# Introducing the sample and the collaborators

Data collection from Khoisan and Bantu speakers of Southern Africa: Namibia, Botswana, Angola and Zambia

Max Planck Institute
for Evolutionary Anthropology

Speaking (of) Khoisan

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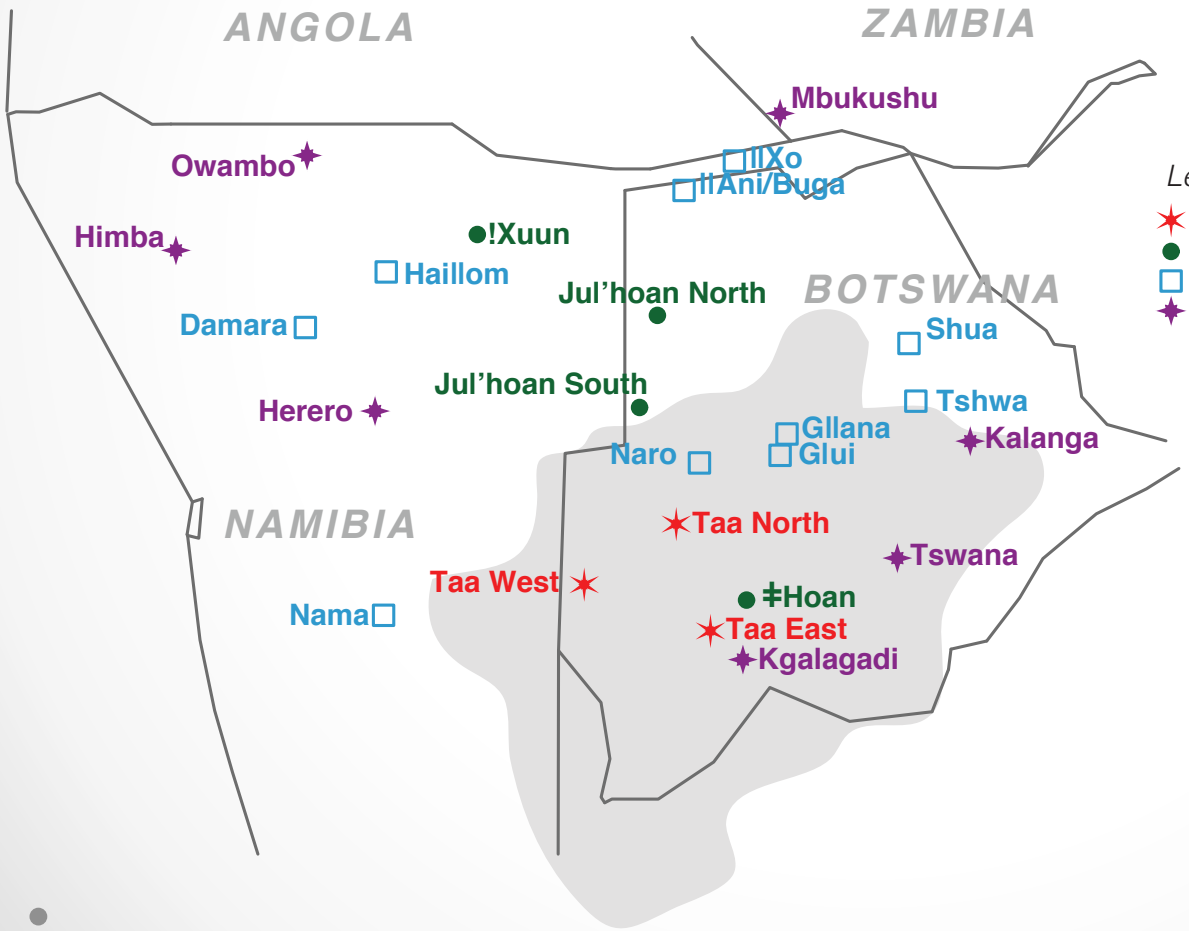
# Kalahari Basin Area

Endangered Language & Population History Research

# Sampling collection

- Khoisan (Kx'a, Khoe-Kwadi, Tuu) and Bantu speaking populations from **Botswana** and **Namibia**
- Samples collected by B Pakendorf, M Stoneking, C Barbieri, T Güldemann, C Naumann, SW Mpoloka, L Gerlach, F Bertholdt, H Nakagawa, B Kure
- Data analyzed for mtDNA sequence, Y chromosome sequence and autosomal SNPs

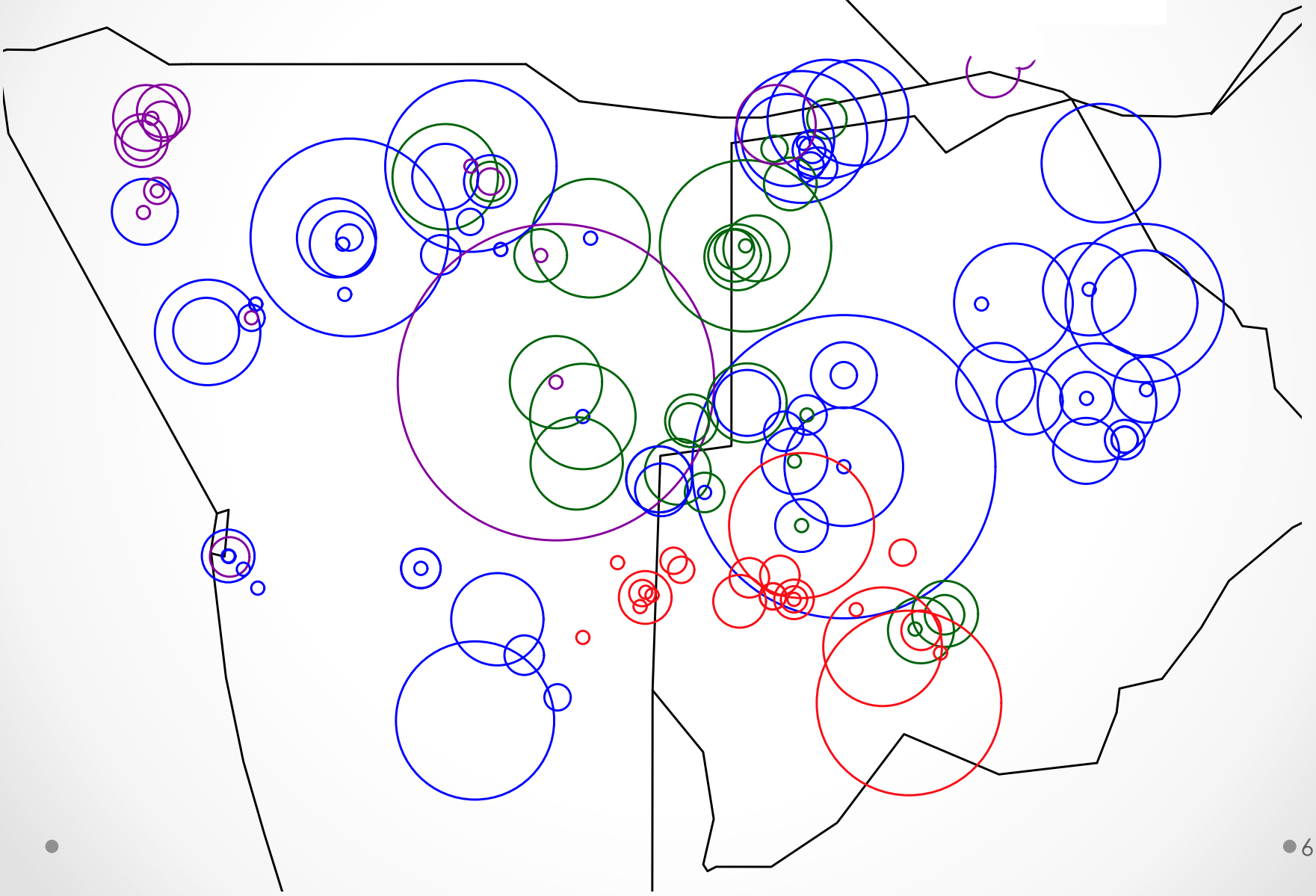
# Dataset KBA




*Legend: Language Family*

- Tuu
- Kx'a
- Khoe-Kwadi
- Bantu

Villages sampled
(circles proportional to sample size)

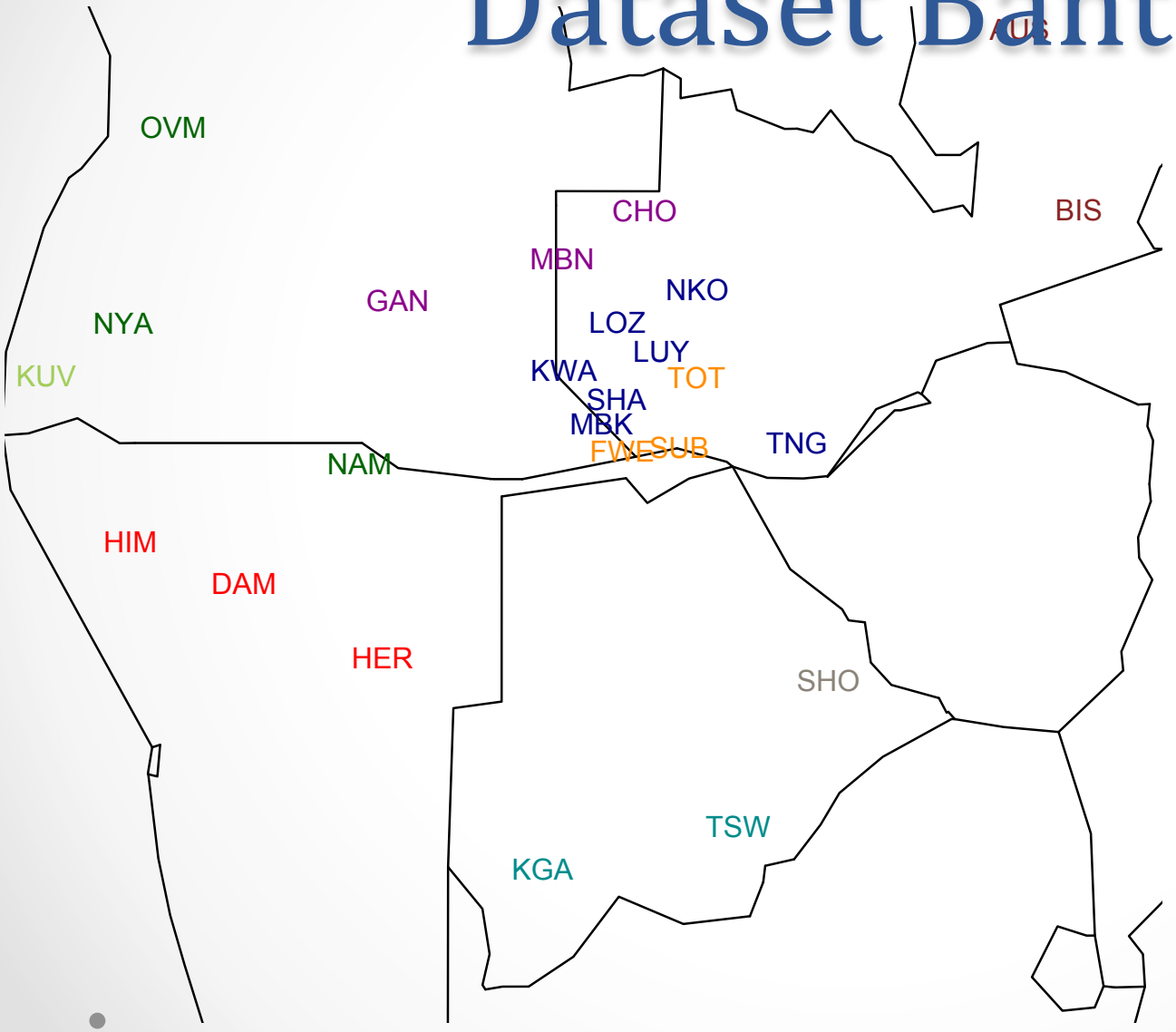


# Bantu speakers project

- Samples from Bantu speaking populations of Angola and Zambia
- Samples collected by B Pakendorf, M Stoneking, J Rocha, S Oliveira, K Bostoen, C de Filippo, E Gunnarsdóttir

- Data analyzed for mtDNA sequence, Y chromosome SNPs, STRs and sequences, and autosomal SNPs

# Dataset Bantu




26 pops, 982 individuals

ANG_NAM
KUV
NW_NAM
TSWA
SHONA
SW_ZAM
SUB
CHOK
NE_ZAM
ZAM_mix

# Main publications

ARTICLE → AUTOSOMAL

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DOI: 10.1038/ncomms2140

## The genetic prehistory of southern Africa

Joseph K. Pickrell[1], Nick Patterson[2], Chiara Barbieri[3,†], Falko Berthold[3,†], Linda Gerlach[3,†], Tom Güldemann[4,5], Blesswell Kure[6], Sununguko Wata Mpoloka[7], Hirosi Nakagawa[8], Christfried Naumann[4,5], Mark Lipson[9,10], Po-Ru Loh[9,10], Joseph Lachance[11,12], Joanna Mountain[13], Carlos D. Bustamante[14], Bonnie Berger[9,10], Sarah A. Tishkoff[11,12], Brenna M. Henn[14], Mark Stoneking[15], David Reich[1,2] & Brigitte Pakendorf[3,†]

→ mtDNA

AMERICAN JOURNAL OF PHYSICAL ANTHROPOLOGY 153:435–448 (2014)

## Unraveling the Complex Maternal History of Southern African Khoisan Populations

Chiara Barbieri,[1*] Tom Güldemann,[2,3] Christfried Naumann,[2,3] Linda Gerlach,[1] Falko Berthold,[1] Hirosi Nakagawa,[4] Sununguko W. Mpoloka,[5] Mark Stoneking,[6] and Brigitte Pakendorf[1*]

# Main publications

AUTOSOMAL

Current Biology 24, 875–879, April 14, 2014 ©2014 Elsevier Ltd All rights reserved

## Tracing Pastoralist Migrations to Southern Africa with Lactase Persistence Alleles

Enrico Macholdt,[1] Vera Lede,[1] Chiara Barbieri,[1,5] Sununguko W. Mpoloka,[2] Hua Chen,[3] Montgomery Slatkin,[3] Brigitte Pakendorf,[4,*] and Mark Stoneking[1,*]

mtDNA

OPEN ACCESS Freely available online

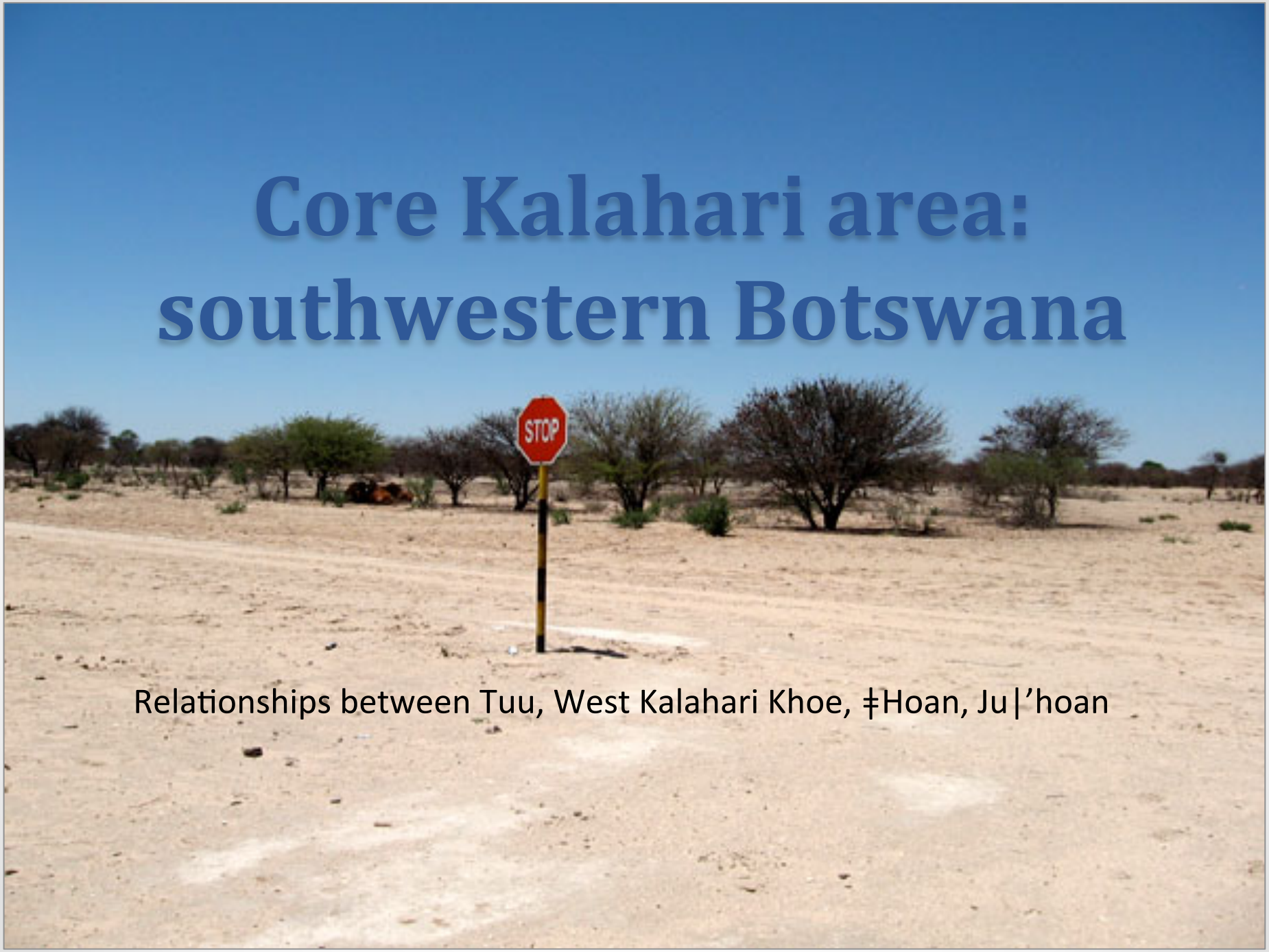
PLOS ONE

## Migration and Interaction in a Contact Zone: mtDNA Variation among Bantu-Speakers in Southern Africa

Chiara Barbieri[1,2*], Mário Vicente[3,4¤], Sandra Oliveira[3,5], Koen Bostoen[6,7], Jorge Rocha[3,5], Mark Stoneking[1], Brigitte Pakendorf[8*]

- Y chromosome in preparation

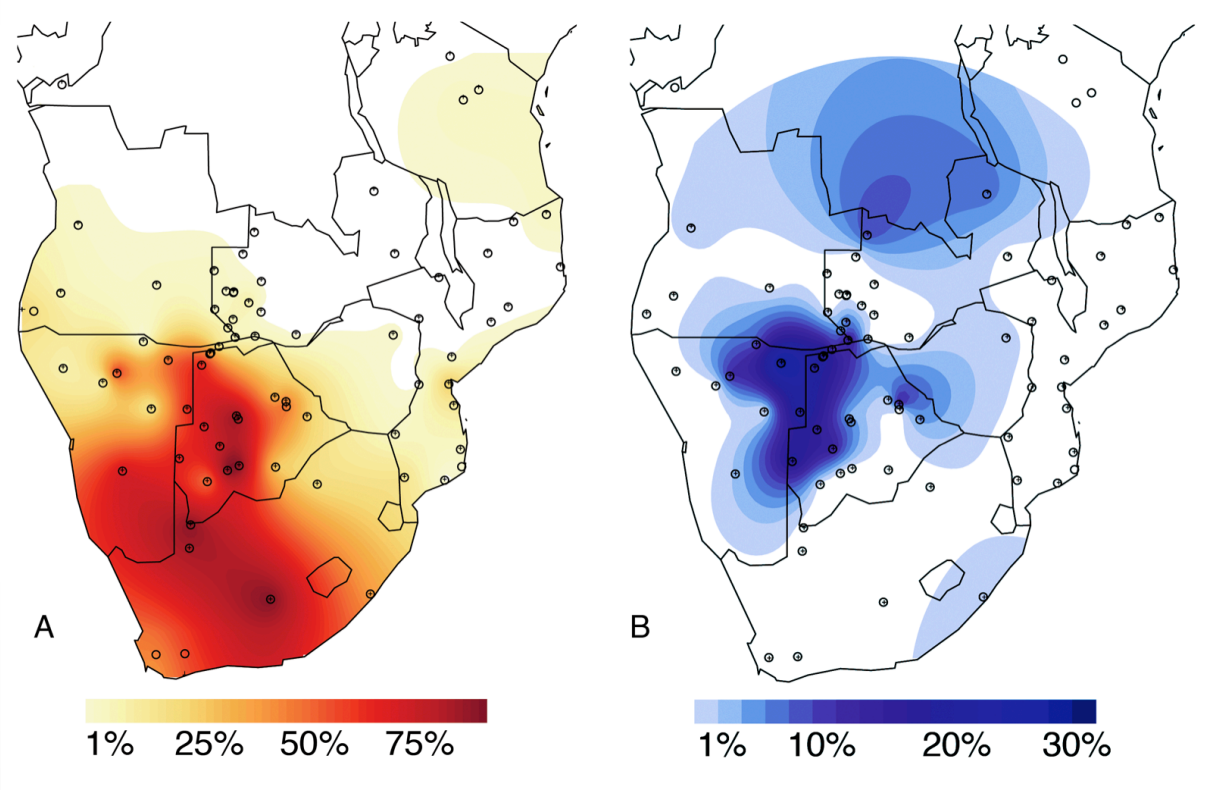
# Core Kalahari area: southwestern Botswana




Relationships between Tuu, West Kalahari Khoe, ǂHoan, Ju|'hoan

# Early diverging mtDNA lineages

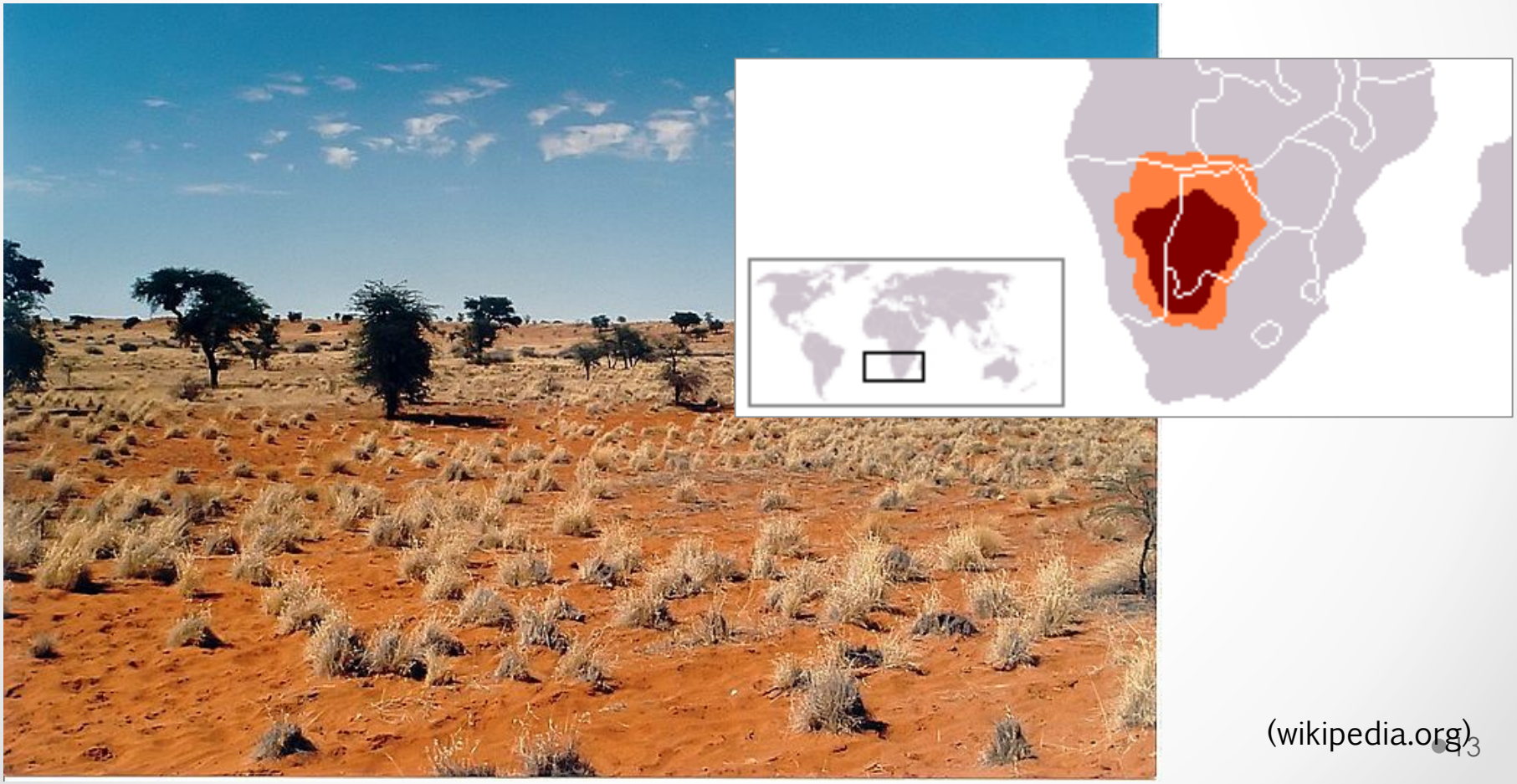
L0d L0k




The most divergent mtDNA lineages ever discovered are found in southern Africa

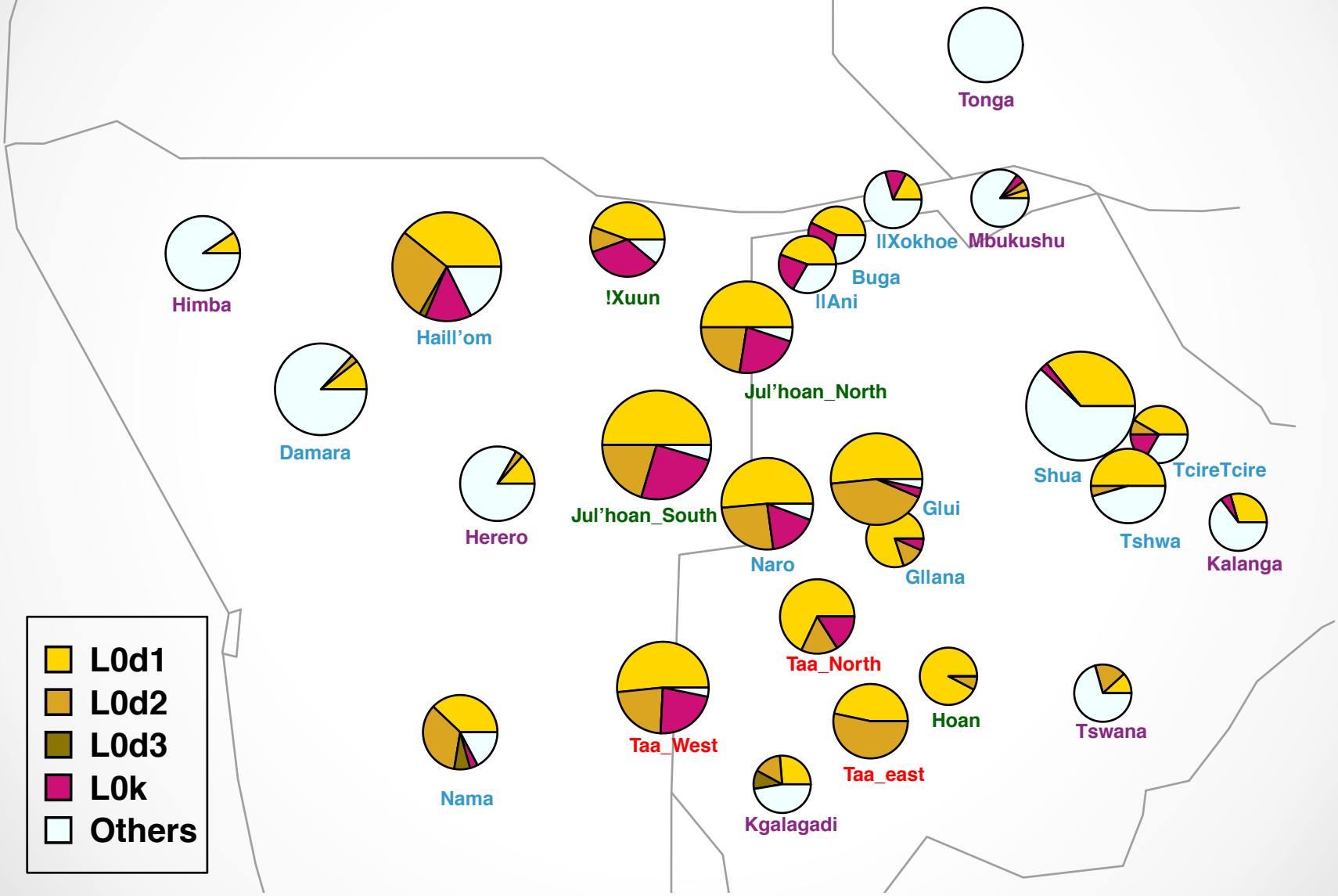
*Barbieri et al. 2013*

# Central Kalahari Basin

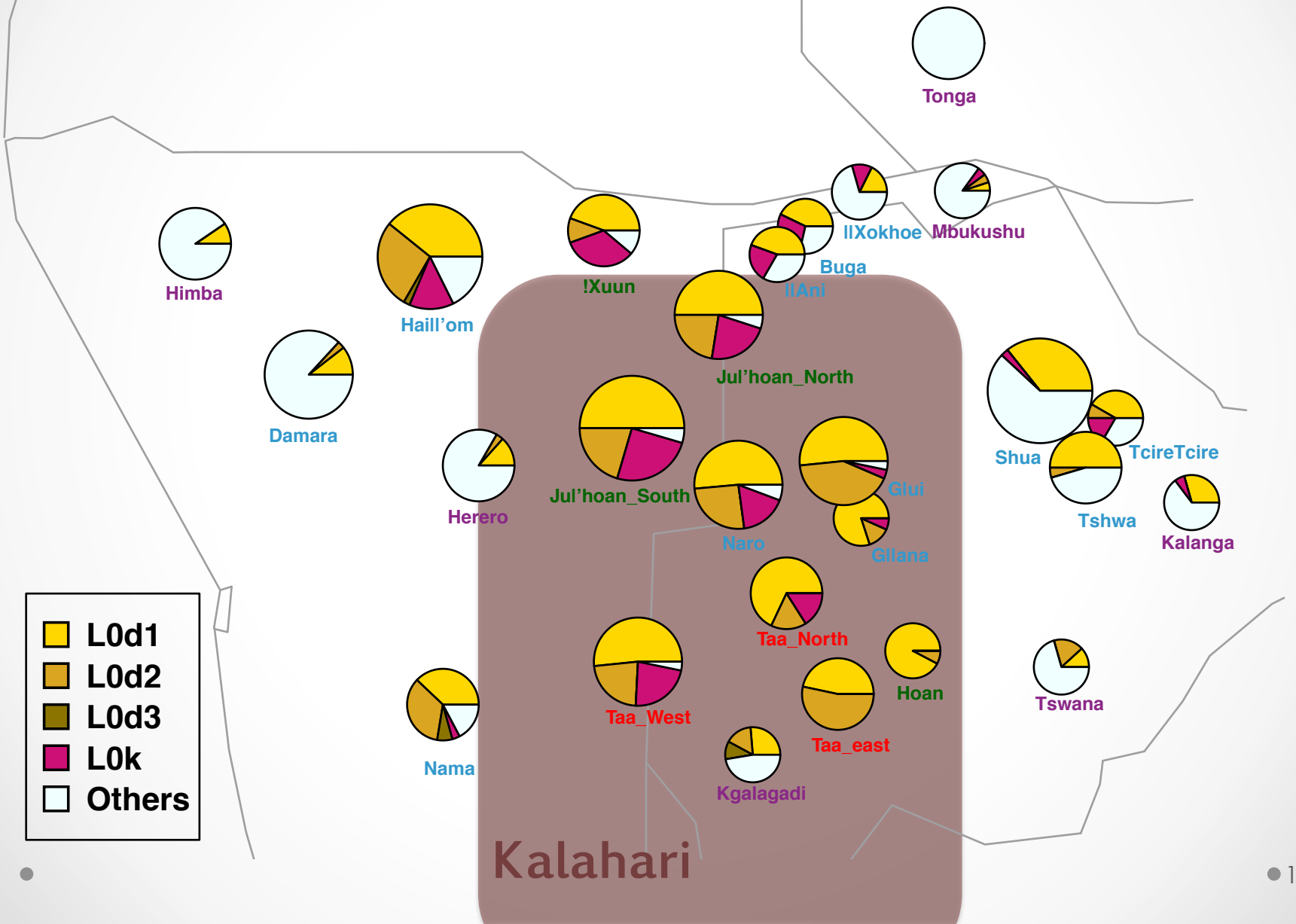


(wikipedia.org)

# Distribution of “Khoisan” characteristic mtDNA haplogroups



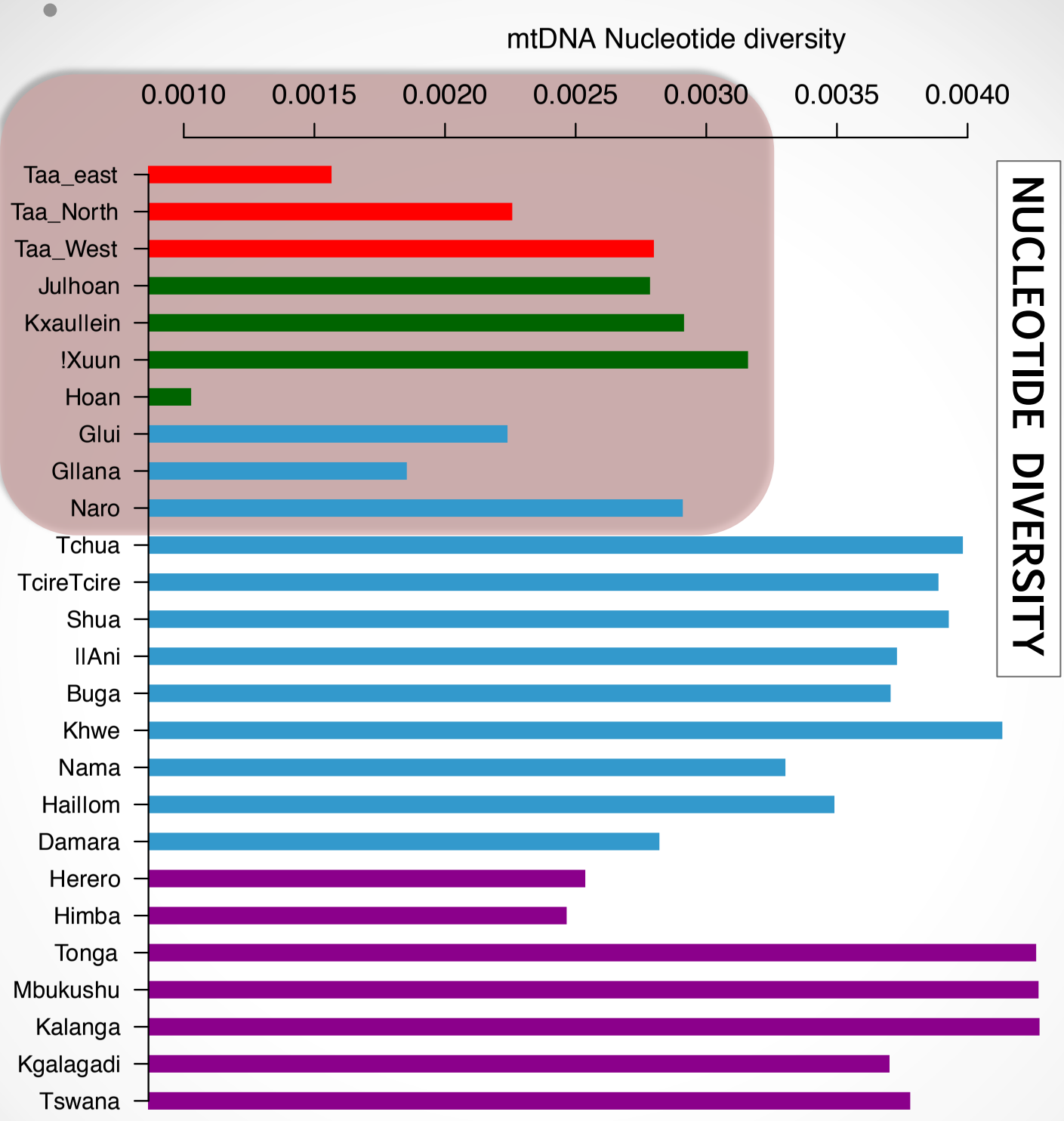
# Distribution of “Khoisan” characteristic mtDNA haplogroups

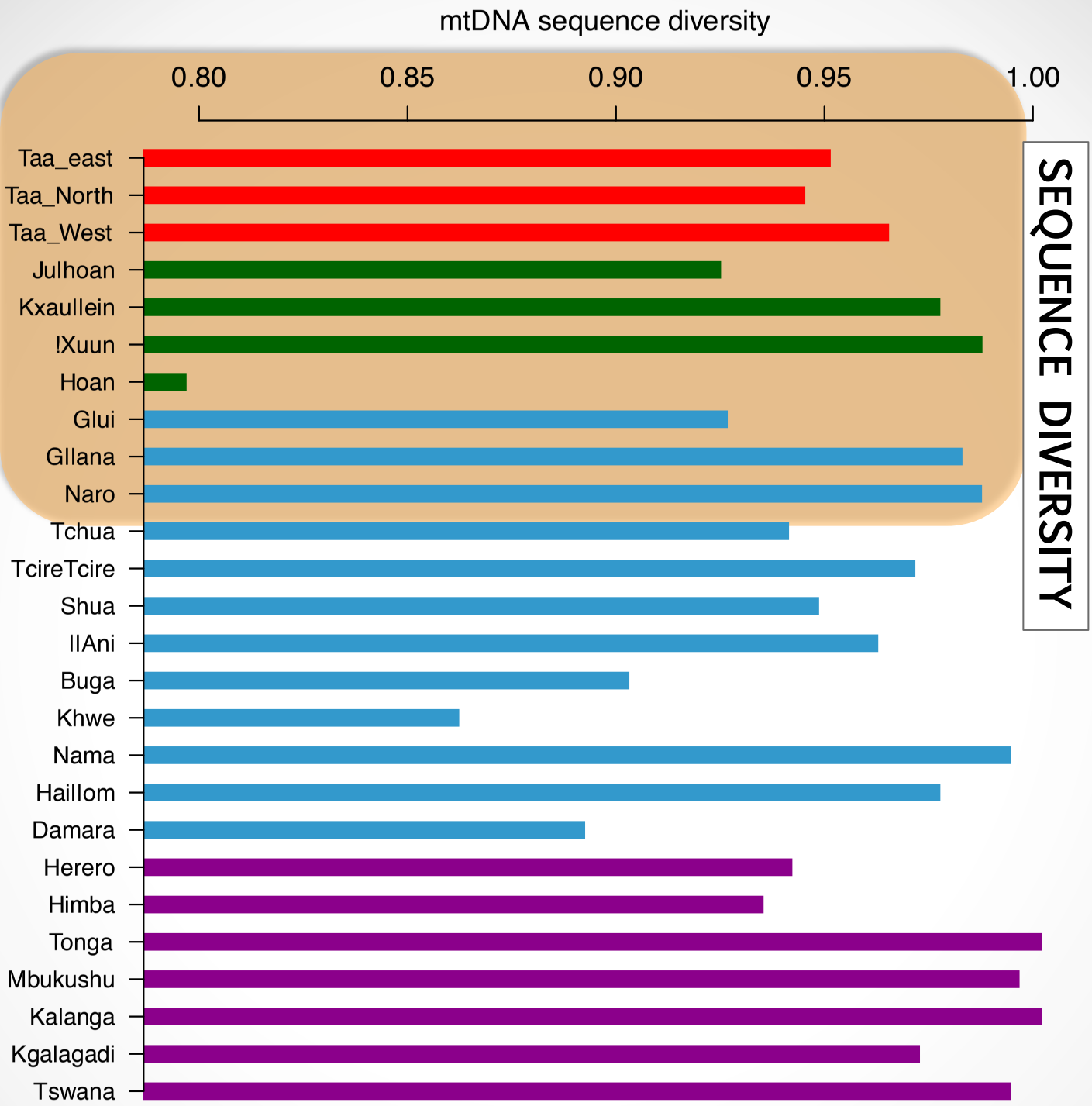


# Central Kalahari Basin mtDNA

- Connections between Tuu, Kx'a and Western Kalahari Khoe
- Higher presence of "Khoisan haplogroups" **L0d** and **L0k**

mtDNA data provides a frame of areal contact between populations who speak languages of the three families


mtDNA Nucleotide diversity
0.0010
0.0015
0.0020
0.0025
0.0030
0.0035
0.0040
Taa_east
Taa_North
Taa_West
Julhoan
Kxaullein
!Xuun
Hoan
Glui
Gllana
Naro
Tchua
TcireTcire
Shua
llAni
Buga
Khwe
Nama
Haillom
Damara
Herero
Himba
Tonga
Mbukushu
Kalanga
Kgalagadi
Tswana
NUCLEOTIDE DIVERSITY

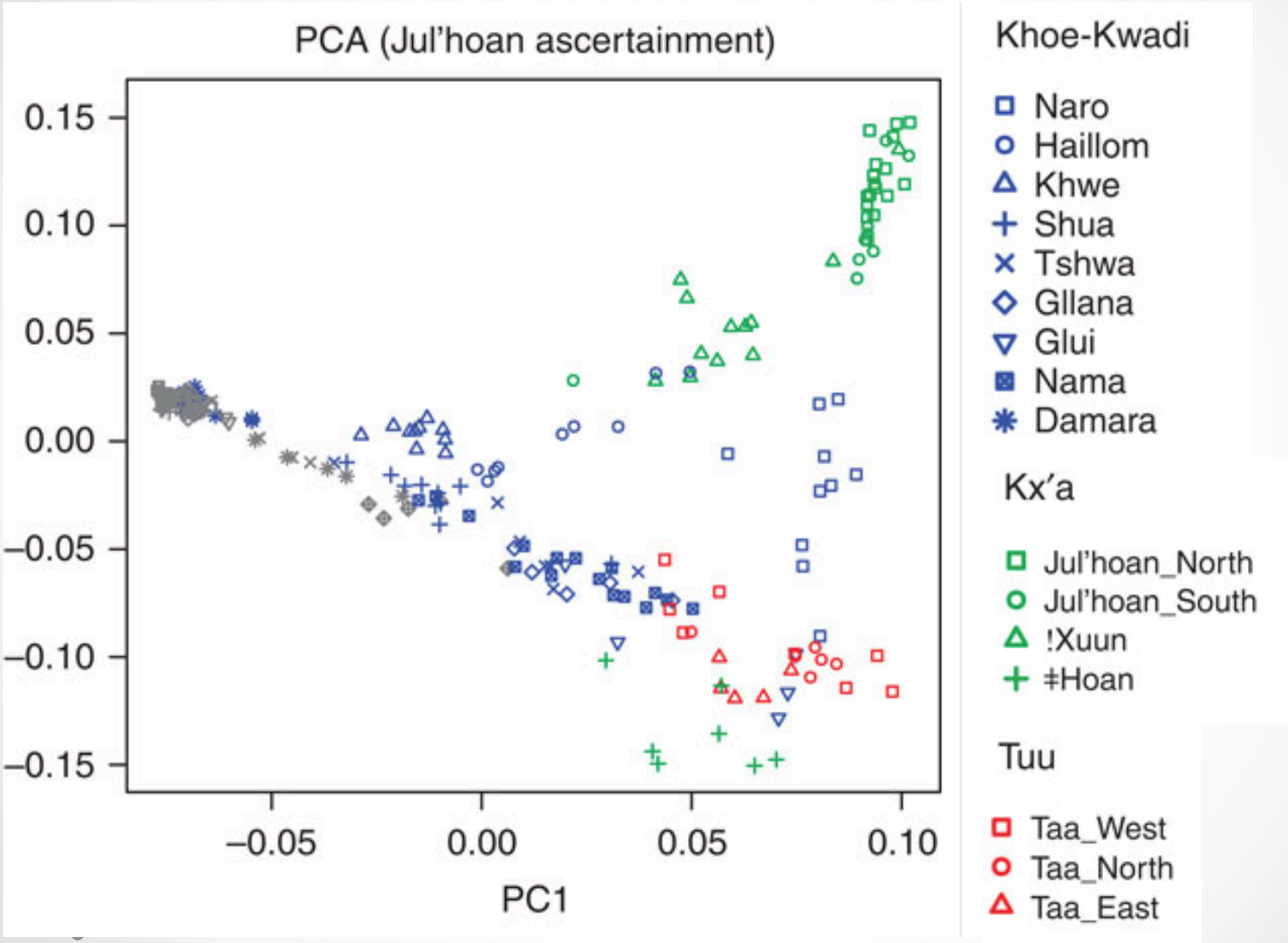

mtDNA sequence diversity
0.80
0.85
0.90
0.95
1.00
Taa_east
Taa_North
Taa_West
Julhoan
Kxaullein
!Xuun
Hoan
Glui
GIlana
Naro
Tchua
TcireTcire
Shua
llAni
Buga
Khwe
Nama
Haillom
Damara
Herero
Himba
Tonga
Mbukushu
Kalanga
Kgalagadi
Tswana
SEQUENCE DIVERSITY

# Core Kalahari Botswana

- Low nucleotide diversity
  - Effect of long term isolation from other migrants (herders, Bantu)
- High sequence diversity
  - Moderate effect of exogamy

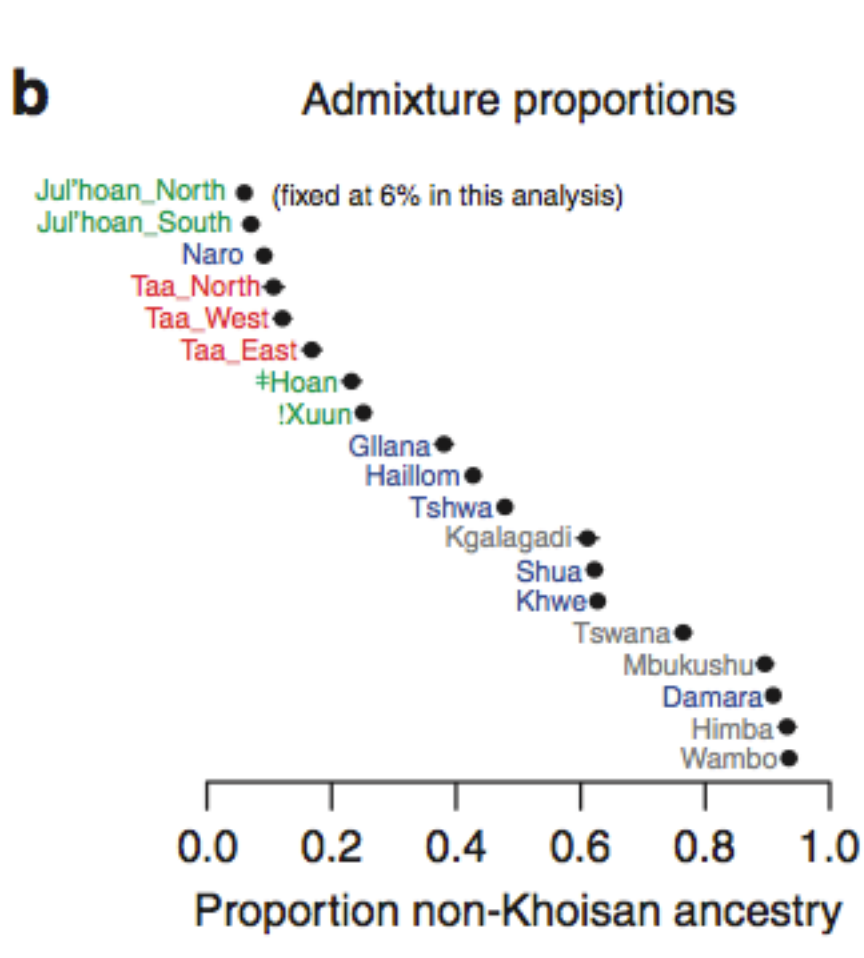
→ Band exogamy, tribal endogamy

# Autosomal DNA - PCA



# Autosomal DNA –

## admixture with non-Khoisan immigrant



# Focus on Kx'a

**Ju**

- Ju'|hoan north and south are genetically close
- Separated in a cluster for autosomal (and Y chromosome)

**ǂHoan**

- mtDNA: distinguished from the rest of the family and the rest of the dataset, but no characteristic lineages
- Share motifs mainly with G|ui, Taa East
- Genetically similar to their neighbors

# Focus on **Khoe**

**West Kalahari**

- **Naro** autosomal: intermediate between Tuu and Ju
- **G|ui** autosomal similar to Tuu
- **G|ui** particularly distinct, with some exclusive motifs within haplogroup L0d1 and B2a
- **G|ui** and **G||ana** are quite different from each other

- Effect of isolation?
- Language shift (from Ju or Tuu?!) to Khoe language?

# Final remarks – Core Kalahari area

- mtDNA: areal effect of exchange
- Retaining early diverging lineages for both mtDNA and Y chromosome
  - Less admixture with Bantu (or other immigrants)
- G|ui and G||ana: possible effect of isolation
  - Not closely related
- Homogeneity of Tuu
- Homogeneity of Ju

→ north/south structure (further discussed in Panel VII)