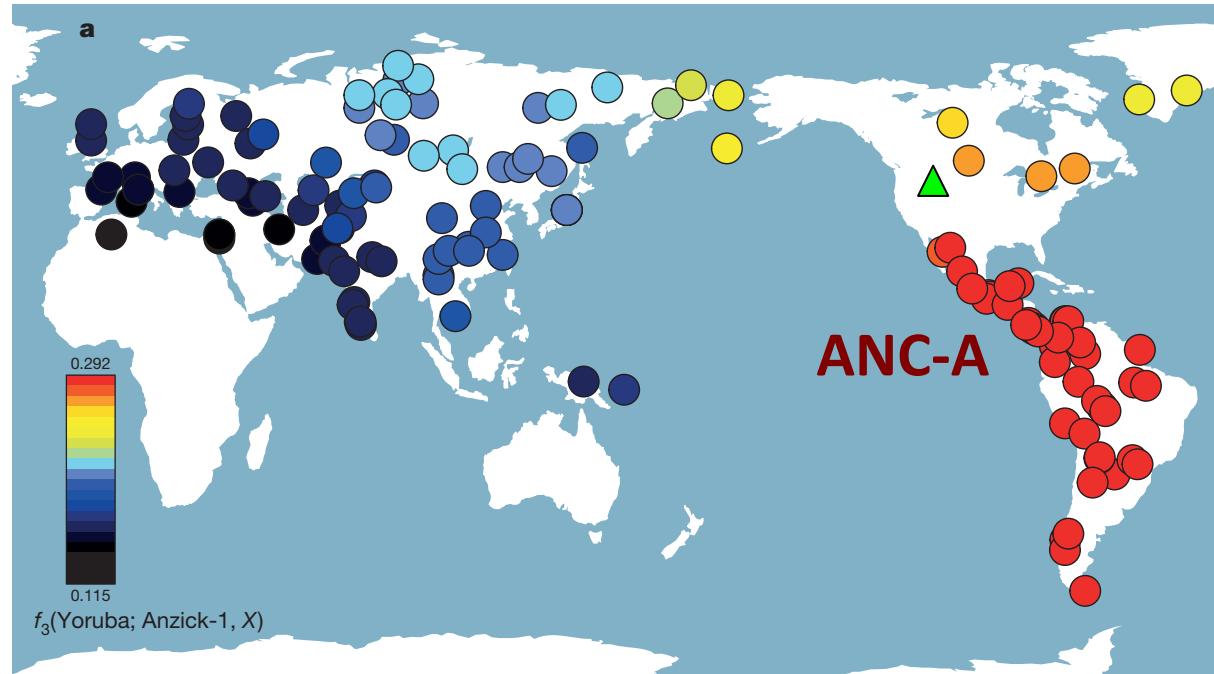
**Raghavan et al. 2015, Skoglund et al. 2015**

Oldest American genome

Anzick-1 ~12,800BP: Clovis-related culture
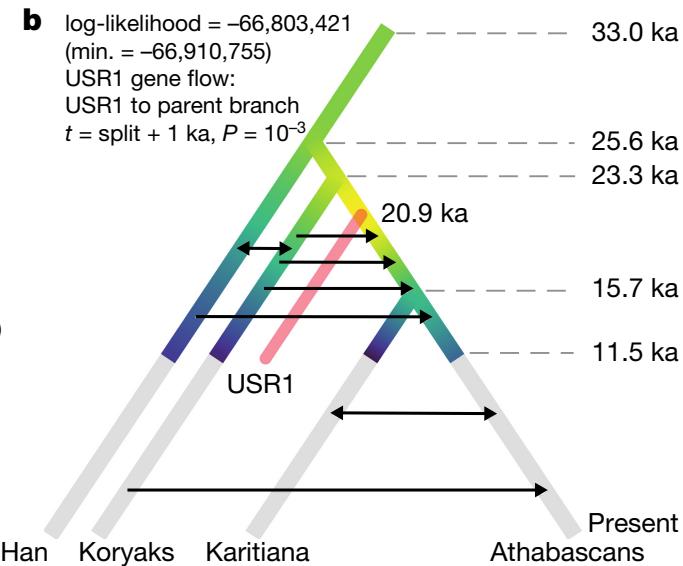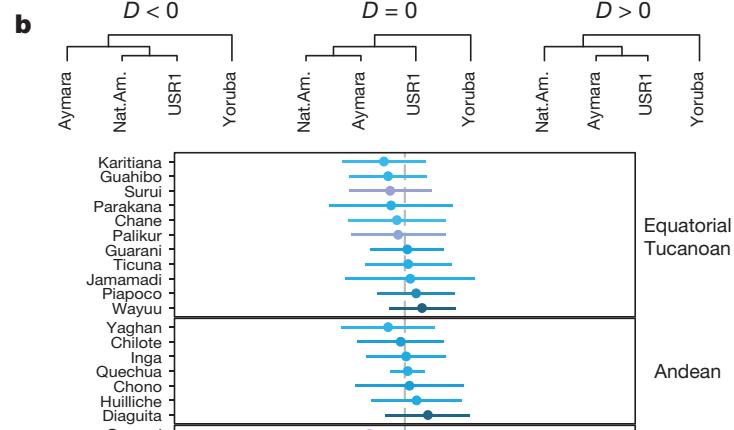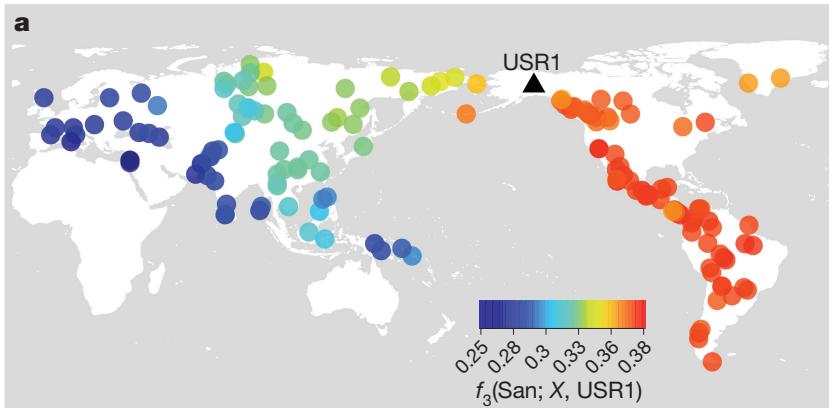
Credits: www.crystalinks.com, Naturex

ANC-A

f_3(Yoruba; Anzick-1, X)

Rasmussen et al. 2014

Ancient Beringians

USR1: ~11,500 BP

f_3(San; X, USR1)

log-likelihood = −66,803,421
(min. = −66,910,755)
USR1 gene flow:
USR1 to parent branch
t = split + 1 ka, $P = 10^{-3}$

33.0 ka
25.6 ka
23.3 ka
20.9 ka
15.7 ka
11.5 ka

USR1

Han   Koryaks   Karitiana   Present Athabascans
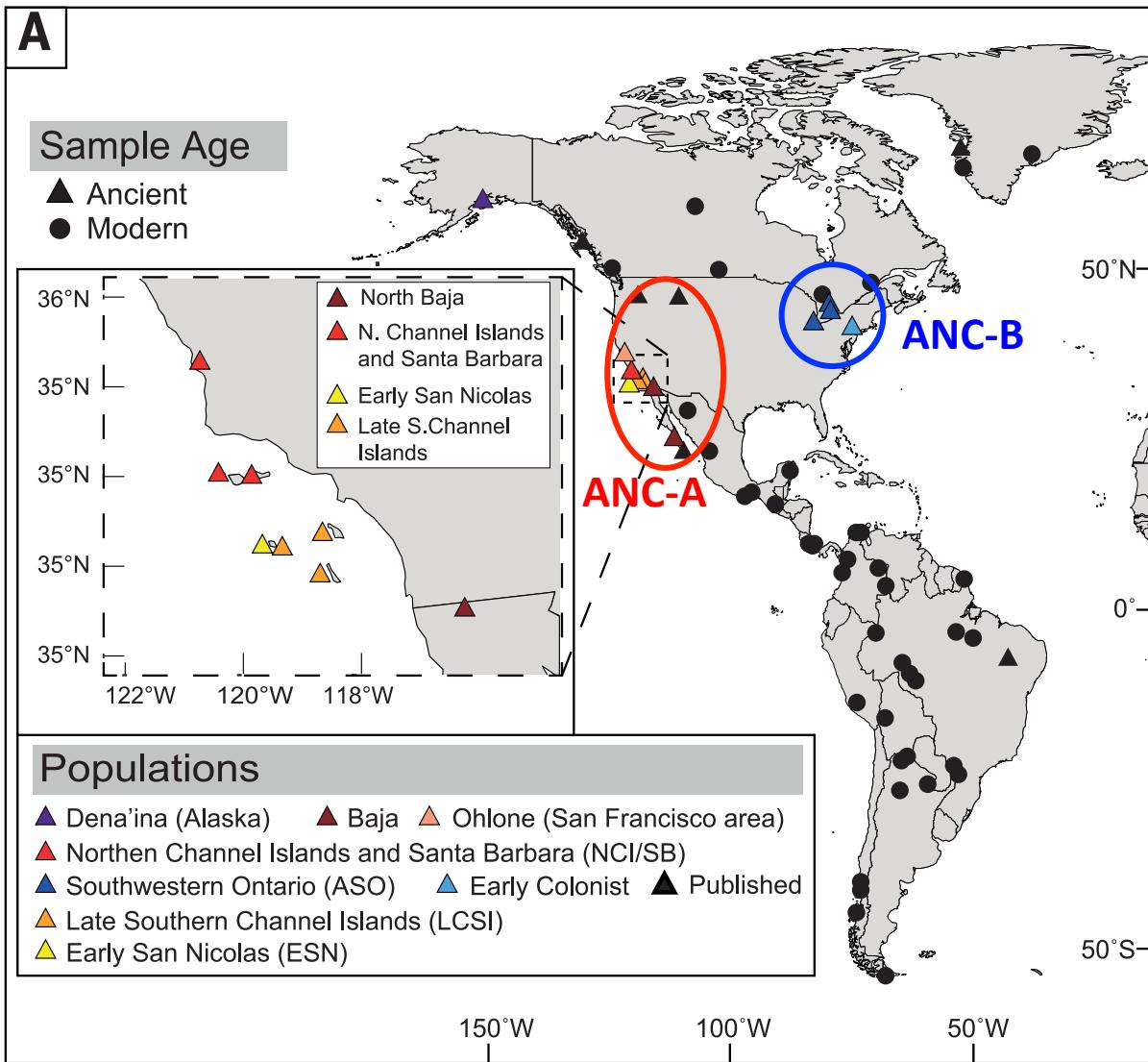
Moreno-Mayar et al. 2018

ANC-A and ANC-B ancestries

- San Nicolas (USA)
- Lucier (Canada)
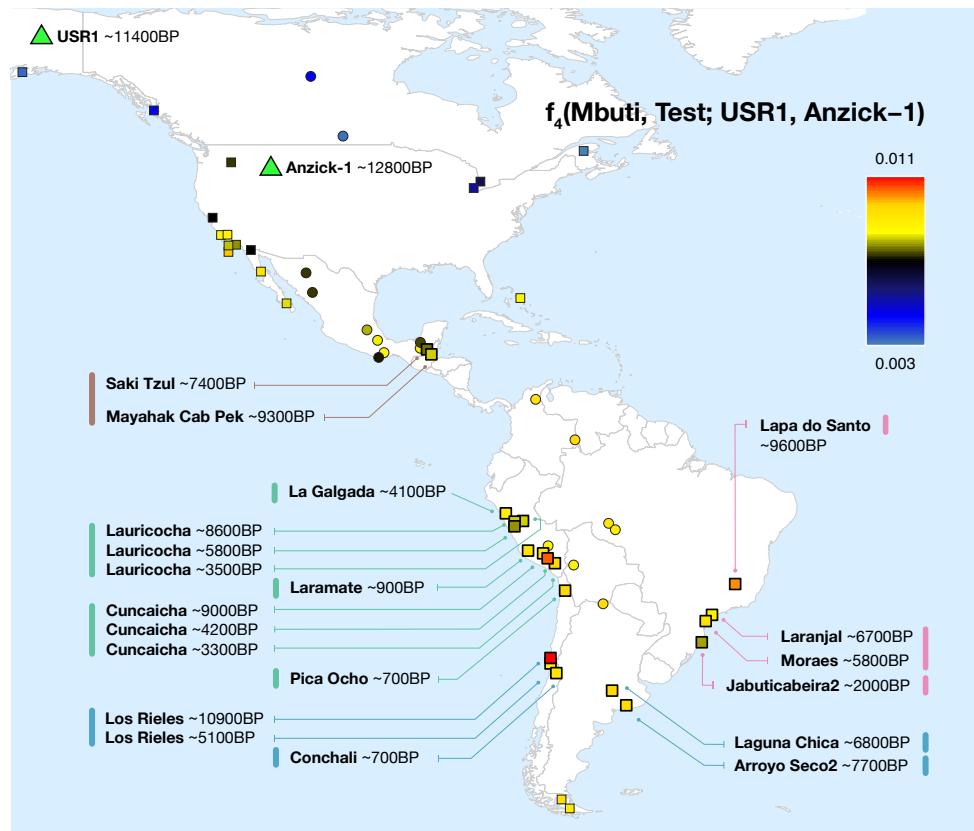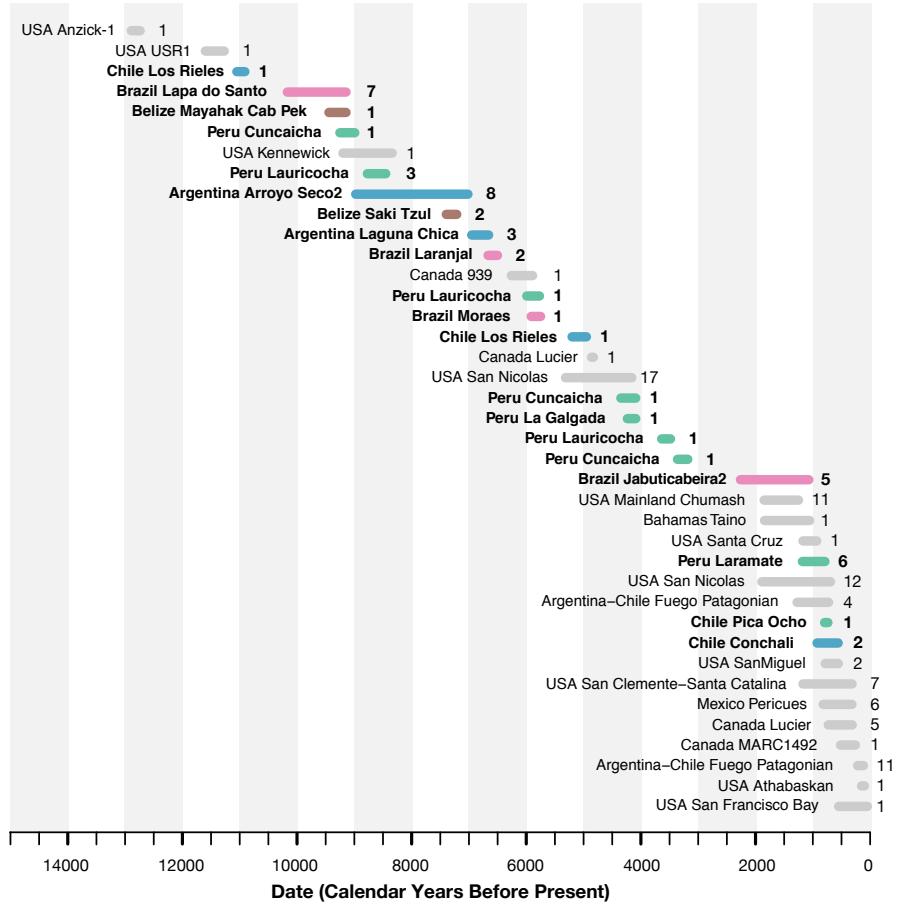
**Less than ~5,000 BP**

Scheib et al. 2018

49 individuals ~11,000-600 BP (35 older than 3,000 BP): four time transects

Posth et al. 2018
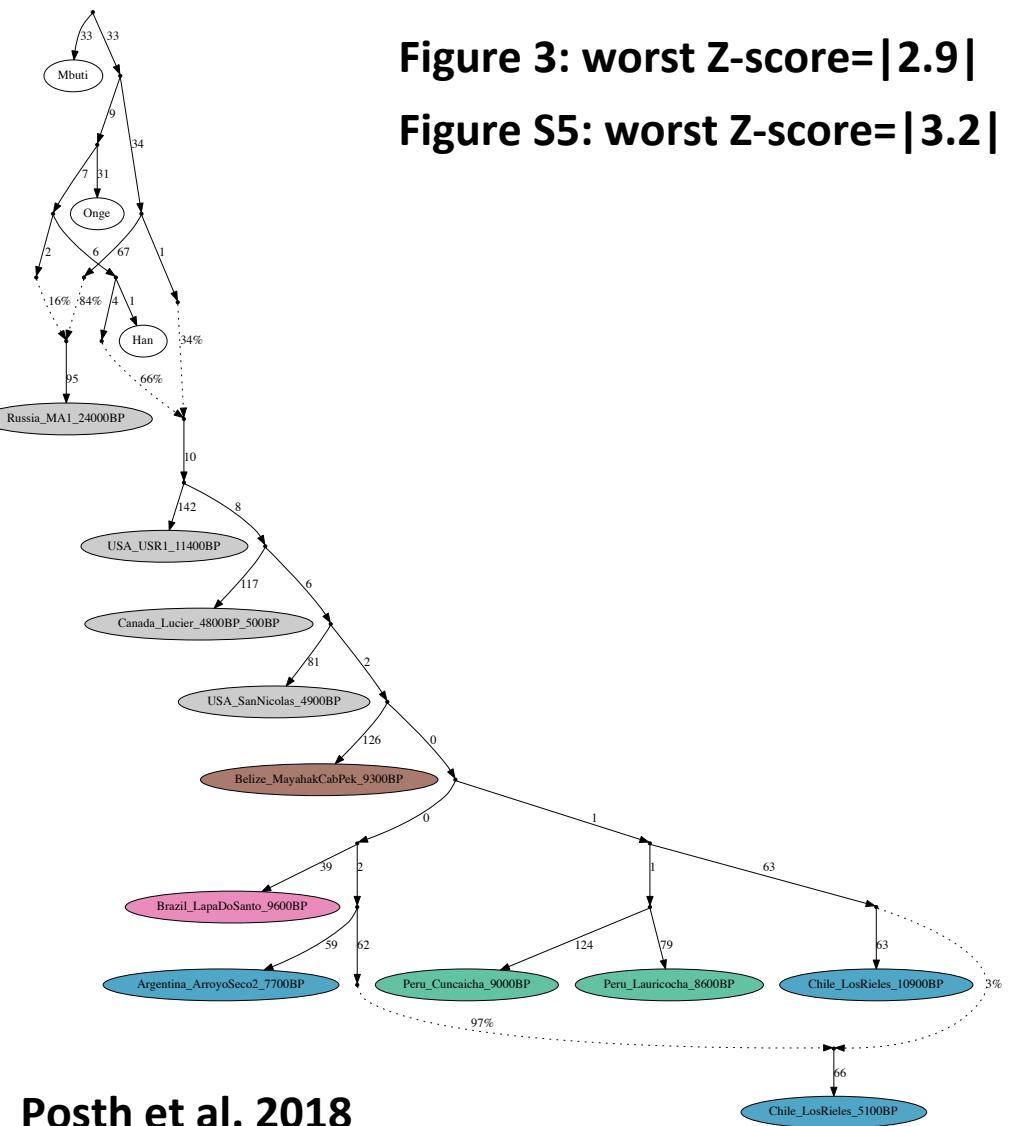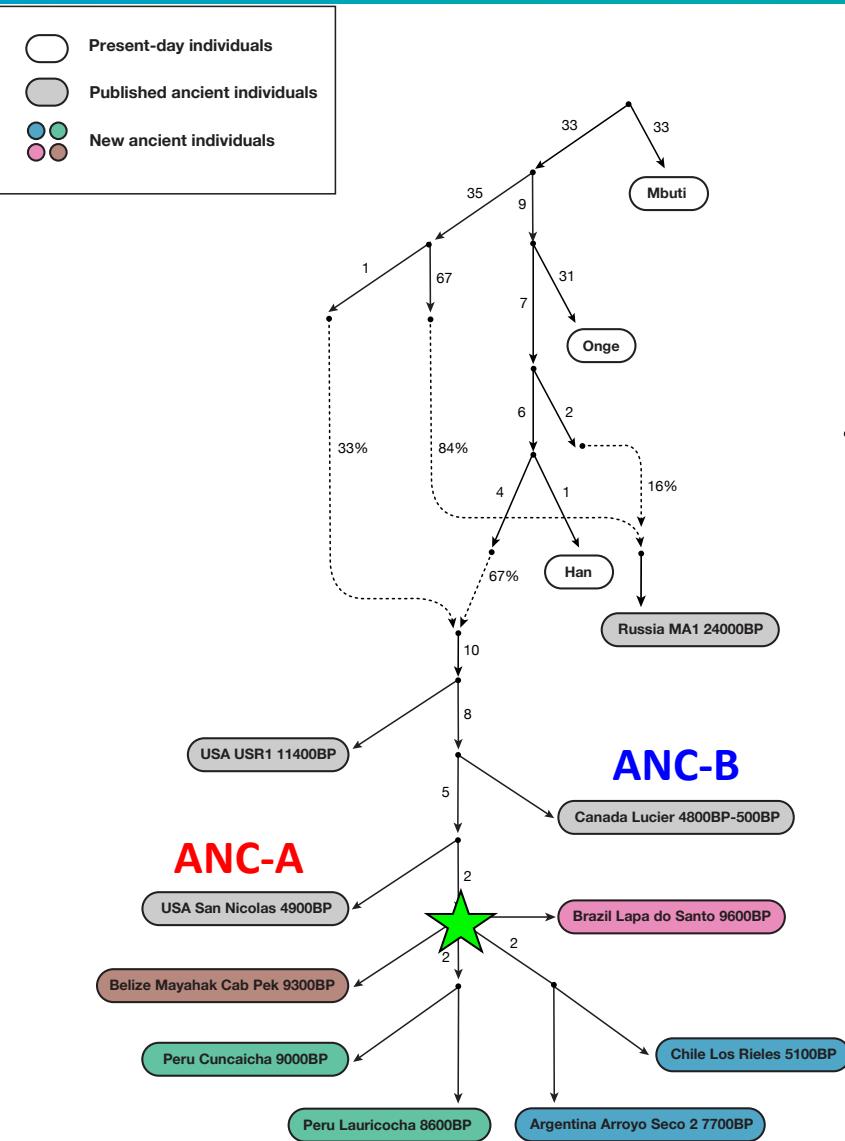
1. Does early Central and South American variation mirror the **population structure** we see today?

2. Minimum **number of genetic exchanges** between ancient South and North Americans?

3. Relationships among the ancient individuals **across regions and through time**?

qpGraph Early Americans

Figure 3: worst Z-score=|2.9|

Figure S5: worst Z-score=|3.2|
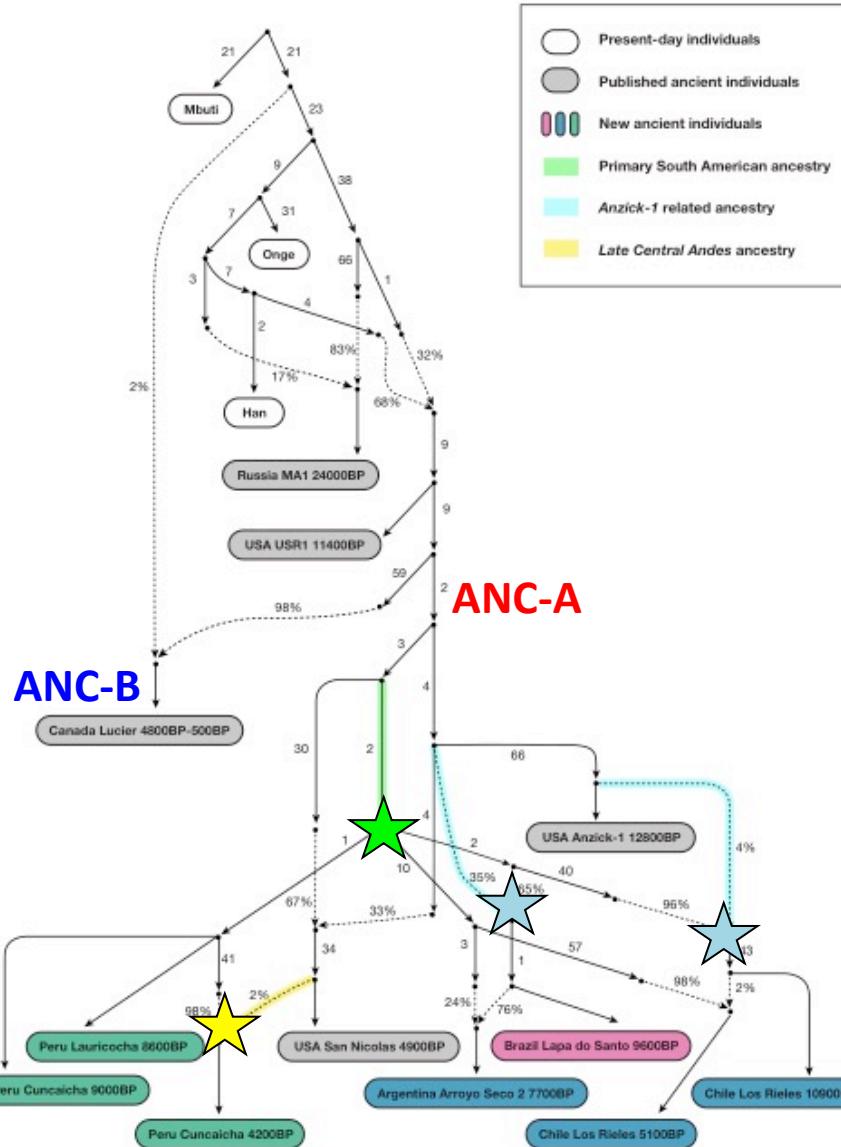
Posth et al. 2018

qpGraph modeling *Anzick-1*

Manual fitting

**Worst Z-score=|3.4|**
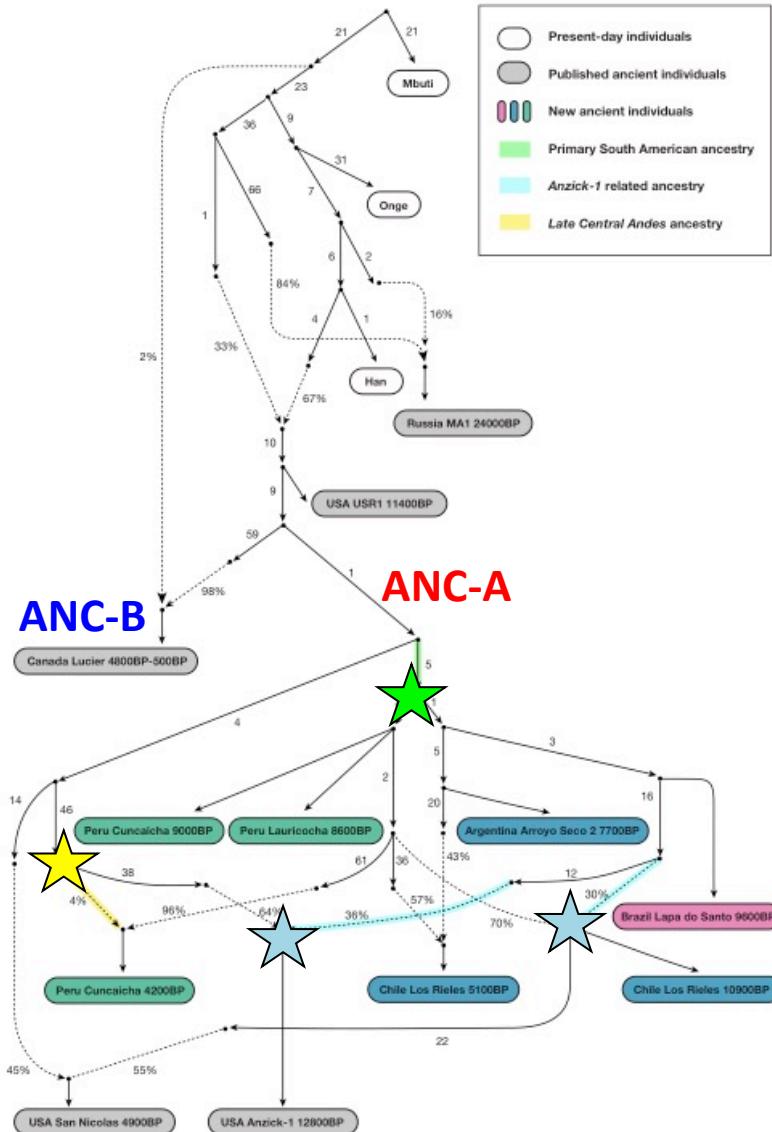
Posth et al. 2018

qpGraph modeling *Anzick-1*

Authomatic fitting Lazaridis et al. 2018 bioRxiv

Worst Z-score=|2.9|

Posth et al. 2018

Let's start building Admixture Graphs with *qpGraph* !

Credits: Michelle O'Reilly,MPI Science of Human History, Jena