

2,000 years of genomic recovery from pre-Columbian agriculture in the Amazon

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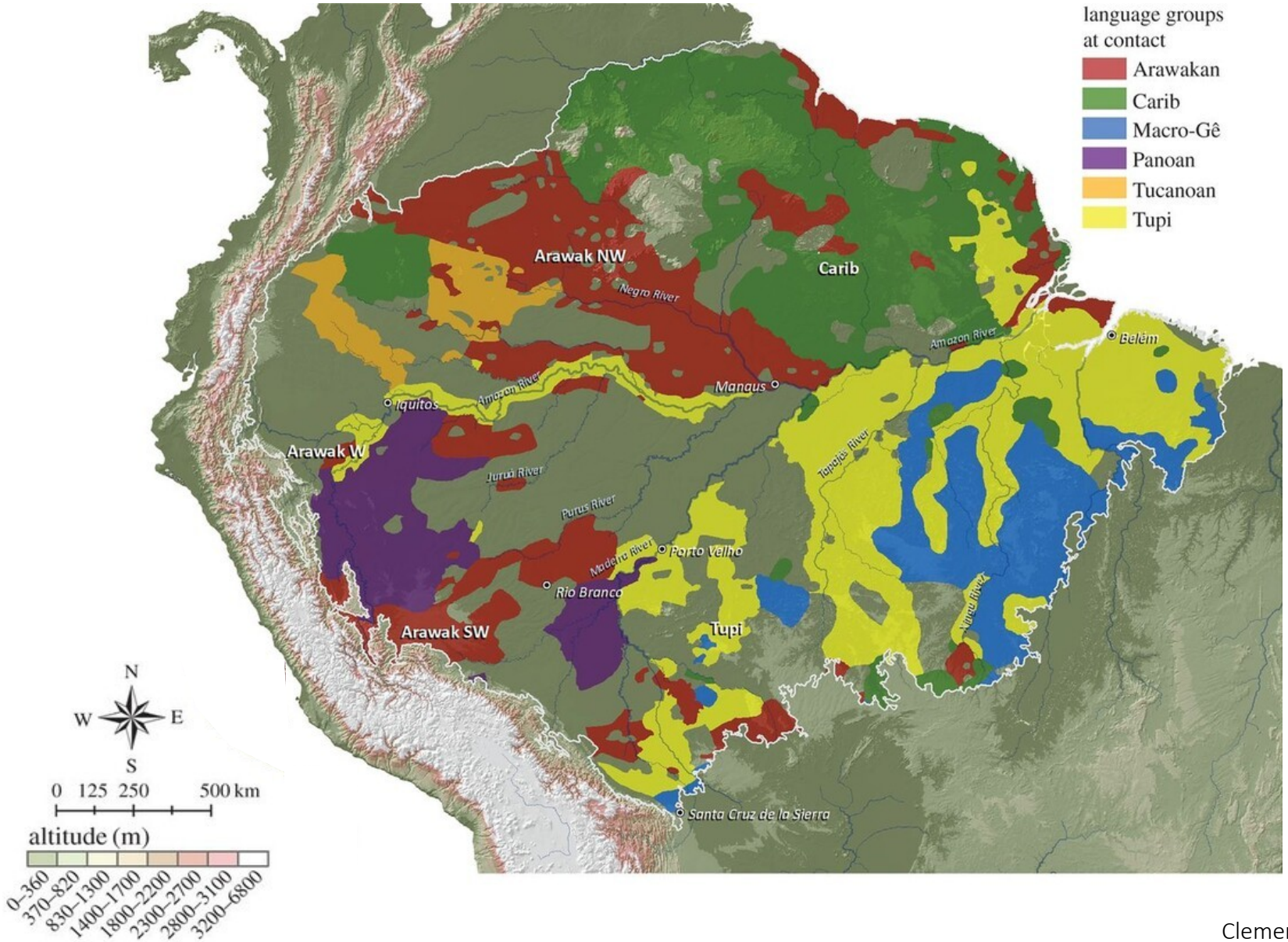
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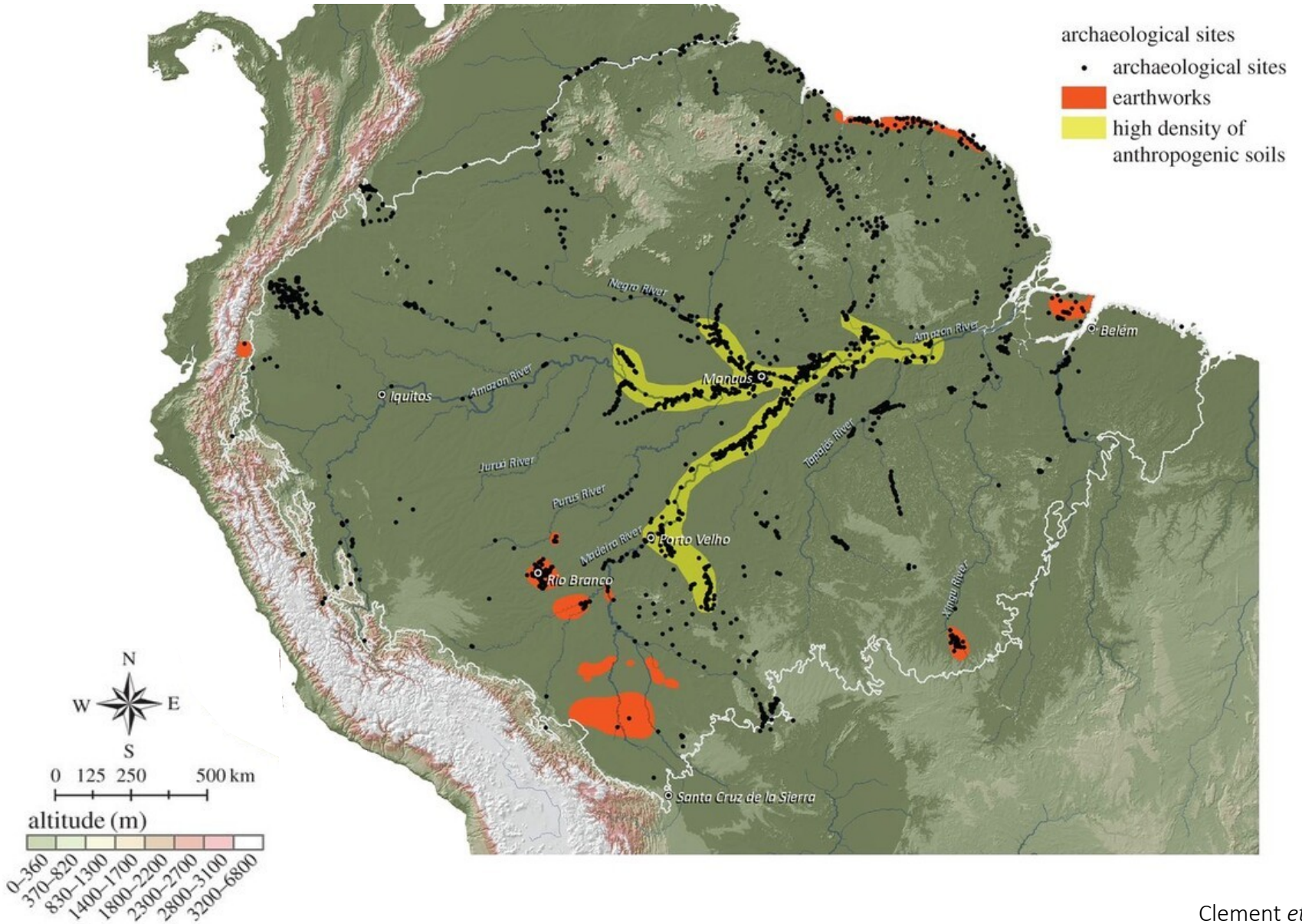
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We investigate the agricultural legacy of a widely populated Amazon



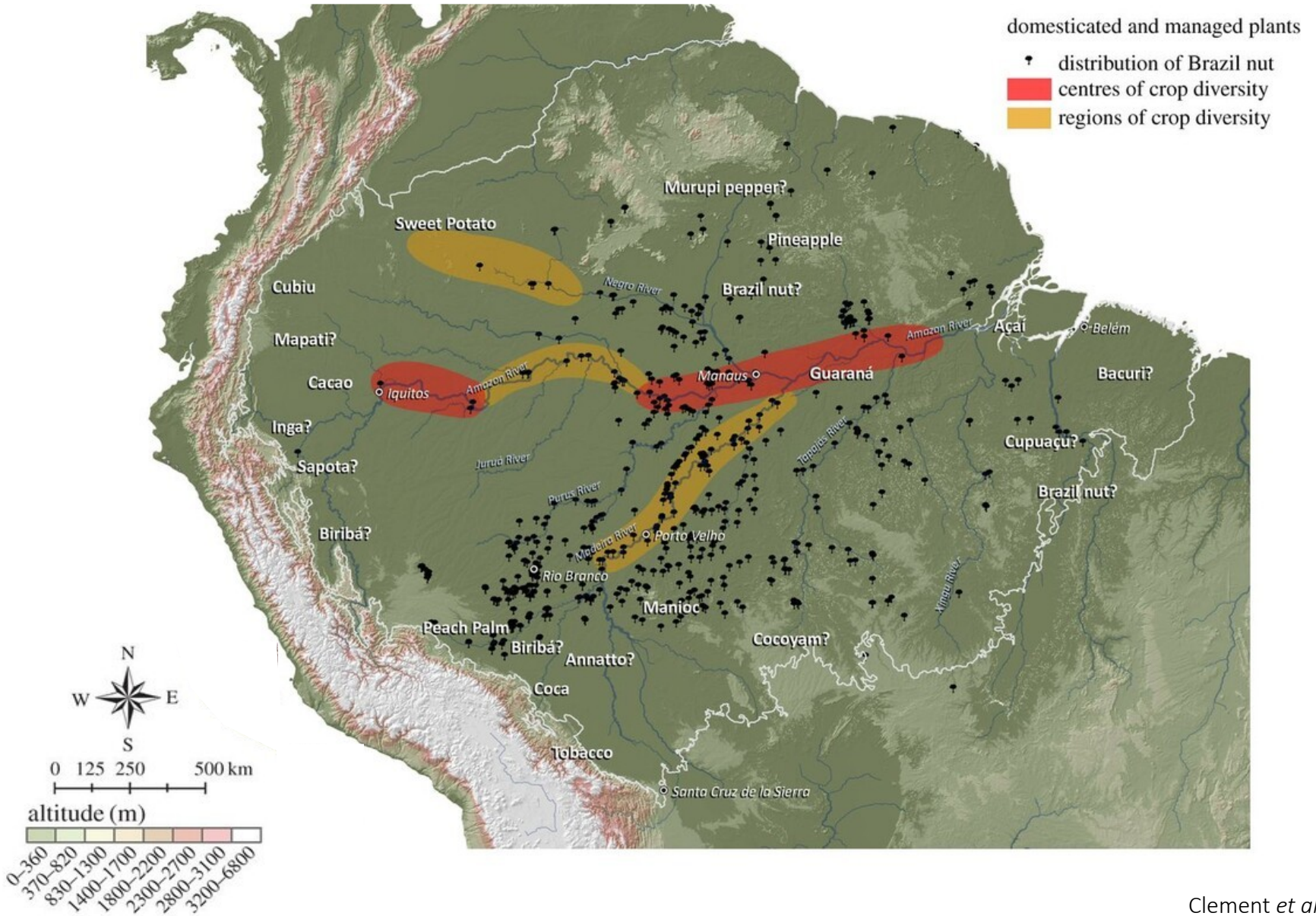
Clement *et al.* 2015. *Proceeding Royal Society B*

We investigate the agricultural legacy of a widely populated Amazon



Clement *et al.* 2015. *Proceeding Royal Society B*

We focus on domesticate species, including the Brazil nut

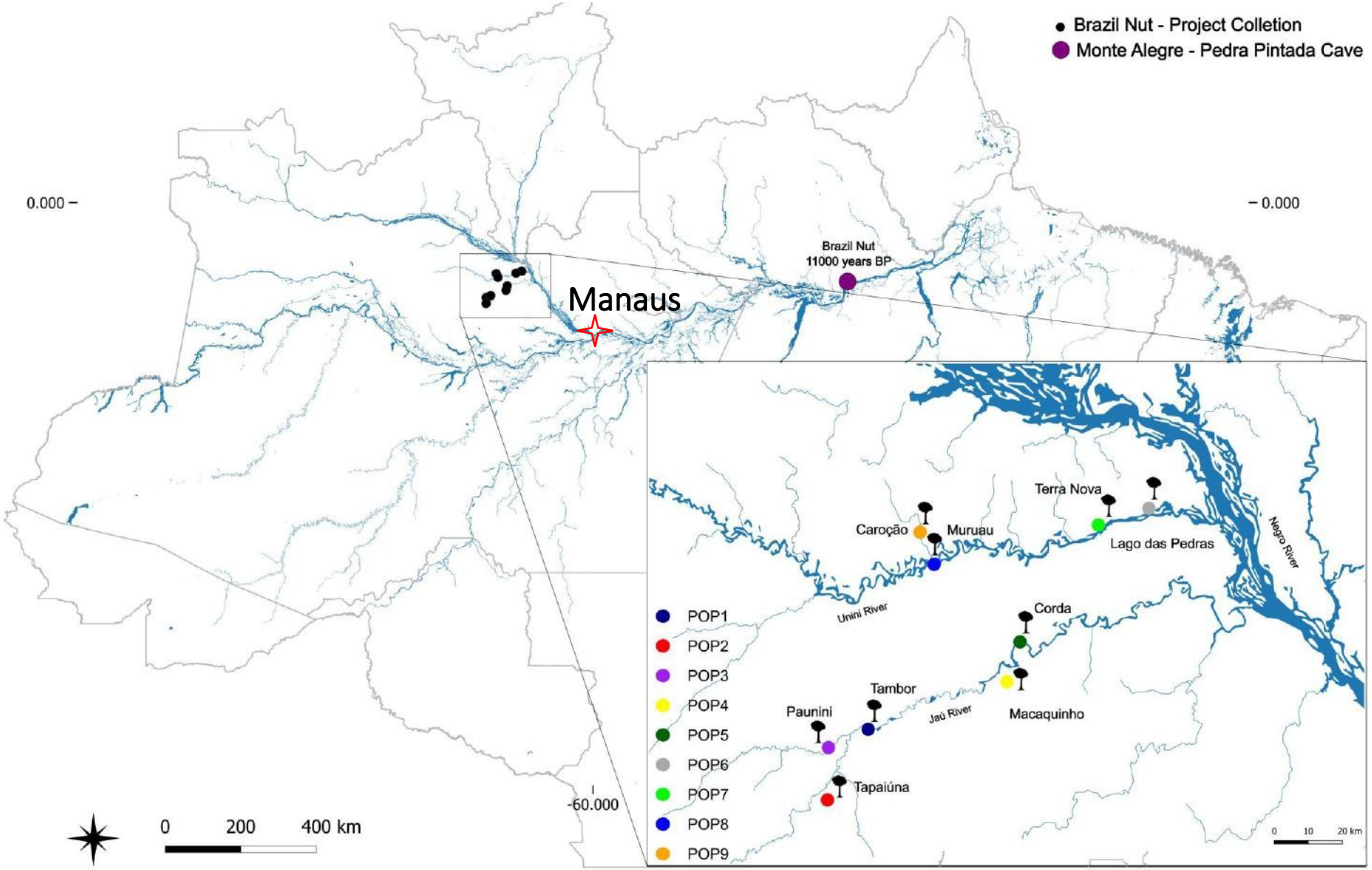


Clement *et al.* 2015. *Proceeding Royal Society B*


TRUM

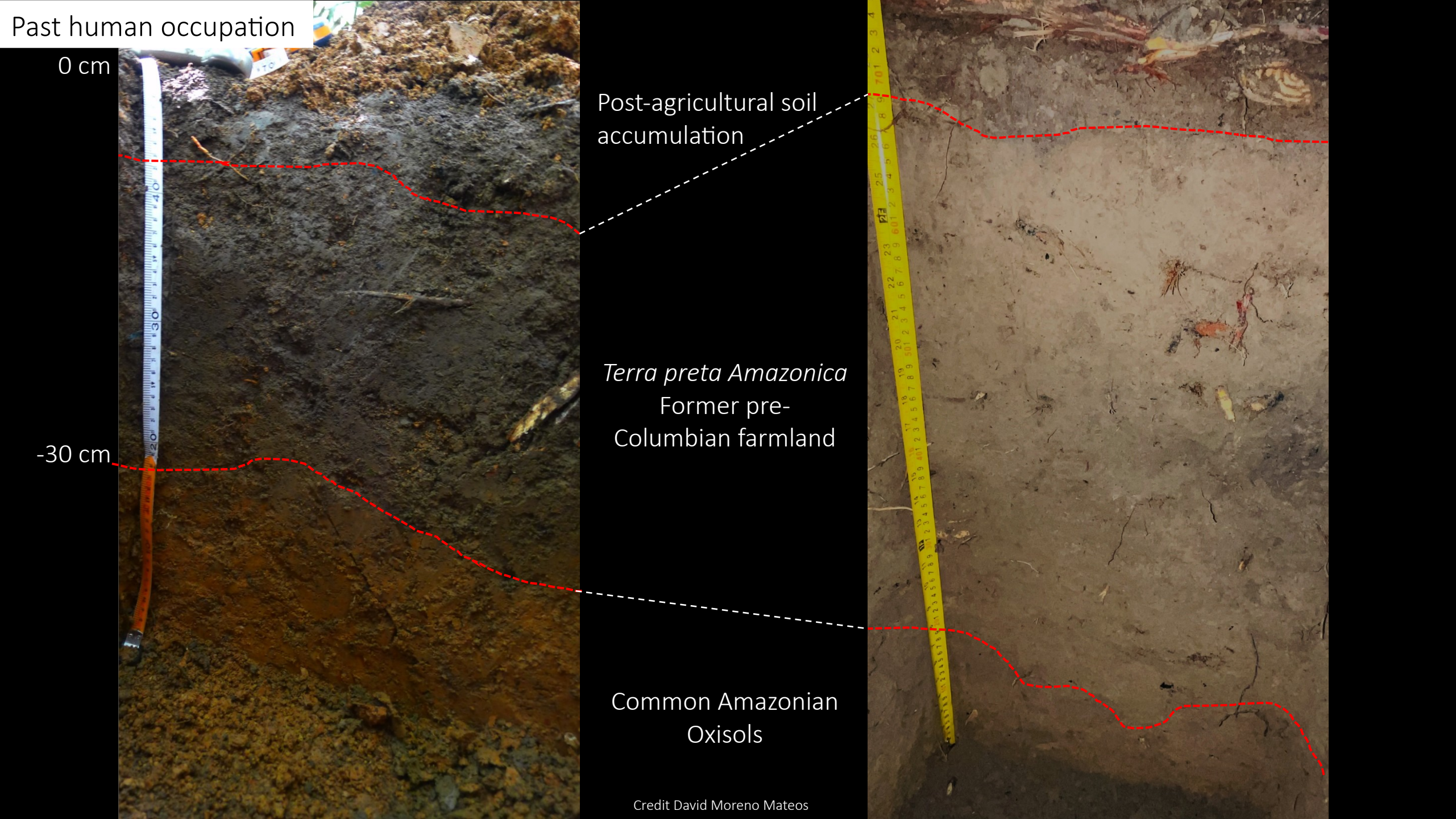
Measuring recovery

We are reconstructing a 2,000-year post-agricultural chronosequence








Past human occupation
0 cm
-30 cm
Post-agricultural soil accumulation
Terra preta Amazonica
Former pre-Columbian farmland
Common Amazonian Oxisols
Credit David Moreno Mateos









We are sequencing the
whole genome at the community level

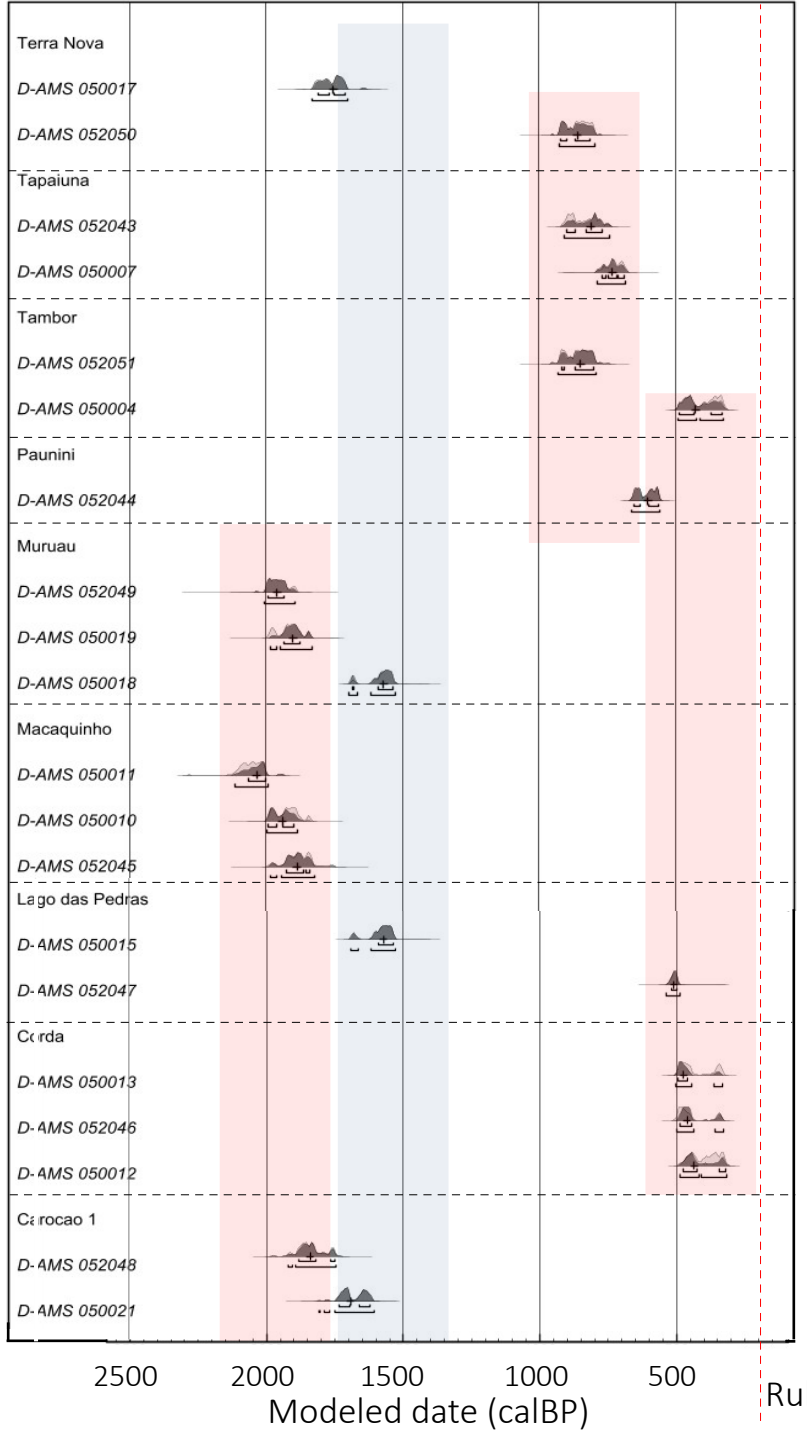
We focus on Brazil nut, Uxi, Piquiá and Mata-mata

1. What regions have changed since the release from domestication?
2. What functions relate to those regions?
3. Has the species recovered its adaptive potential?

Pre-Columbian agricultural occupation lasted for 2,000 years

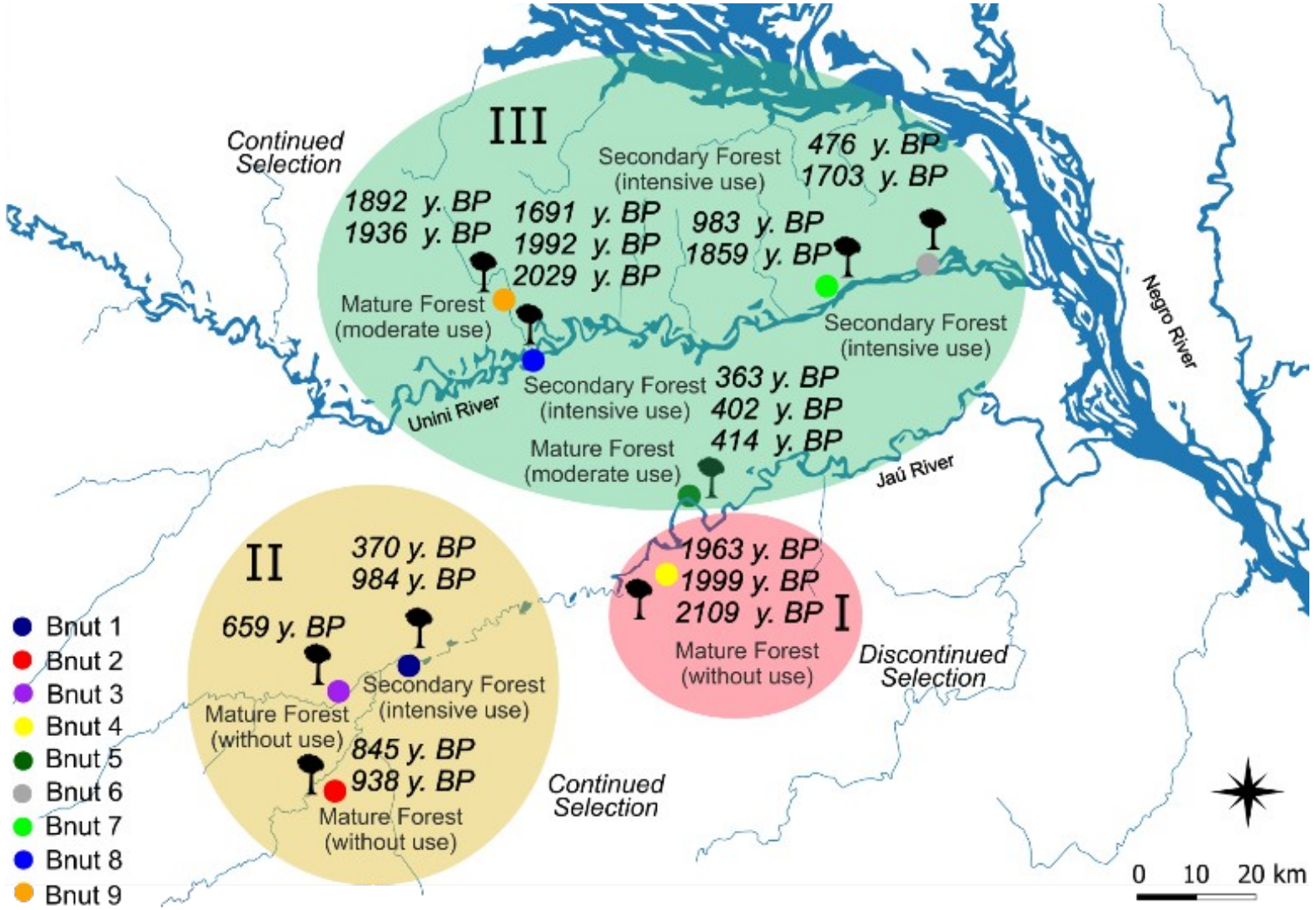
Based on ^{14}C dating

1. Farms either had a short-term agricultural signal, likely <100 years
2. Or have a 300-year occupation periods
3. Alternative, there could be discrete occupation events



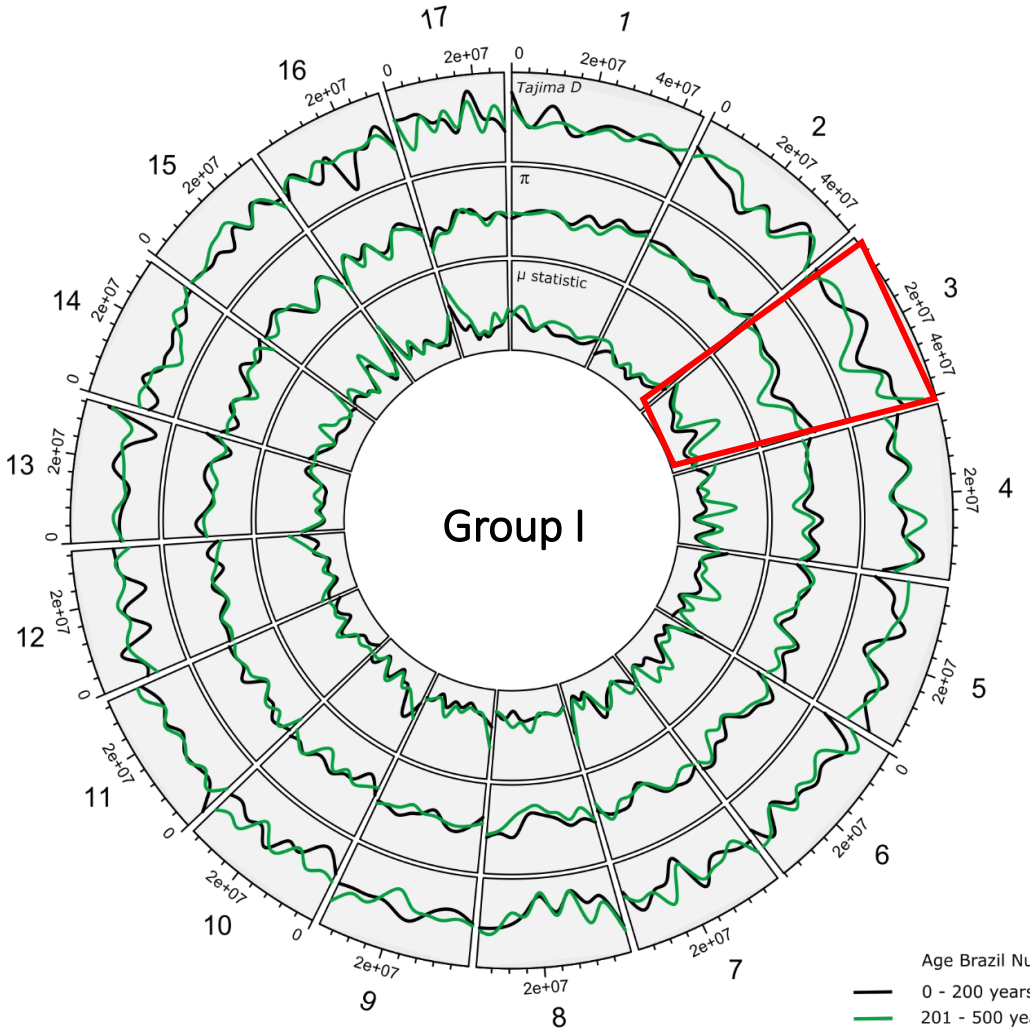
Population structure indicates possible human historic dispersal

Three populations with many unique gene outliers

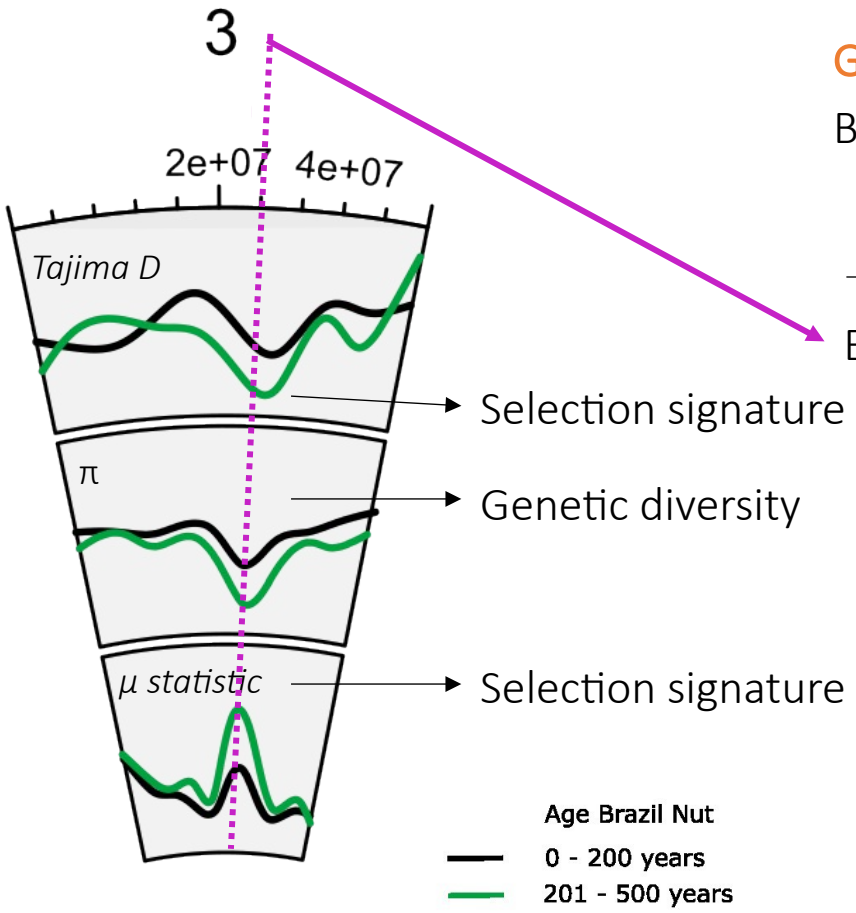


Whole-genome sequencing shows signs of genome recovery from domestication within 500 years

Using dendrochronologies



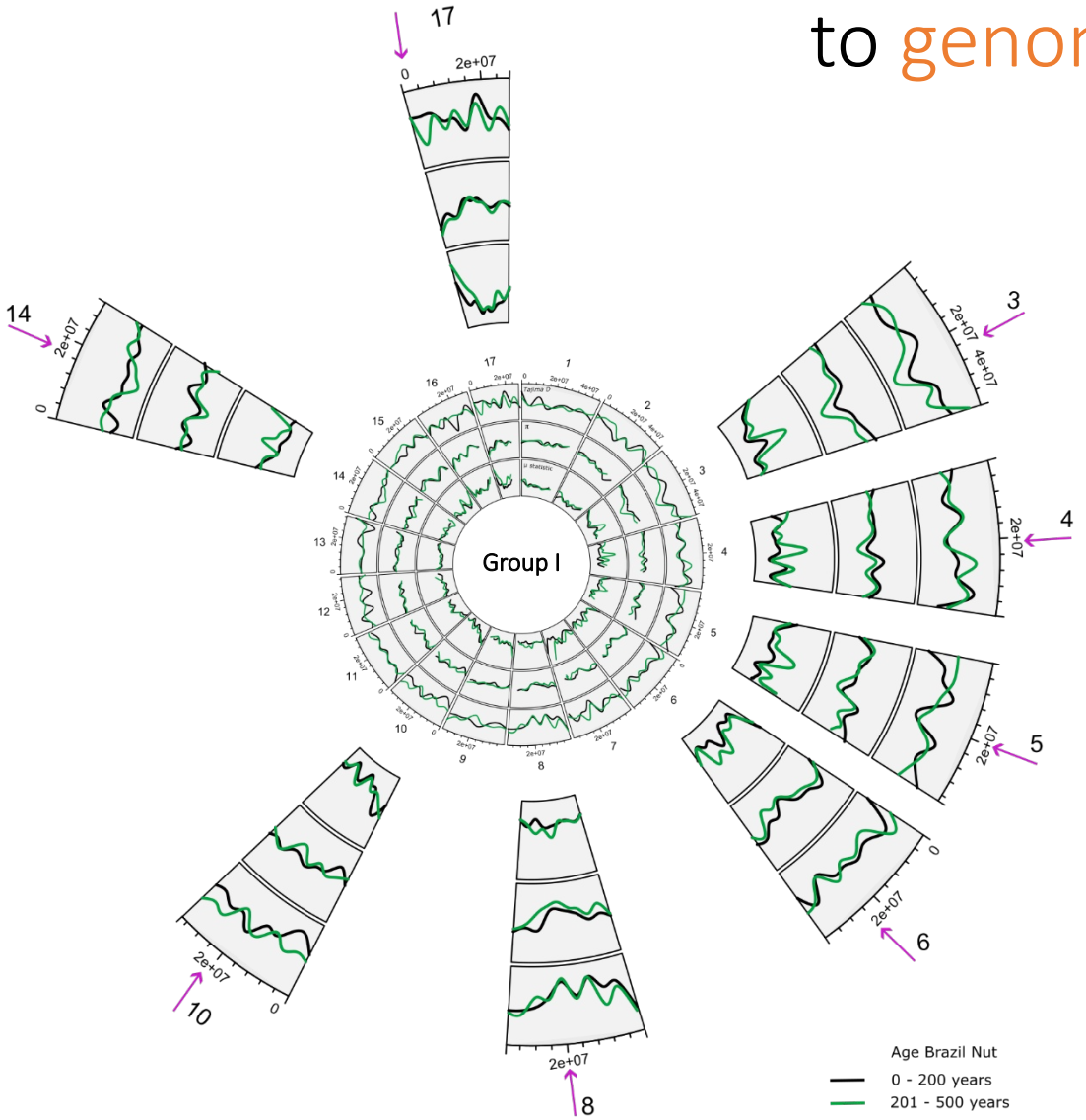
Are selection signatures related to domestication genes and hence to genomic recovery?



Gene (chromosome)	Annotation	Function
Bex-01:01821 (1)	C2-domain-(Calcium/lipid-binding-domain,-CaLB)	Intracellular communication, stress response, cell growth
Bex-04:22670 (3)	Bifunctional-inhibitor/lipid-transfer-protein/seed-storage-2S-albumin	Lipid transport, reserve storage, protection against pathogens

Maybe showing changes in seed resources allocation and size?

Are selection signatures related to domestication genes and hence to genomic recovery?



We found at least eight chromosomes with genes showing some kind of selection signatures in one of the populations

Summary

1. Archeological chronologies can help reconstruct agricultural past
2. Waves of human occupation may have shaped the structure of the current Brazil nut populations
3. We are starting to find changes in selection signatures, potentially indicating genomic recovery
4. Will we find an ecosystem level genomic recovery signal?

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