



# **Linguistic, cultural and genetic perspectives on human diversity in west-central Africa**

***A JOINT ESF EUROCORES PROJECT***

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**David Comas (*UBE, UPF, Barcelona*)**



# Acknowledgments

- **ESF**
- **The organisers of the final OMLL conference**
- **All funding organisms (CNRS, MEC, DFG)**
- **All collaborators (Africa, Europe, ...)**
- **All individuals who accepted to be sampled**



# Outline

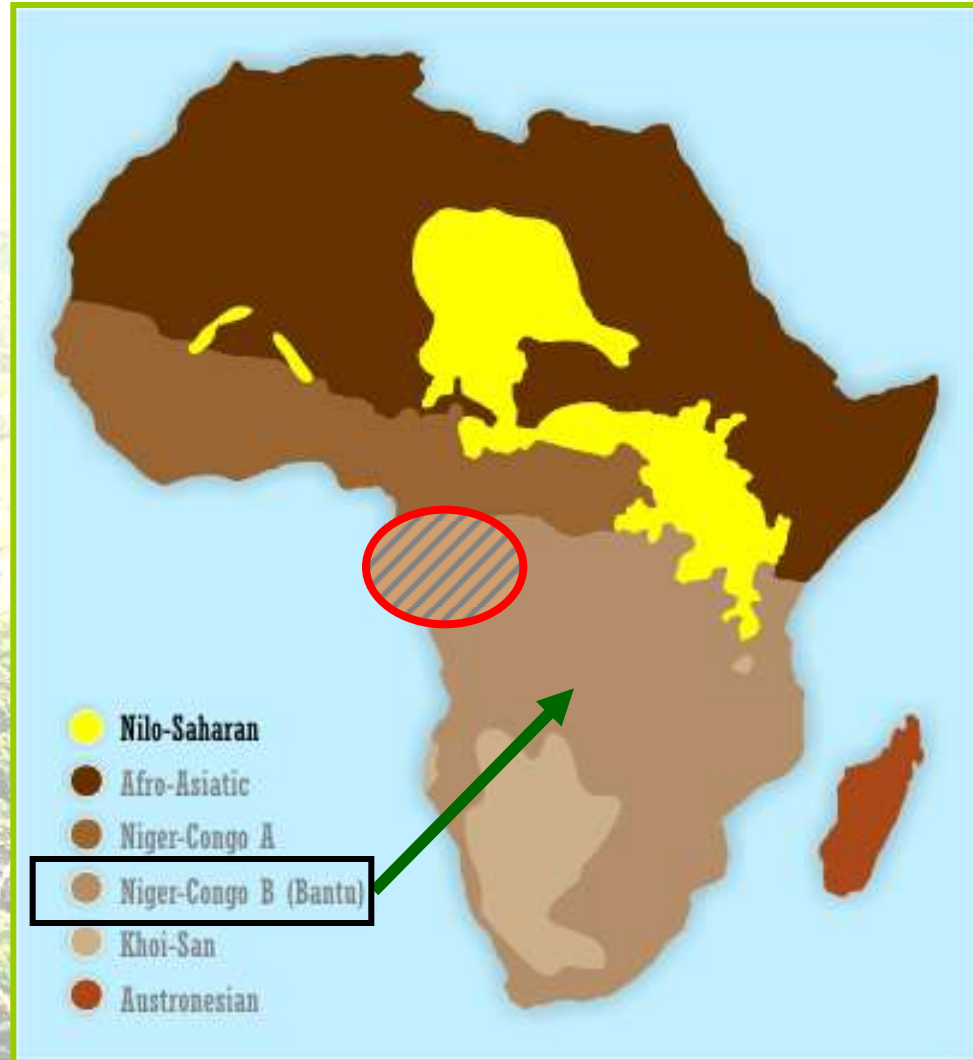
- **Linguistic and cultural diversity**
- **Objectives of project**
  - ☞ Lolke Van der Veen (Lyon)
- **Results mtDNA variation analysis**
  - ☞ Lluís Quintana-Murci (Paris)
- **Results Y-chromosome variation analysis**
- **Conclusions and ongoing work**
  - ☞ David Comas (Barcelona)

# The Bantu languages

Language family comprising some 500 languages spread over most of sub-Saharan Africa

One of the many branches of the Niger-Congo phylum

Focus on the Northwest

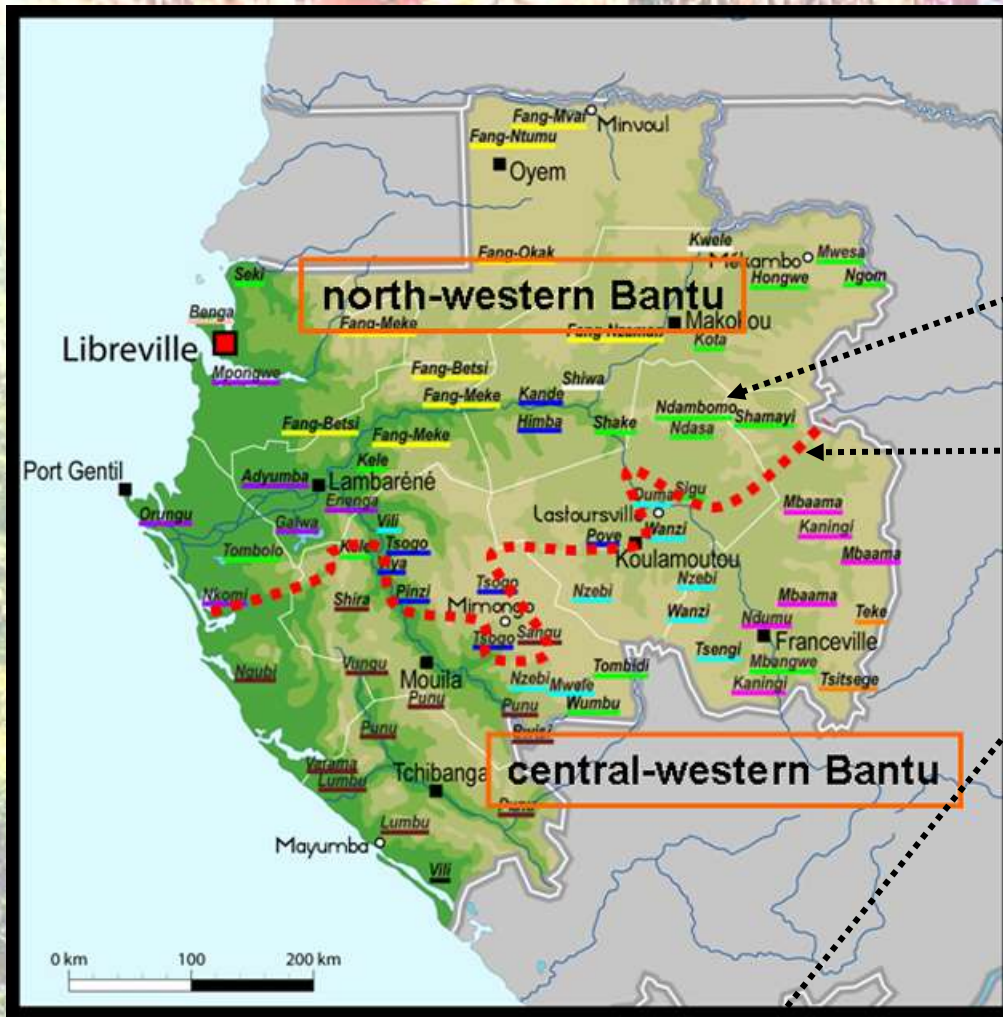


# Linguistic and cultural diversity

## PATTERNS

- Taking **Gabon** as a representative example:
  - **High degree of linguistic and cultural diversity** (at regional level)
    - Some **50+ ethno-linguistic communities**
    - Varieties belonging to **11 higher-level linguistic clusters**
    - **Farming villagers vs. hunter-gathering (semi-)nomads**
      - **Hunter-gathering groups:** all, except one (i.e. Baka), are Bantu-speaking communities
    - **Major linguistic boundary:** north-western vs. central-western Bantu
      - *Cf. (i.a.) Bastin et al. 1999 ; Holden and Gray 2006*
    - More or less widespread **convergence phenomena** due to **cohabitation** and **contact**

# Linguistic diversity and major linguistic boundary



- ☐ Centres of gravity of individual languages and language varieties
  - ☐ Boundary between north-western and central-western Bantu
  - ☐ Eleven clusters represented (colour code)
- Baka (Ubangian) ignored here!*

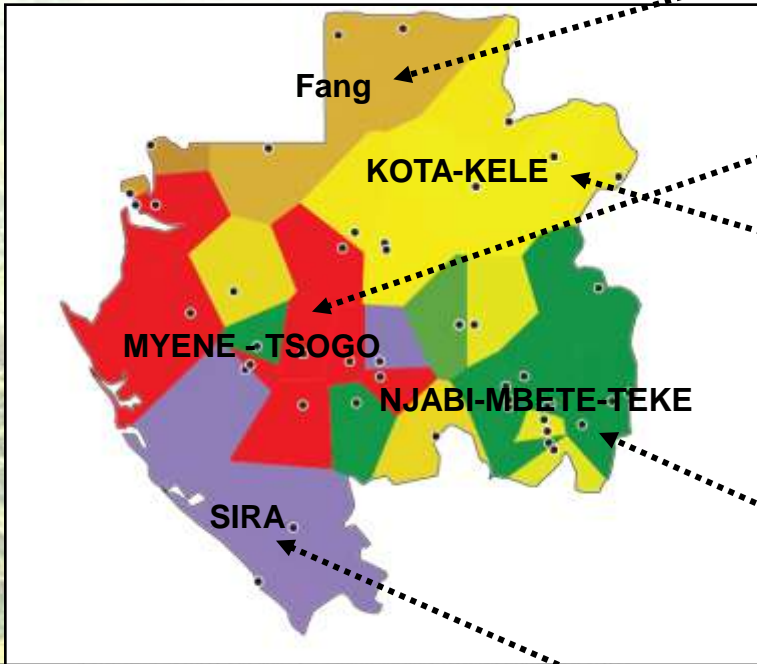
A30	A80	B20	B40	B60	H12b
A70	B10	B30	B50	B70	



# Linguistic and cultural diversity

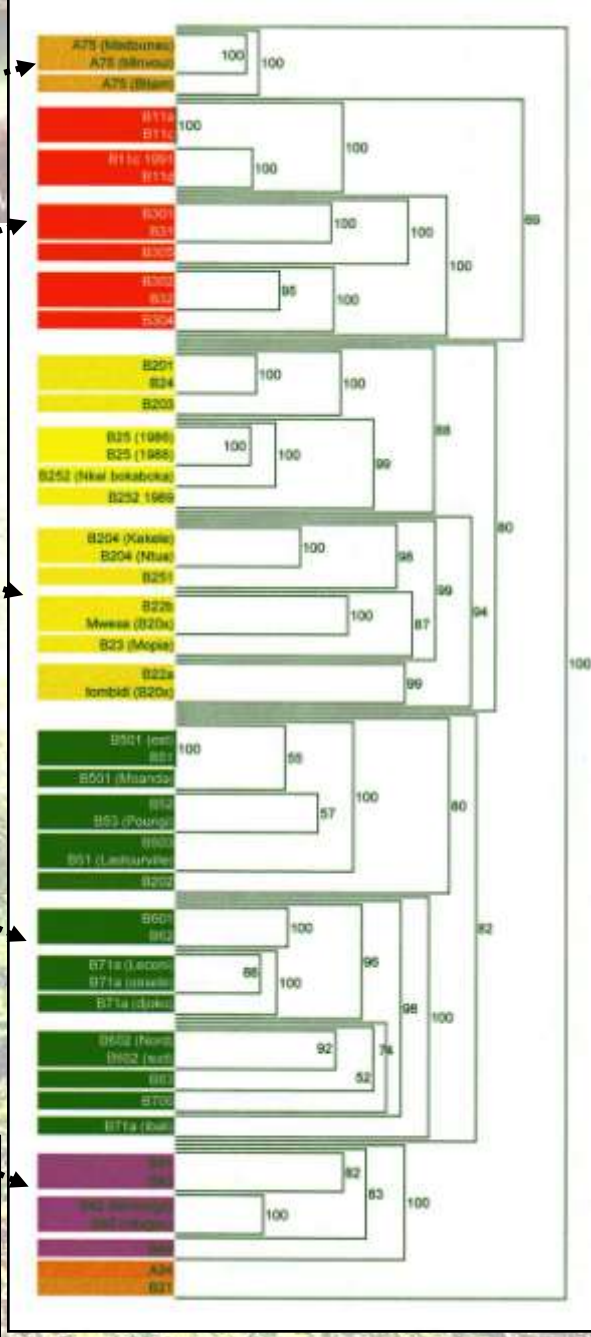
- **Ongoing fieldwork** improves understanding of the often complex linguistic relations
- **Recent advances in classification:** Alewijnse et al. (2007)
  - **Computational approach** (J. Nerbonne, RUG, Netherlands)
  - **ALGAB database (DDL, Lyon):** 53 sampling sites, phonetic data points for 160 glosses
  - Overall, **results corroborate previous views**
  - Some **innovative results**
    - **KOTA-KELE (B20)** emerging as a unified group in spite of clear signs of admixture
    - Link between **MYENE-TSOGO (B10-B30)**, but less solid as previously thought (due to convergence?)
    - Special position of **Benga (A34)** and **Seki (B21)**

# Alewijnse et al. (2007)



First three dimensions of the results of MDS applied to the mean cophenetic distances used in the bootstrapped clustering procedure. (Dots: sampling sites.)

Consensus dendrogram. Labels coloured as in map. Numbers associated with the groups indicate how reliably that group emerged, from a total of 100 runs.





# Linguistic and cultural diversity

## PATTERNS

- **Cultural traits**

- Overall, cultural traits and clusters of such traits **reinforce the linguistic subdivisions**, at different levels

- **Mating patterns** (exogamy, endogamy)
- **Descent systems** (patrilineal, matrilineal)
- **Artefacts** (masks, reliquaries, etc.)
- **Traditional technological traits** (ironwork, hunting, fishing, travelling by pirogue, weaving, sculpture, etc.)
- **Initiation rituals**
- **Dances, songs and music** (types, styles, etc.)
- **Taboos** (food, sex, naming predators, etc.)
- **Toponymy** (manners of naming places)

- The Ogooué river as some (relative) **natural barrier**

# Gabon: masks as an example of cultural diversity

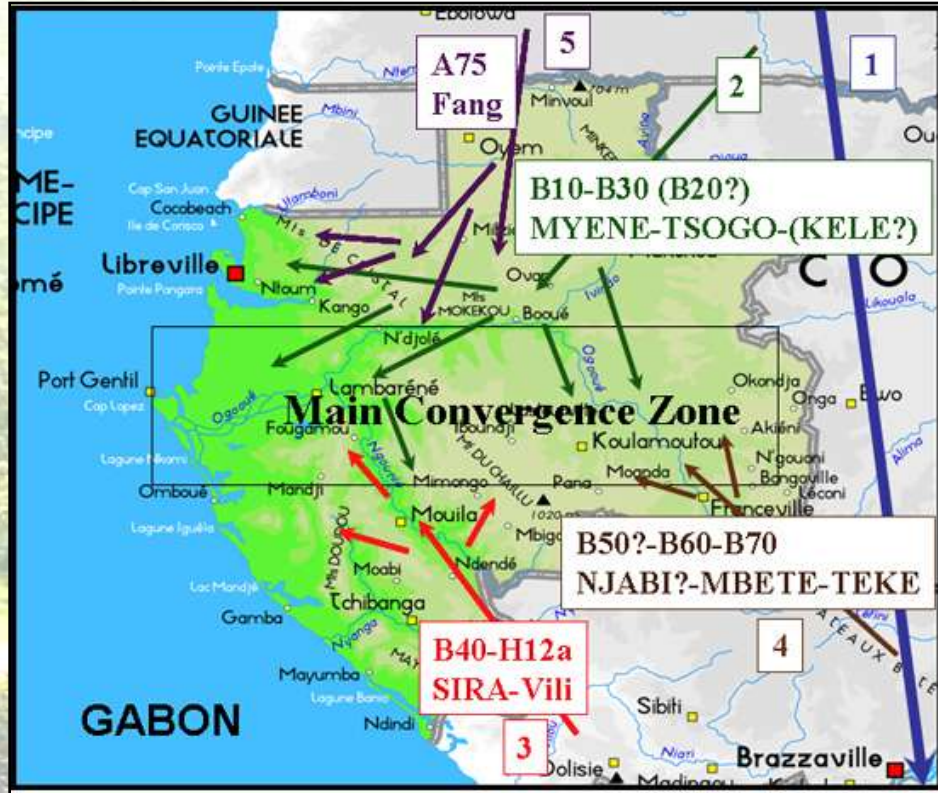


# Linguistic and cultural diversity

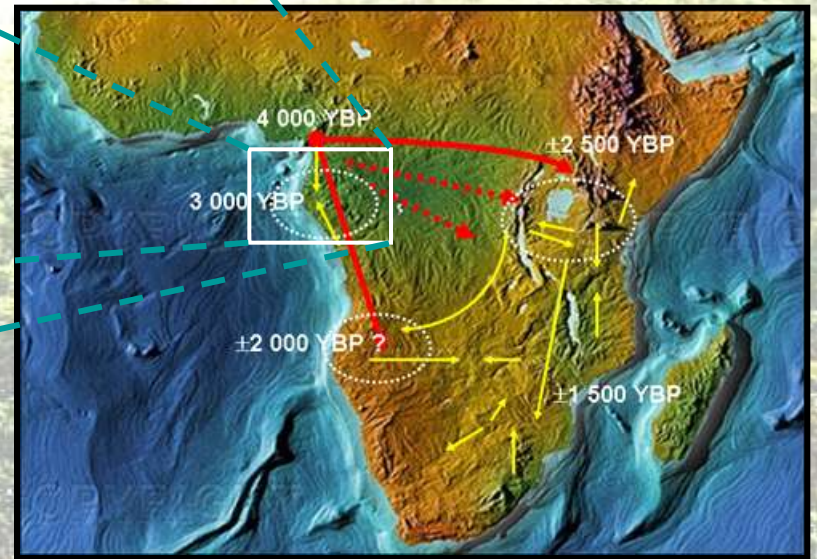
## PROCESSES

- **Peopling of the area**
  - Hypotheses based on **extensive language studies** and **oral tradition**, and (indirectly) on **recent archaeological findings**
- **Demic western Bantu expansion**
  - **Three millennia** of progressive peopling
  - Small groups of **hunter-gatherers** already in situ!
  - **Bantu-speaking villagers** practising some more or less developed form of **agriculture**
    - **Successive waves**
    - **Relatively small groups**
    - **Different time depths**
      - *Cf. Recent arrival of Fang in the Estuary and centre (19-20<sup>th</sup> c. AD)*
    - **High rate of between-group interaction**
  - Some extent of **interaction** with the hunter-gathering communities

# Peopling of Gabon area and western Bantu expansion



Bantu expansion (schematic representation)



Peopling of the Gabon area by Bantu-speaking villagers as suggested by language studies and oral tradition (relative chronology: (1)2-5)

# Objectives of the project

- **Improve understanding of human diversity in west-central Africa on basis of uniparental markers (*mtDNA and Y-chromosome variation*)**
  - Test the hypothesis of a **demic** Bantu expansion
  - Look for possible **correlations between languages and genes** for Bantu-speaking populations (test case with a limited time depth (4000 YBP)!)
  - Determine, if possible, the **pre-Bantu gene pool**
  - Determine differences between **agriculturalists (villagers)** and **hunter-gatherers (semi-nomads)**
    - Impact of lifestyle!
  - Look for evidence of **exchanges** between populations
  - Look for possible **sexual asymmetries** in migratory patterns
  - Examine the odd '**Out-of-Egypt**' hypothesis for the Bantu-speaking Fang population (Gabon, Cameroon)

# Objectives of project

- **Rigorous sampling with well-defined criteria:**
  - Generally, **2 populations** per major linguistic cluster
  - **50 individuals** per sampled population
  - Sampling **in the field** with **individuals' consent**
  - Both **parents of subject** belonging to same ethno-linguistic group
  - As a rule, **male subjects of 35 years and older**
  - Use of an **ethno-linguistic questionnaire** for detailed study of the affiliation through lineages (over 4 generations) and the relations between these lineages (*clans*) and the villages over time

# Objectives of project



Populations and numbers of individuals sampled in Gabon  
Total: 960 samples from 21 populations (1 non Bantu-speaking pop.)

# Objectives of project

- **Additional samples (440)** from previous and more recent projects taken into account (west-central Africa)
  - E.g. project coordinated by E. Heyer and S. Bahuchet
- Total of some **1400 individuals**
  - Some 980 agriculturalists (**20 populations**)
  - Some 420 hunter-gatherers (**9 populations**)
- Central Africa: at present, **one of the best documented areas of Africa**, from the genetic point of view!
  - Major progress since Salas et al. (2002): “very poorly represented”

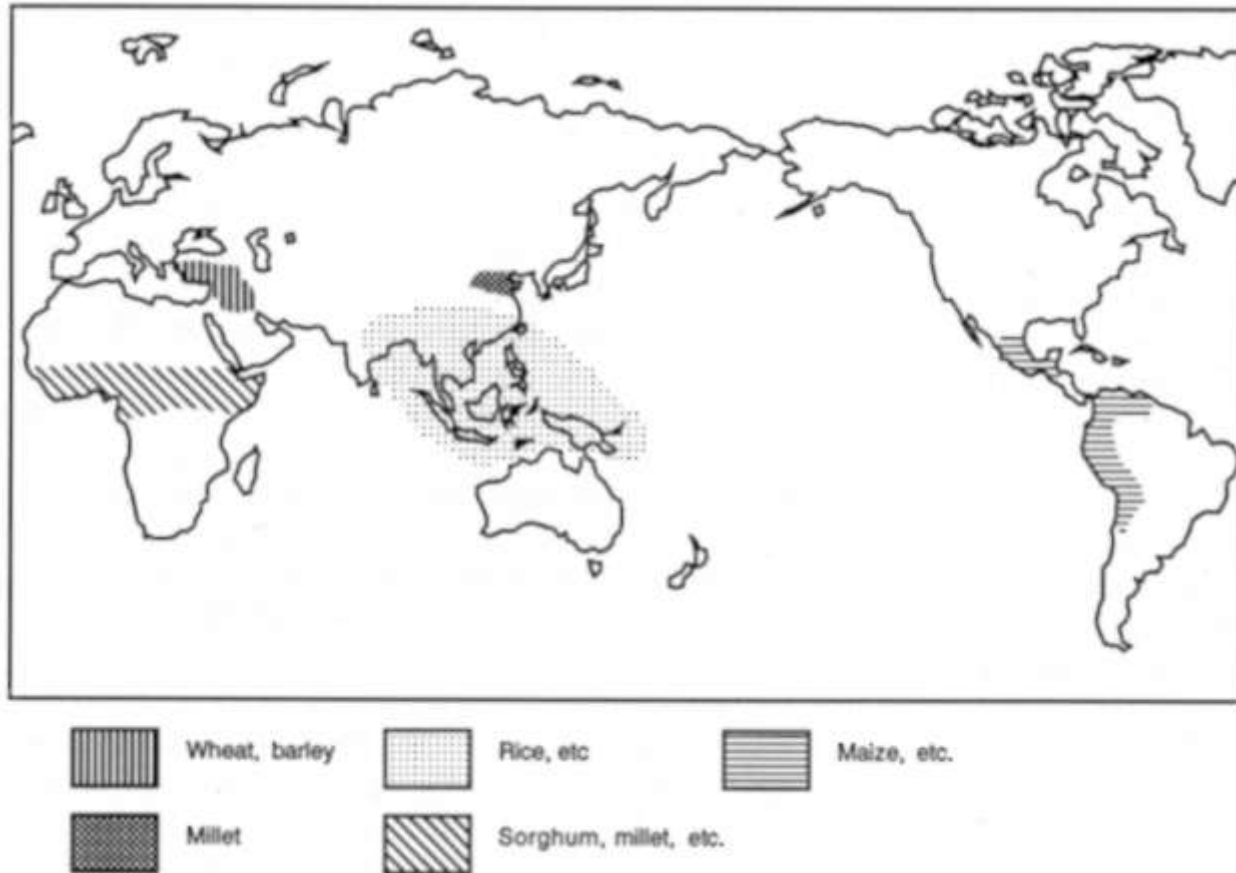


# Maternal DNA variation of Bantu-speaking agriculturalists and Pygmy hunter-gatherers from central-west Africa

- **Institut Pasteur, Paris:** Helene Quach, Francesca Luca, Etienne Patin, Blandine Massonnet
- **Institut de Sciences de l'Homme (Lyon):** Lolke van der Veen, Jean-Marie Hombert, Patrick Mouguiama-Daouda
- **Musée de l'Homme, Paris:** Paul Verdu, Evelyne Heyer, Serge Bahuchet, Alain Froment
- **Universitat Pompeu Fabra, Barcelona:** Jaume Bertranpetit, David Comas
- **Other collaborators:** Doron Behar, Antonio Salas, Ken Kidd, Lucas Sica, etc
- **Funding:** CNRS, ESF, French Ministry of Research (Prosodie)

ESF Eurocores, OMLL Final Conference, Rome, December 12-14 2007

# The first major change in human history: Transition from hunter-gathering to agriculture



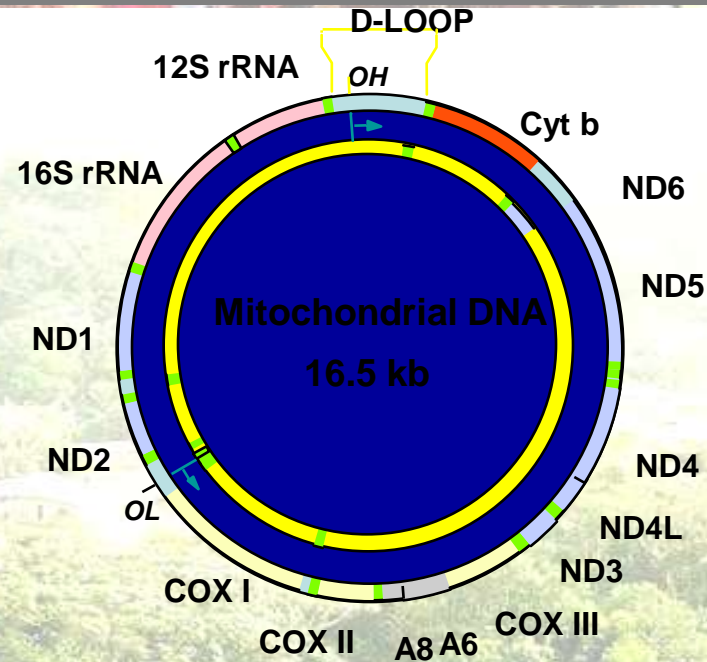
# In Africa



# The transition from hunter-gathering to agriculturalism

- Increase of population densities:
  - More resources available
  - Higher reproductive capacities:
    - Longer lifespan
    - Earlier reproductive age
- Change in lifestyle: from nomadism to sedentarism
- Different relation with pathogens:
  - Higher densities: higher transmission
  - Sedentary lifestyle: higher contamination
  - Pastoralism: zoonosis

# mtDNA genome

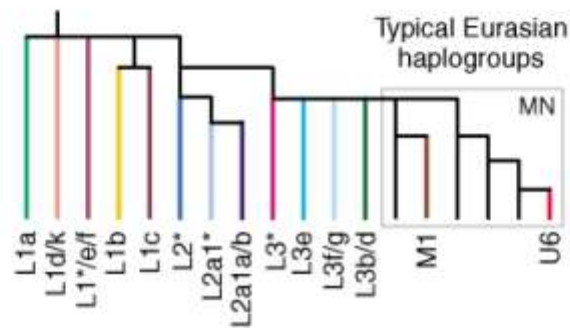
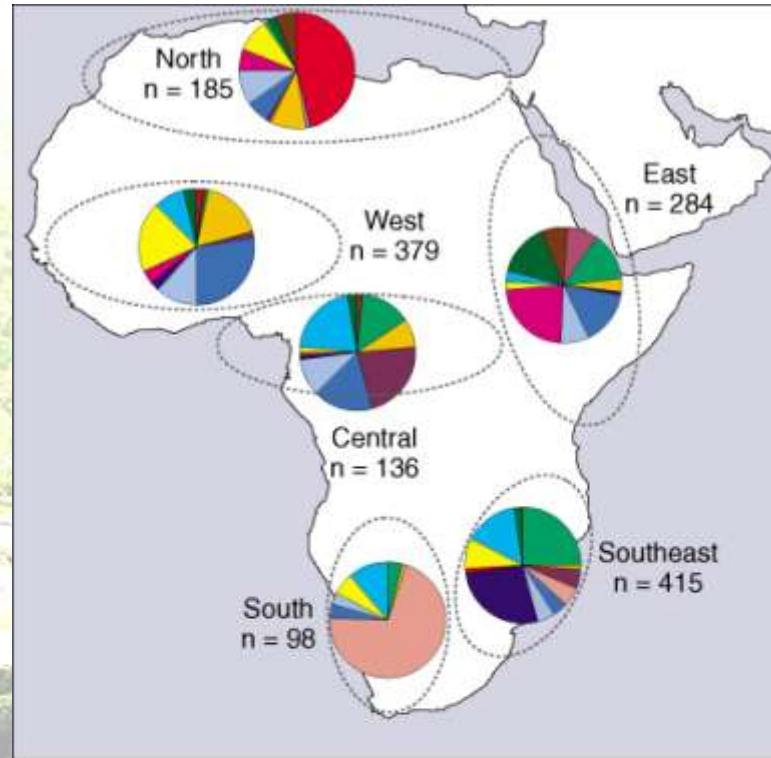


- 1981 Human mitochondrial genome was sequenced
- Strict maternal inheritance
- No recombination
- High mutation rate

# Central African questions

- Get a mtDNA panorama of central African populations
- Better understand the maternal gene pool of population located near the initial Bantu-expansions
- Evaluate the genetic exchange between agriculturalists and hunter-gatherers
- Get insights into the gene pool of Pygmy populations: unique origin? Different origins? Common initial gene pool with agriculturalists?

# mtDNA African landscape



# State of the collection: final samples sizes analyzed

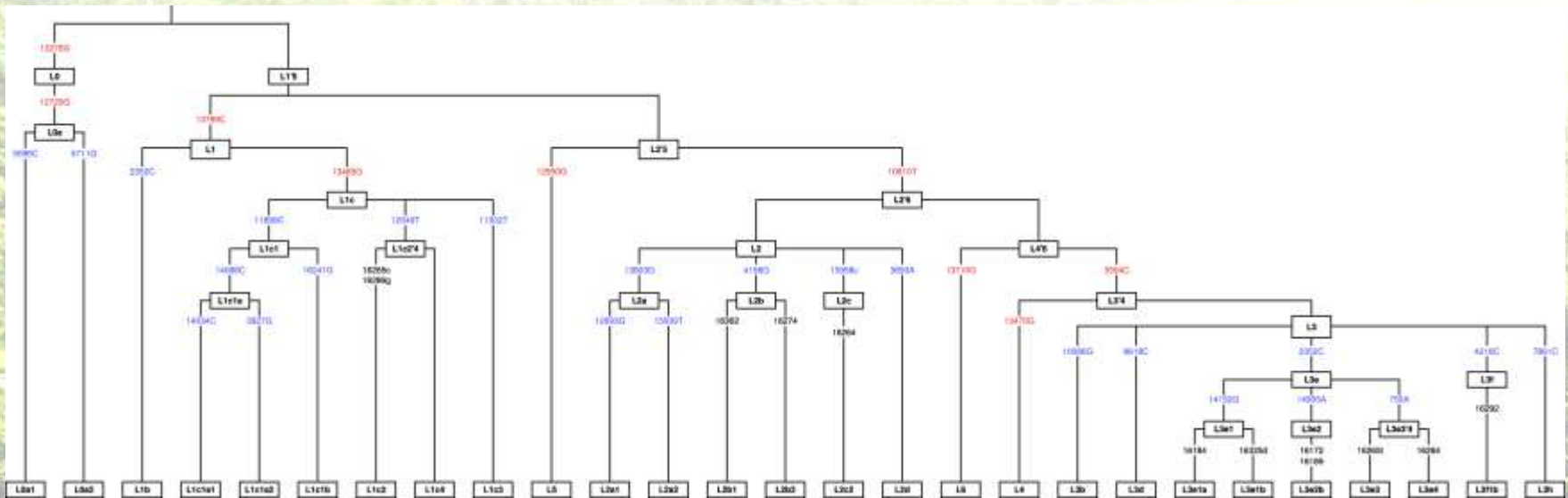
POP CODE	POPULATION	COUNTRY	LIFESTYLE	N
BEN	BENGA	GABON	AGR	50
DUM	DUMA	GABON	AGR	47
EVI	EVIYA	GABON	AGR	38
EWD	EWONDO	CAMEROON	AGR	25
FAN-CM	FANG	CAMEROON	AGR	39
FAN-GB	FANG	GABON	AGR	66
GAL	GALOA	GABON	AGR	51
GIS	ESHIRA	GABON	AGR	40
KEL	AKELE	GABON	AGR	48
KOT	KOTA	GABON	AGR	56
MAK	MAKINA	GABON	AGR	45
NDU	NDUMU	GABON	AGR	39
NGU	NGUMBA	CAMEROON	AGR	88
NZE	NZEBI	GABON	AGR	63
OBA	OBAMBA	GABON	AGR	47
ORU	ORUNGU	GABON	AGR	20
PUN	PUNU	GABON	AGR	52
SHA	SHAKE	GABON	AGR	51
TEK	ATEKE	GABON	AGR	54
TSO	MITSOGO	GABON	AGR	64
BAB	PYGMY-BABONGO	GABON	HG	45
BAK-CC	PYGMY-BAKA	CAMEROON-CENTRE	HG	30
BAK-CW	PYGMY-BAKA	CAMEROON-WEST	HG	58
BAK-GB	PYGMY-BAKA	GABON	HG	39
BAKO	PYGMY-BAKOLA	CAMEROON	HG	88
BEZ	PYGMY-TIKAR	CAMEROON	HG	35
BIA	PYGMY-BIAKA	C.A.R.	HG	56
BKY	PYGMY-BAKOYA	GABON	HG	31
MBU	PYGMY-MBUTI	D.R.C.	HG	39

-a total of 1404 individuals  
 -20 Bantu-speaking  
 agriculturalists populations  
 (983 individuals)  
 -9 Pygmy hunter-gatherer  
 populations (421 individuals)





# Genotyping strategy based on complete mtDNA sequences



# Our analyses

- **Coding-regions SNPs:**

33 coding-region SNP analyses taking into consideration previous phylogenies AND complete mtDNA sequence data phylogenies: coding-regions SNPs provide information about the main lineages in the mtDNA tree

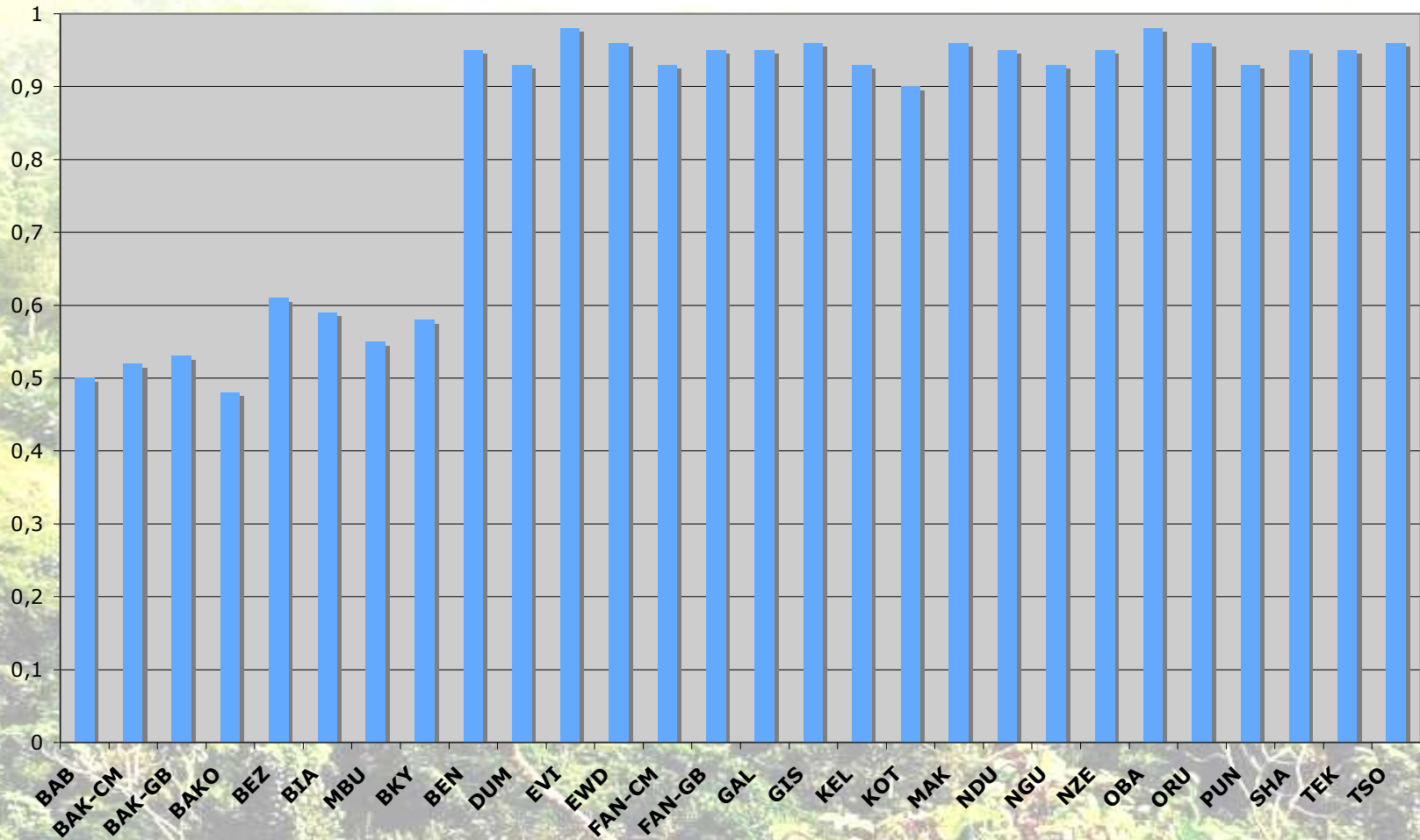
- **Sequence of HVS-I region:**

the hyper-variable region can provide information about the time-depth of the different mtDNA lineages

# Population diversity

Pygmies

Bantus



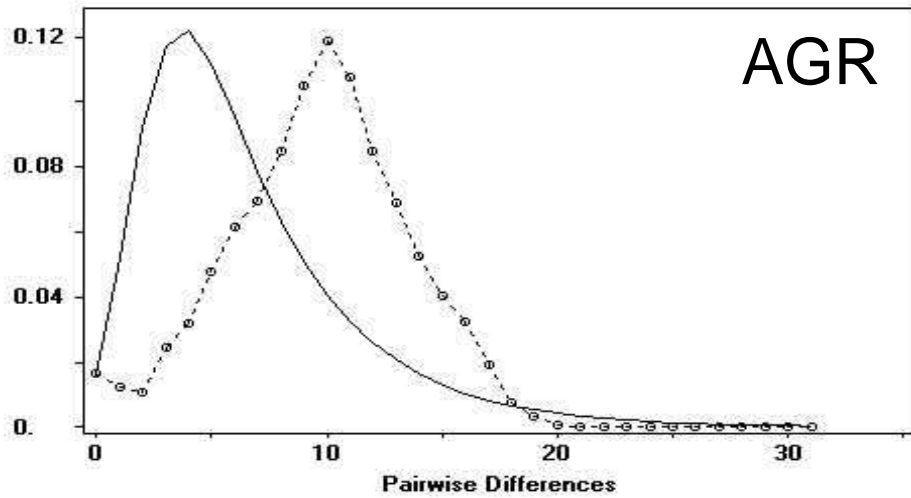
# Population diversity and demographic regimes

Table 1. General diversity indices and neutrality tests for the different agriculturalist and hunter-gatherer populations here studied.

Population	Location	<i>n</i> *	Hg D (SE)	Ht D (SE) <sup>a</sup>	Pi (SE) <sup>o</sup>	Tajima's <i>D</i> ( <i>P</i> ) <sup>†</sup>	Fu's <i>F<sub>s</sub></i> ( <i>P</i> ) <sup>‡</sup>
<b>Bantu-speaking agriculturalists</b>							
Akele	Gabon-West	48	.925 (.022)	.985 (.008)	9.811 (4.571)	-0.70 (.262)	-16,76
Ateke	Gabon-Southeast	54	.945 (.012)	.985 (.007)	9.088 (4.248)	-0.76 (.231)	-21,96
Benga	Gabon-Northwest	50	.931 (.016)	.952 (.015)	9.922 (4.616)	-0.67 (.307)	-4.53 (.101)
Duma	Gabon-East	47	.925 (.016)	.973 (.010)	9.258 (4.332)	-0.92 (.193)	-9,09
Eshira	Gabon-West	40	.939 (.016)	.971 (.012)	10.077 (4.703)	-0.68 (.293)	-5.84 (.060)
Eviya	Gabon-Centre	38	.898 (.023)	.932 (.018)	9.135 (4.297)	-0.52 (.299)	-0.08 (.539)
Ewondo	Cameroon-West	25	.900 (.023)	.933 (.023)	9.933 (4.702)	0.05 (.571)	0.95 (.692)
Fang-CM	Cameroon-South	39	.880 (.028)	.970 (.014)	9.333 (4.381)	-0.44 (.402)	-9,46
Fang-GB	Gabon-North	66	.930 (.012)	.971 (.009)	8.849 (4.132)	-0.78 (.235)	-12,99
Galoa	Gabon-West	51	.925 (.019)	.965 (.011)	9.002 (4.214)	-0.96 (.172)	-6.13 (.047)
Kota	Gabon-East	56	.900 (.023)	.967 (.010)	10.562 (4.885)	-0.61 (.283)	-8.28 (.021)
Makina	Gabon-Centre	45	.928 (.017)	.962 (.016)	9.306 (4.356)	-0.71 (.269)	-7.28 (.027)
Mitsogo	Gabon-Centre	64	.898 (.025)	.961 (.011)	9.058 (4.224)	-0.84 (.219)	-9,50
Ndumu	Gabon-Southeast	39	.953 (.013)	.973 (.013)	9.417 (4.418)	-0.92 (.178)	-8,01
Ngumba	Cameroon-West	88	.932 (.010)	.969 (.007)	10.090 (4.655)	-0.35 (.435)	-14,10
Nzebi	Gabon-Southeast	63	.949 (.010)	.976 (.010)	8.955 (4.181)	-1.16 (.110)	-22,92
Obamba	Gabon-Southeast	47	.942 (.016)	.988 (.007)	9.741 (4.542)	-1.13 (.108)	-17,49
Orungu	Gabon-West	20	.905 (.041)	.974 (.025)	10.895 (5.173)	-0.13 (.508)	-3.53 (.090)
Punu	Gabon-Southwest	52	.946 (.014)	.982 (.007)	9.124 (4.266)	-1.24 (.096)	-15,94
Shake	Gabon-East	51	.899 (.022)	.973 (.011)	10.195 (4.733)	-0.68 (.275)	-13,01
<b>Eastern Pygmy</b>							
Mbuti	D.R.C	39	.710 (.041)	.823 (.034)	6.877 (3.307)	1.05 (.886)	2.69 (.851)
<b>Western Pygmy</b>							
Babongo	Gabon-Southeast	45	.721 (.052)	.749 (.058)	6.945 (3.327)	-0.27 (.493)	1.75 (.799)
Baka-CC	Cameroon-Centre	30	.540 (.080)	.830 (.035)	5.425 (2.688)	0.26 (.655)	3.34 (.899)
Baka-CW	Cameroon-Southwest	58	.654 (.040)	.786 (.037)	5.667 (2.757)	-0.75 (.256)	1.52 (.766)
Baka-GB	Gabon-Northeast	39	.533 (.034)	.757 (.052)	4.124 (2.098)	0.08 (.569)	2.76 (.886)
Bakola	Cameroon-West	88	.455 (.033)	.722 (.024)	3.509 (1.805)	2.01 (.971)	5.05 (.942)
Bakoya	Gabon-Northeast	31	.333 (.096)	.548 (.087)	3.011 (1.614)	-0.99 (.190)	4.26 (.954)
Biaka	C.A.R	56	.724 (.030)	.823 (.030)	6.006 (2.906)	0.05 (.632)	2.42 (.857)
Tikar	Cameroon-North	35	.464 (.054)	.703 (.027)	2.911 (1.565)	1.46 (.923)	4.38 (.955)

\* Sample size; Gene diversity based on haplogroup profiles (Hg D) and standard error (SE); <sup>a</sup>Gene diversity based on HVS -I sequence-based haplotypes (Ht D); <sup>o</sup>Average number of pairwise differences (Pi); <sup>†</sup>All *P* values are < .05 (for Tajima's *D*) and < .02 (for Fu's *F<sub>s</sub>*), except where noted.

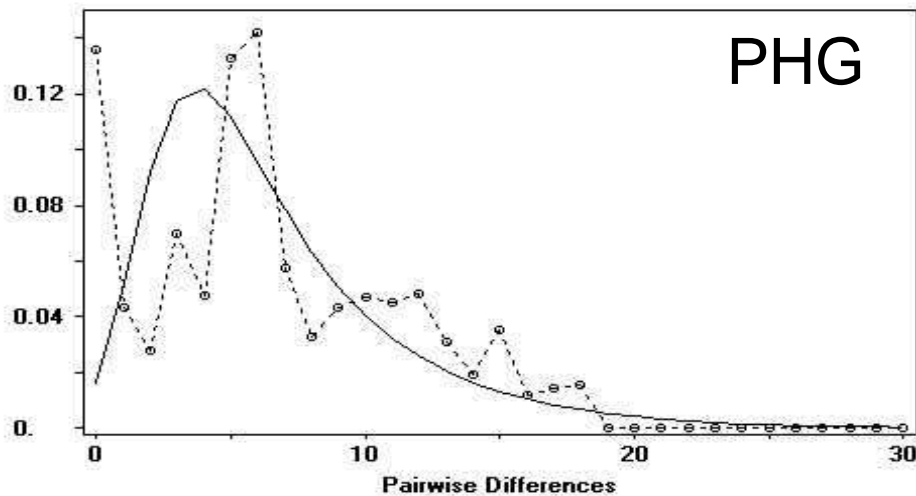
# Mismatch HVS-I distributions



— Exp

- - ○ - Obs

Most farmers show signs of population growth



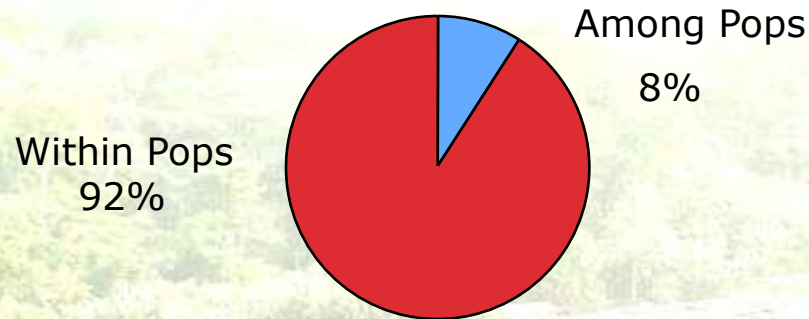
— Exp

- - ○ - Obs

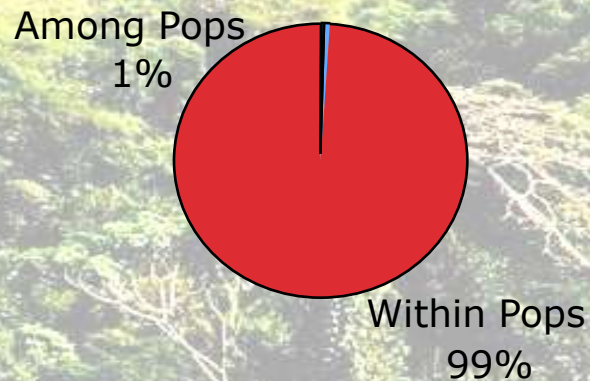
Most Pygmies show signs of small population sizes and strong drift

# Analysis of MOlecular Variance (AMOVA)

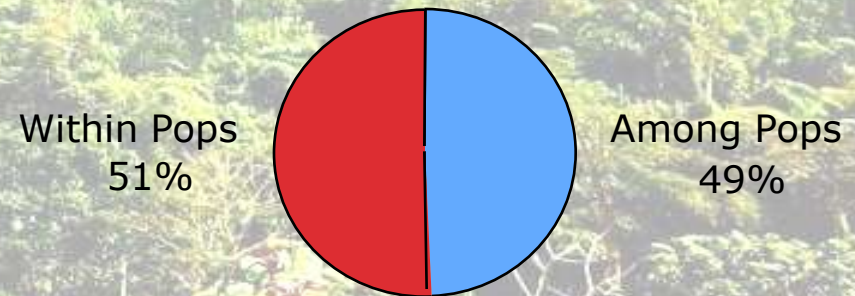
## Percentages of Molecular Variance in the entire collection



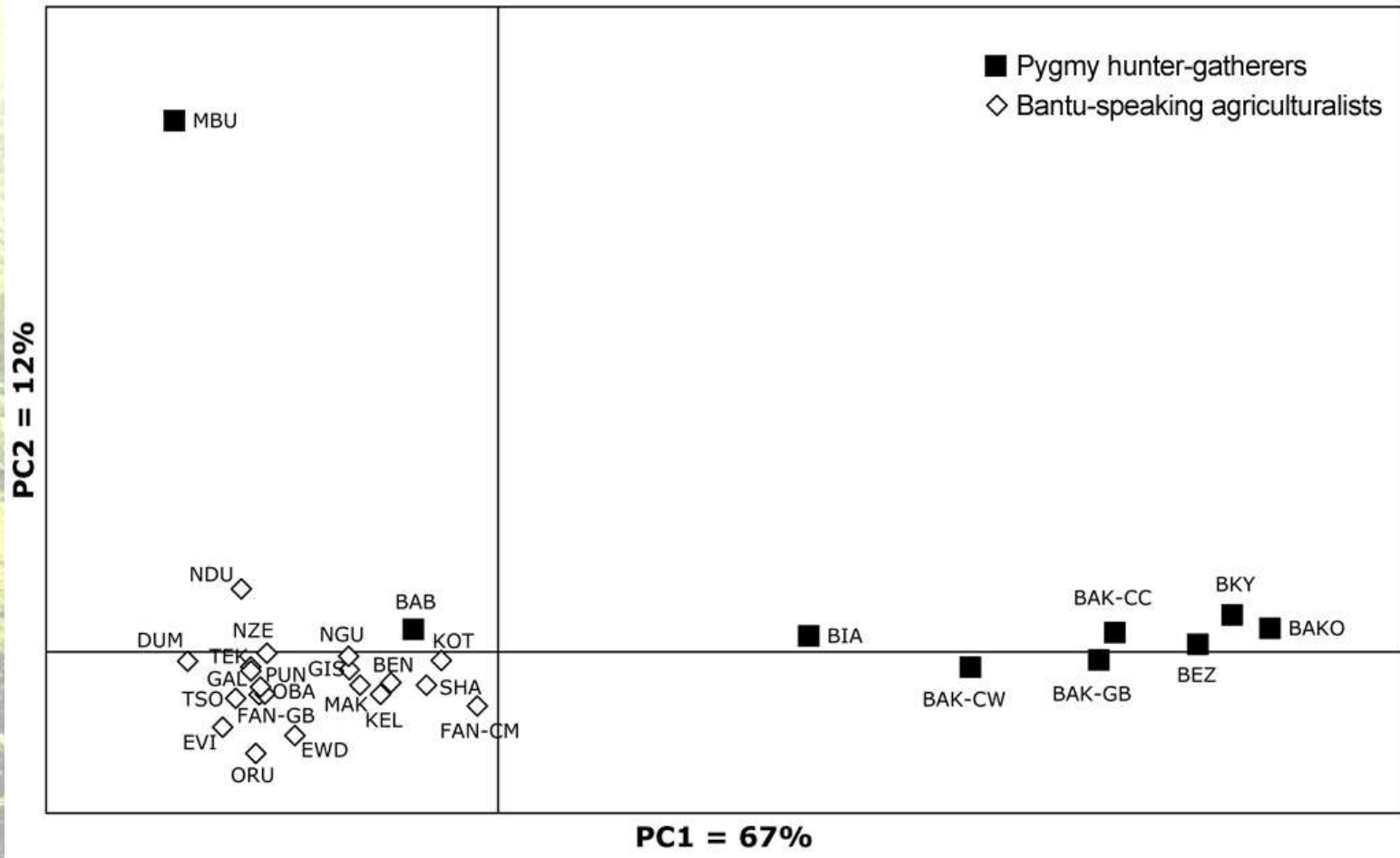
## Percentages of Molecular Variance in Bantu-speaking farmers



## Percentages of Molecular Variance in Pygmy hunter-gatherers



# Population relationships: entire collection



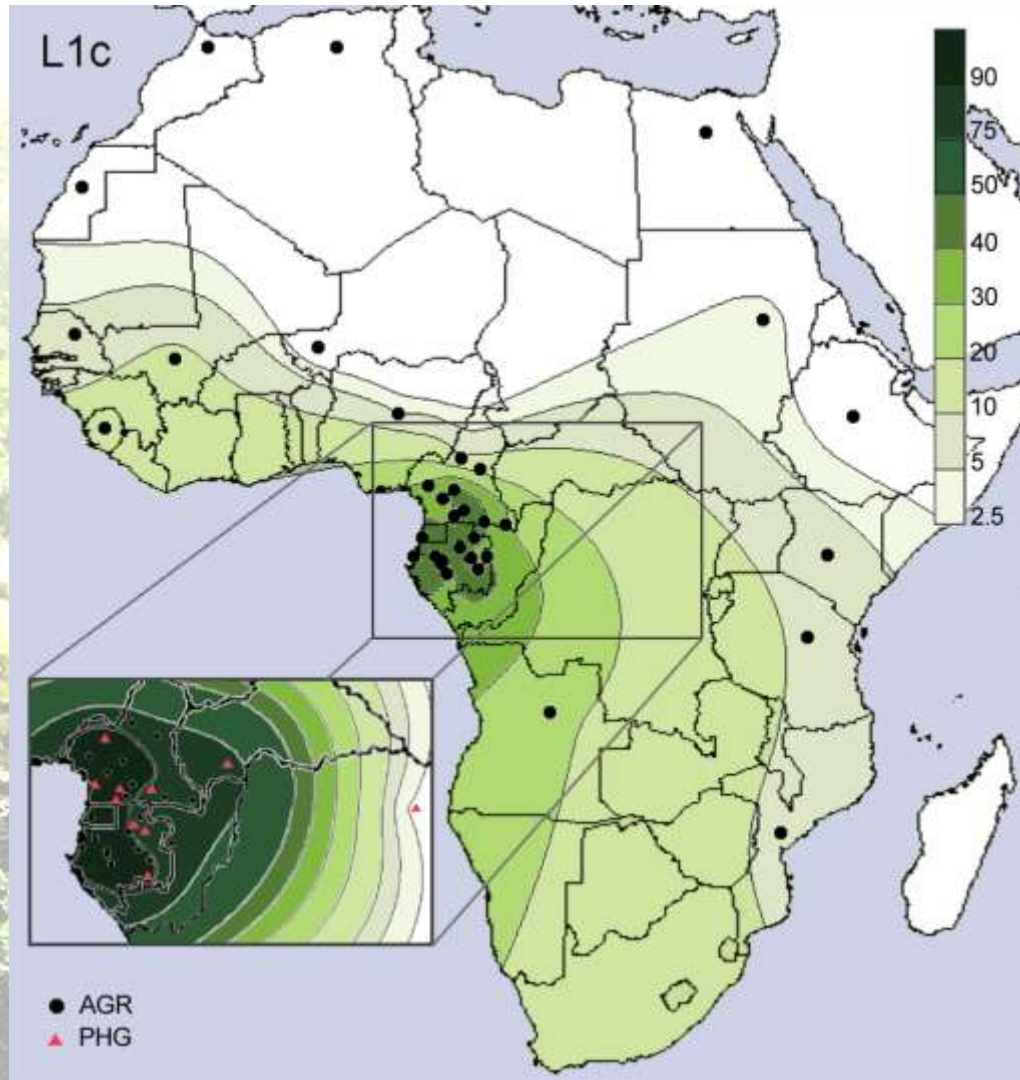
# Hg profiles

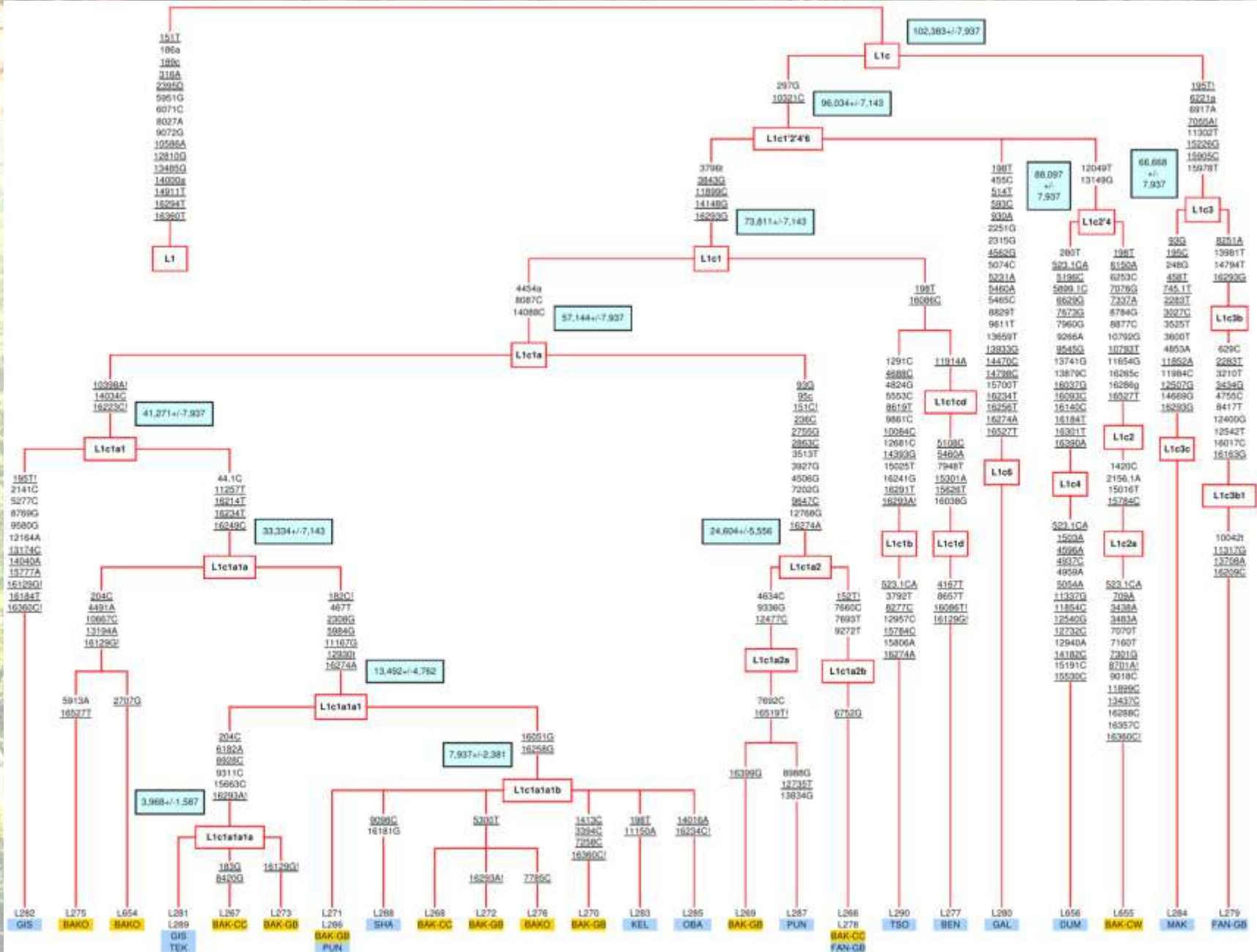
Haplogroup	AGR		Western PHG		Eastern PHG	
	N	%	N	%	N	%
L0a1	64	6.5%	3	0.8%	0	0.0%
L0a2	26	2.6%	7	1.8%	10	25.6%
L1b	63	6.4%	0	0.0%	0	0.0%
L1c*	5	0.5%	0	0.0%	0	0.0%
L1c1	14	1.4%	1	0.3%	0	0.0%
L1c1a1	113	11.5%	204	53.4%	0	0.0%
L1c1a2	87	8.9%	115	30.1%	0	0.0%
L1c1b	27	2.7%	21	5.5%	0	0.0%
L1c2	28	2.8%	5	1.3%	0	0.0%
L1c3	44	4.5%	0	0.0%	0	0.0%
L1c4	33	3.4%	13	3.4%	0	0.0%
L2*	3	0.3%	2	0.5%	0	0.0%
L2a*	1	0.1%	0	0.0%	8	20.5%
L2a1	131	13.3%	0	0.0%	0	0.0%
L2a2	4	0.4%	0	0.0%	17	43.6%
L2b1	13	1.3%	0	0.0%	0	0.0%
L2b2	2	0.2%	0	0.0%	0	0.0%
L2c2	16	1.6%	0	0.0%	0	0.0%
L2d	12	1.2%	1	0.3%	0	0.0%
L3*	8	0.8%	0	0.0%	0	0.0%
L3b	30	3.1%	0	0.0%	0	0.0%
L3d	38	3.9%	2	0.5%	0	0.0%
L3e1*	23	2.3%	2	0.5%	0	0.0%
L3e1a	28	2.8%	0	0.0%	0	0.0%
L3e1b	5	0.5%	0	0.0%	0	0.0%
L3e2*	17	1.7%	0	0.0%	0	0.0%
L3e2b	40	4.1%	0	0.0%	0	0.0%
L3e3	29	3.0%	0	0.0%	0	0.0%
L3e4	7	0.7%	0	0.0%	0	0.0%
L3f1b	56	5.7%	6	1.6%	0	0.0%
L3h	8	0.8%	0	0.0%	0	0.0%
L4	8	0.8%	0	0.0%	0	0.0%
L5	0	0.0%	0	0.0%	4	10.3%

L1 clades accounts for by 37% of agriculturalists and 95% of western Pygmies



# A likely central African origin of L1c





ESF Eurocores, OMLL Final Conference, Rome, December 12-14 2007

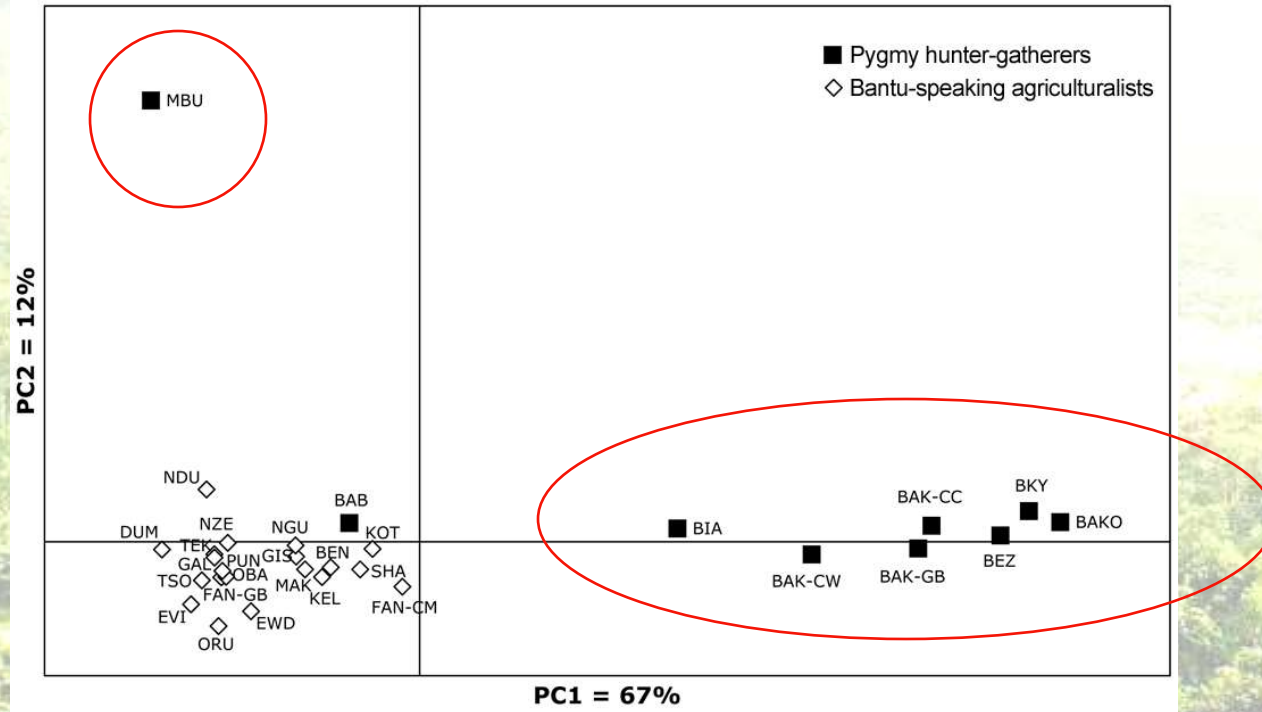
## A central African origin of L1c1a

- SNP typing of the whole collection for the internal SNPs within L1c
- L1c1a is present in 20.3% of AGR populations and 83.5% in PHG populations
- L1c1a is restricted to central Africa, presenting a coalescent time of ~57,100 YBP
- Our analyses show a central African origin of this lineage, suggesting that the ancestral population giving rise to both proto-farmers and Pygmies was mainly composed of this lineage

# The maternal gene pool of (proto) agriculturalists

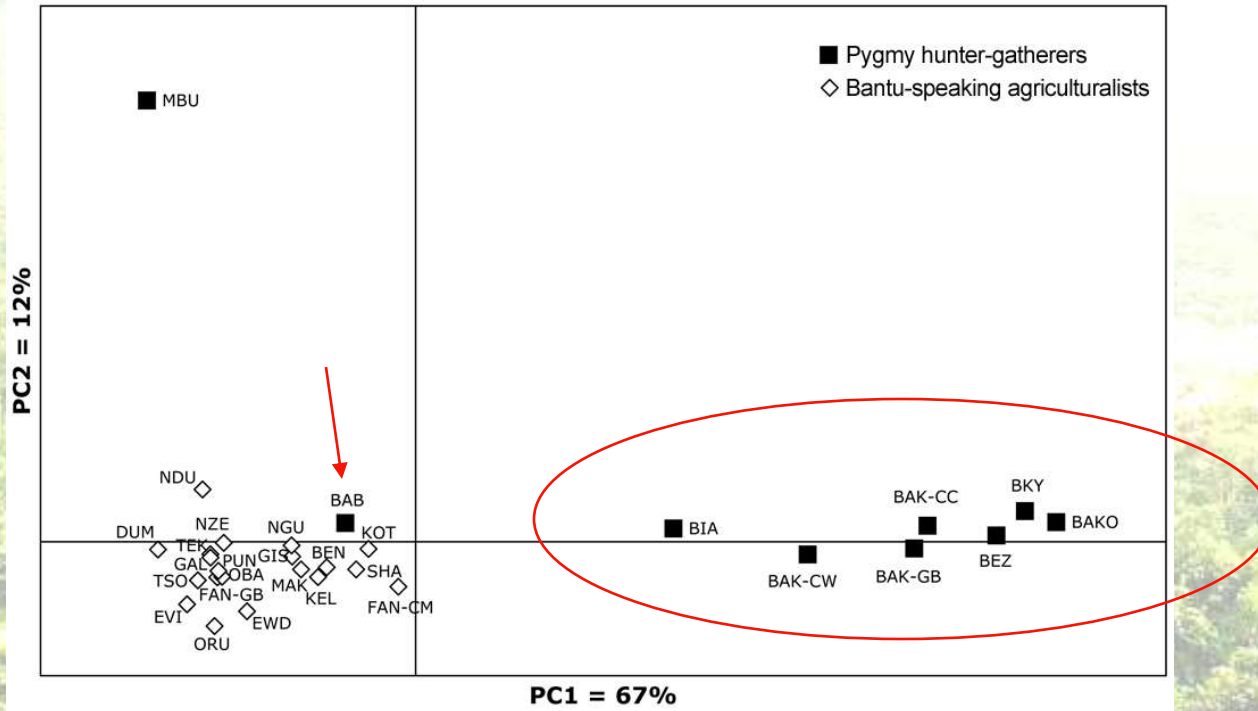
- The maternal gene pool of AGR is homogeneous (PC plot, AMOVA and 60% of FST are not significant)
- **L1c1a (20.3%)**, L2a1 (13.3%), L0a1 (6.5%), L1b (6.4%), L3e2 (5.8%), L3e1 (5.7%) and L3f1b (5.7%)
- The coalescence time of L1c1a (57,000 YBP) is 25,000 years older than the remaining Hgs, suggesting an initial central African gene pool dominated by L1c and later enriched by the arrival/or expansion of the carriers of other Hgs.

# The maternal gene pool of Pygmy hunter-gatherers



- All  $F_{st}$  are significant involving Mbuti
- Phylogeographically, no hgs shared, completely different genetic background
- Clear lack of common maternal ancestry
- Real lack of common ancestry? Convergence?

# Western Pygmies

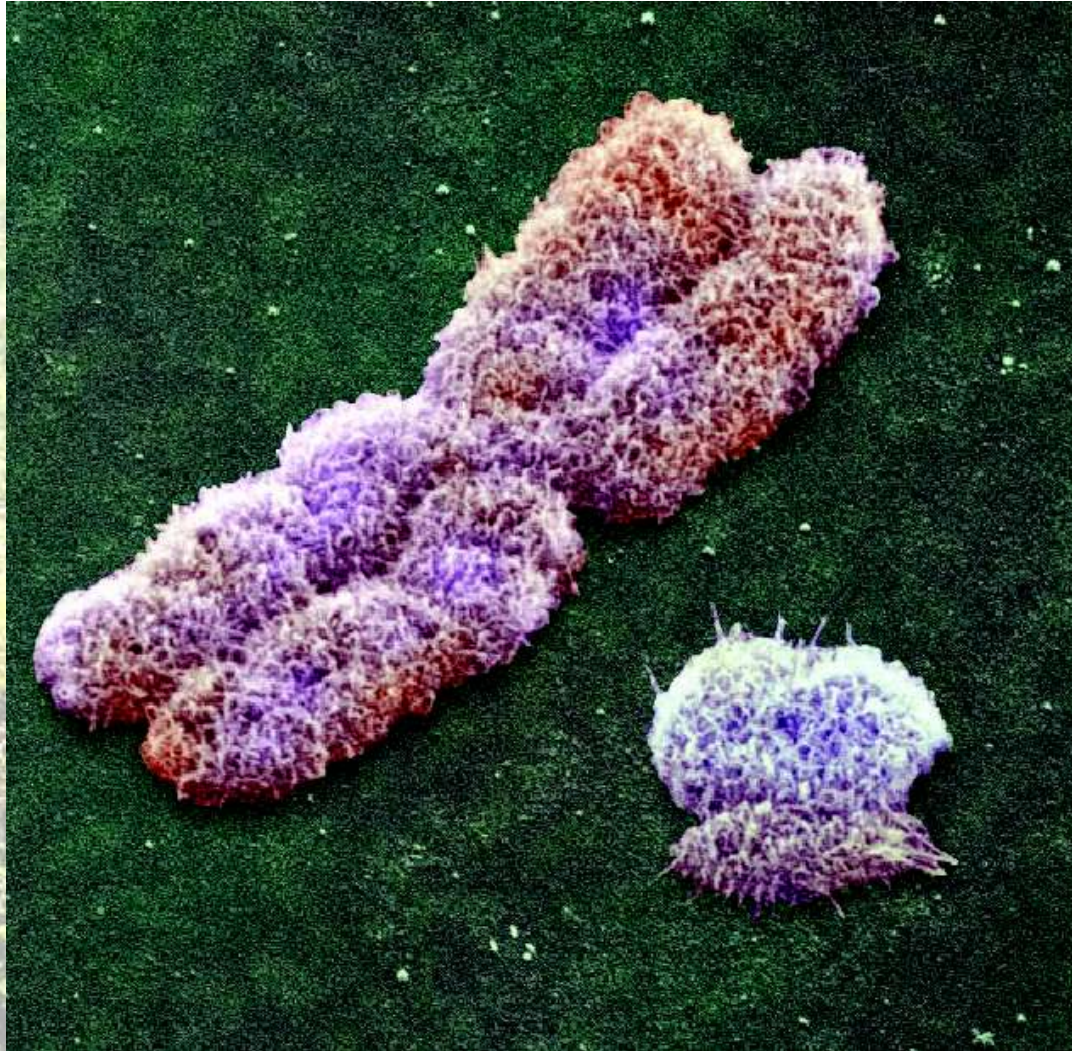


- More heterogeneous (12% of inter-pop) than the group of agriculturalists
- Babongo? Gene flow? Inter-cultural marriages are more common
- ~83.5% of contemporary western PHG share a single maternal ancestor in the form of the autochthonous Central African Hg L1c1a (in the form of the two sister clades L1c1a1 and L1c1a2).

# Conclusions

- initial divergence of the ancestors of contemporary Pygmies from an ancestral Central African population starting not earlier than ~70,000 years ago (their last common ancestor)
- a period of isolation between the two groups needed to explain their phenotypic differences
- long-standing and asymmetrical maternal gene flow from Pygmies to agriculturalists, starting not earlier than ~40,000 years ago (the time when the two shared lineages appeared) and persisting until the last few thousands of years (sharing of recently appeared lineages between the two groups)
- enrichment of the proto-agriculturalist maternal gene pool by the arrival and/or posterior demographic expansion of L0a, L2 and L3 carriers.

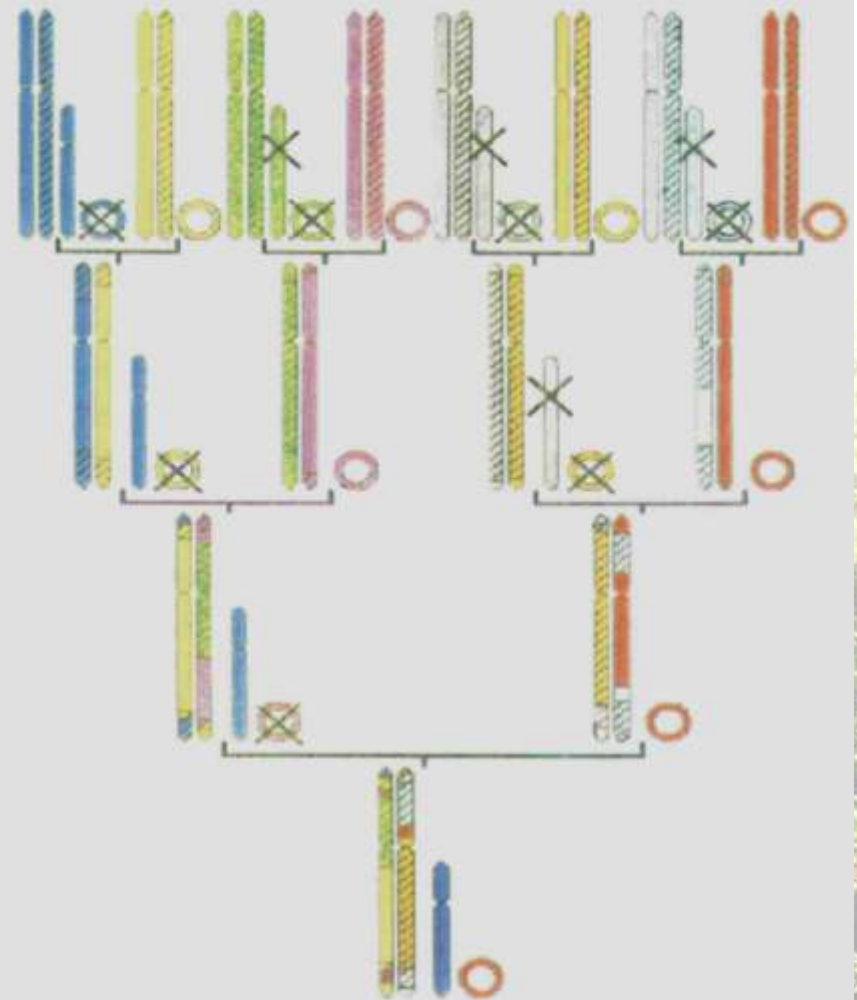
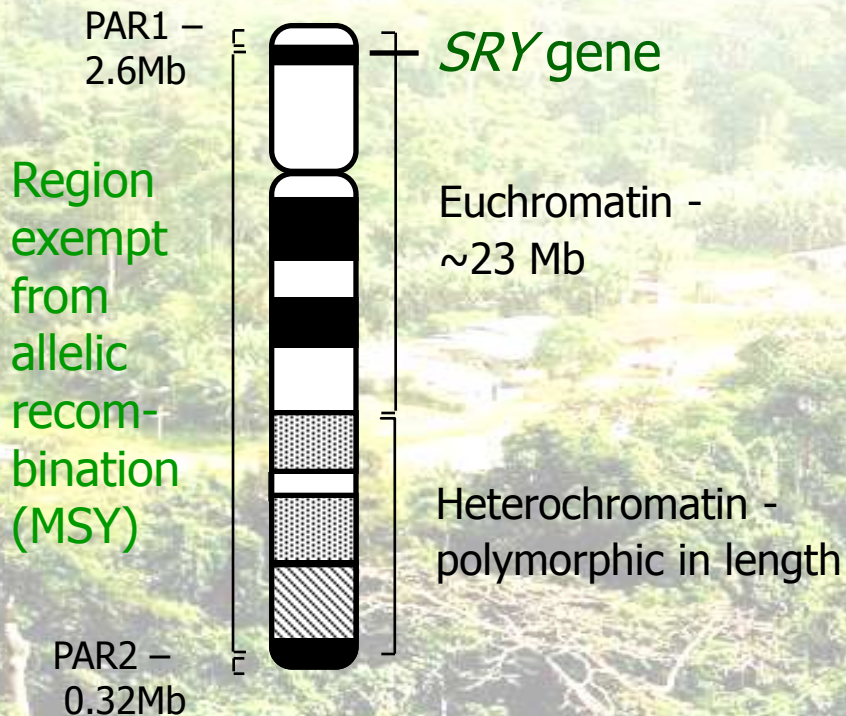
# Y-chromosome diversity in W-C Africa



ESF Eurocores, OMLL Final Conference, Rome, December 12-14 2007



# Y-chromosome diversity in W-C Africa



# Y-chromosome diversity in W-C Africa

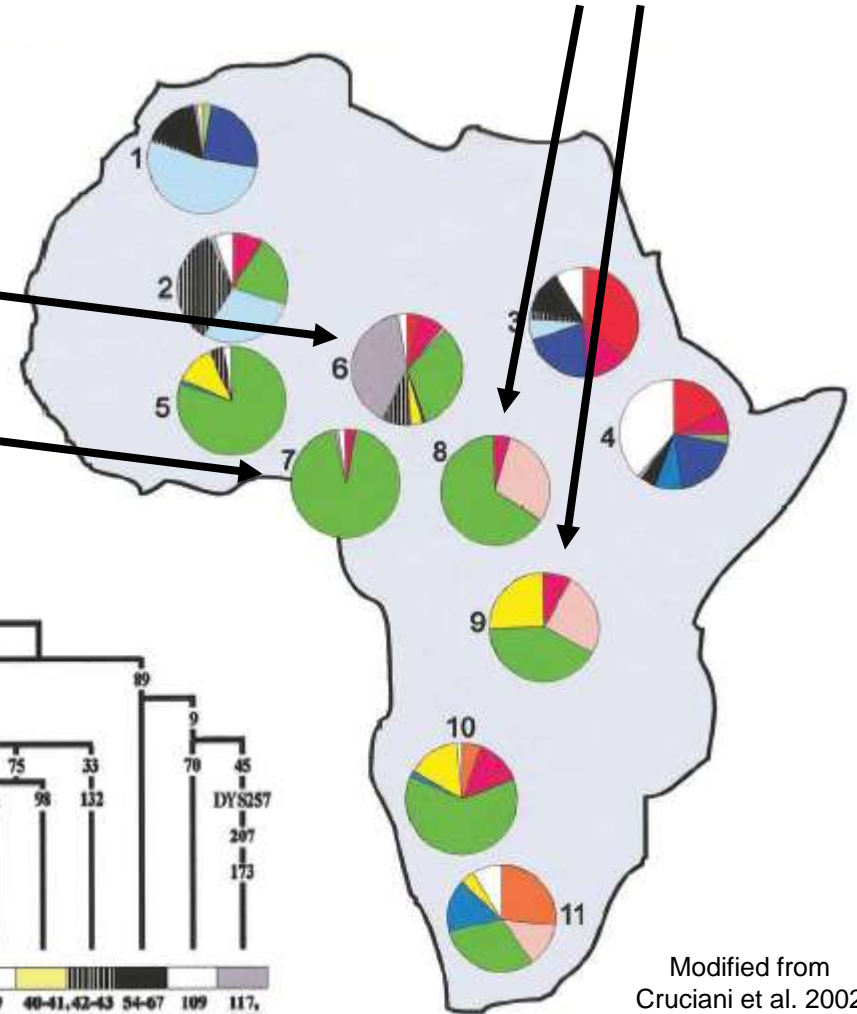
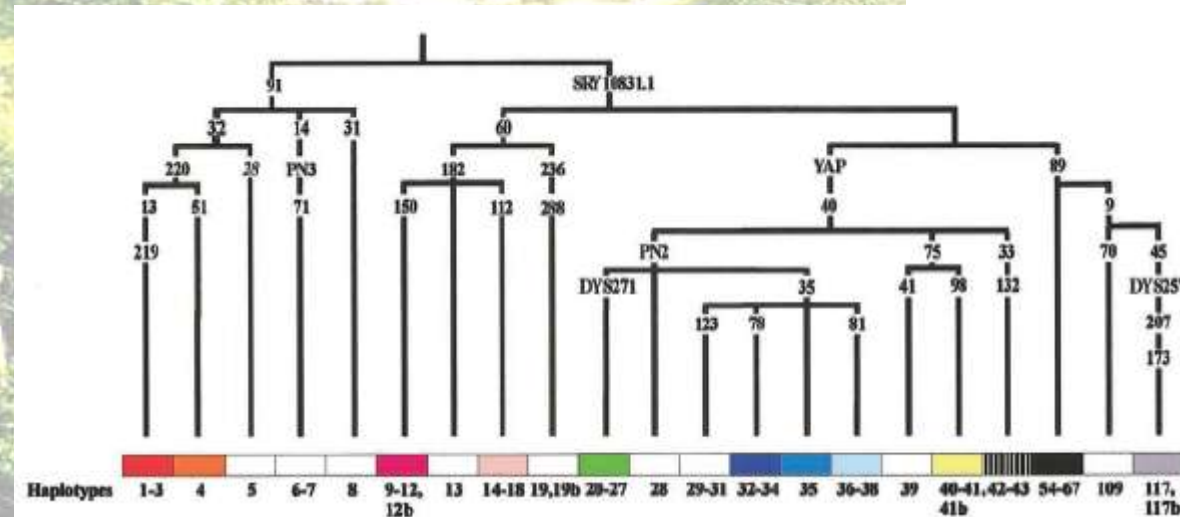
Specific lineages in Pygmy

Eurasian lineage in Northern Cameroon:  
back migration from Asia ?

Northern Cameroon

Southern Cameroon

Eastern Pygmies



Modified from  
Cruciani et al. 2002

# Y-chromosome diversity in W-C Africa



## Central/West African collection:

- ~900 samples from Gabon and Cameroon
  - 3 Pygmy samples
  - 20 Bantu-speaking agriculturalists

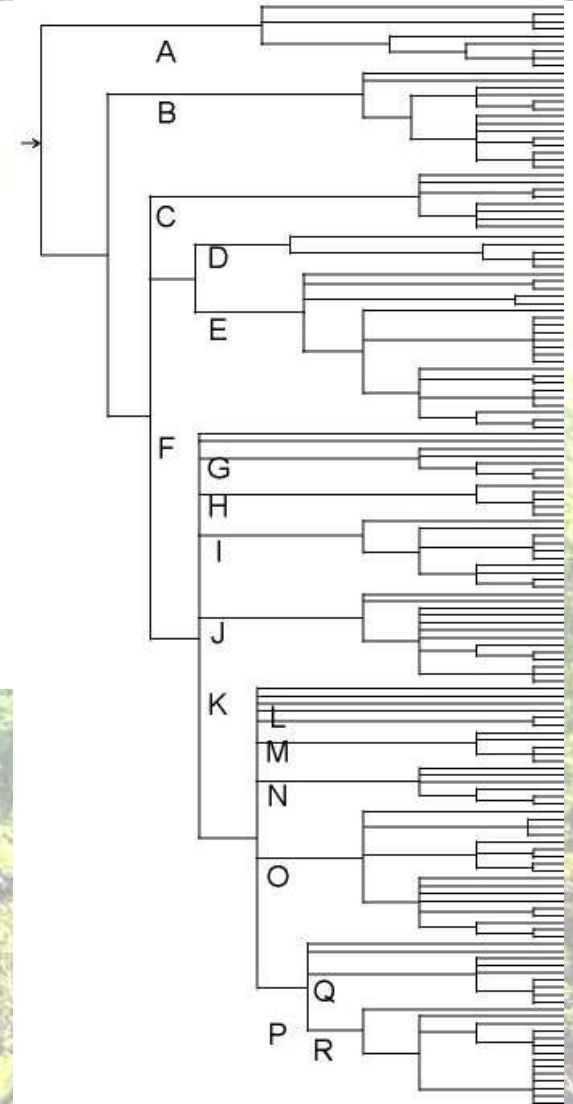
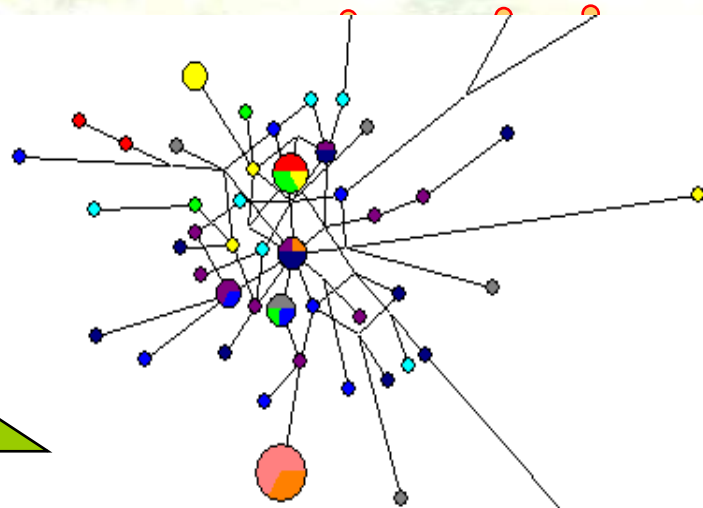
## - 20 Bantu-speaking agriculturalists pops:

**Gabon:** Benga, Duma, Eviya, Fang, Galoa, Eshira, Kele, Kota, Makina, Ndumu, Nzebi, Obamba, Orungu, Punu, Shake, Teke, Tsogo, Bekwil, Ngumba, Okande

## - 3 Pygmy populations:

- 1 Baka population from Central/East Cameroon
- 1 Baka population from Gabon
- 1 Bakola population from Cameroon

# Y-chromosome diversity in W-C Africa



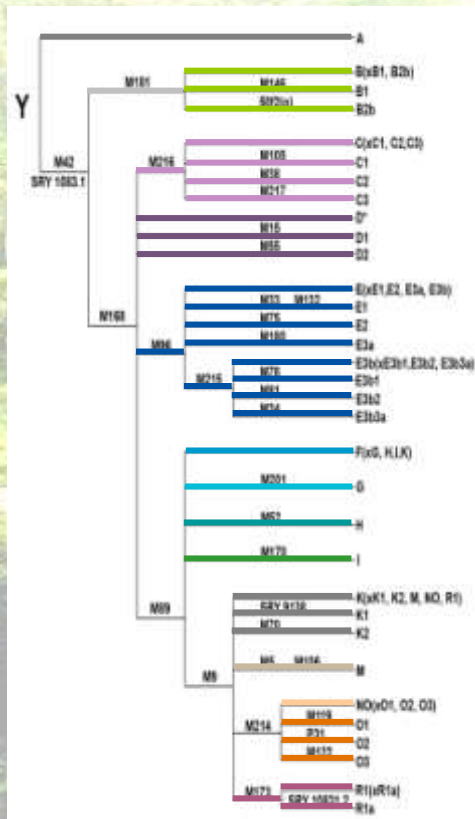
STRs

18 STR markers

Biallelic markers

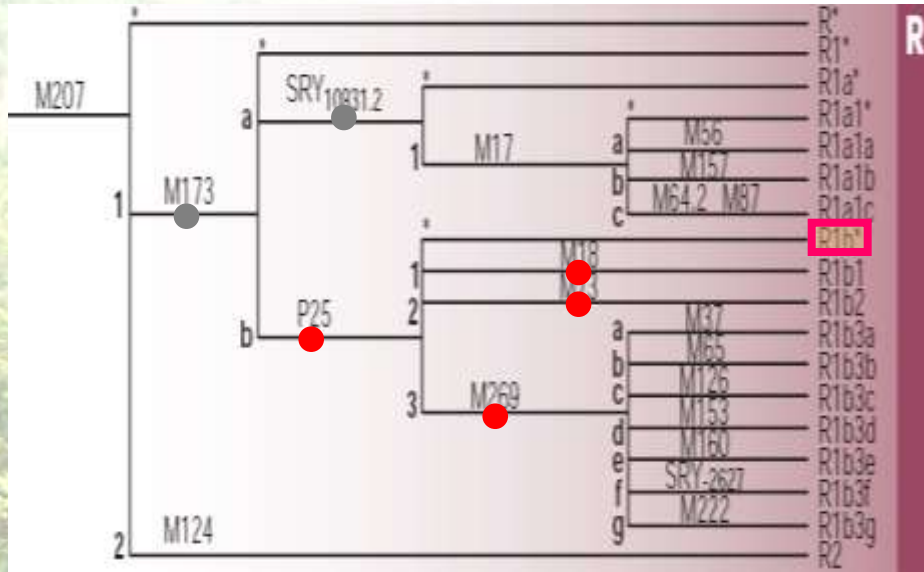
~ 40 SNP markers

# Y-chromosome diversity in W-C Africa



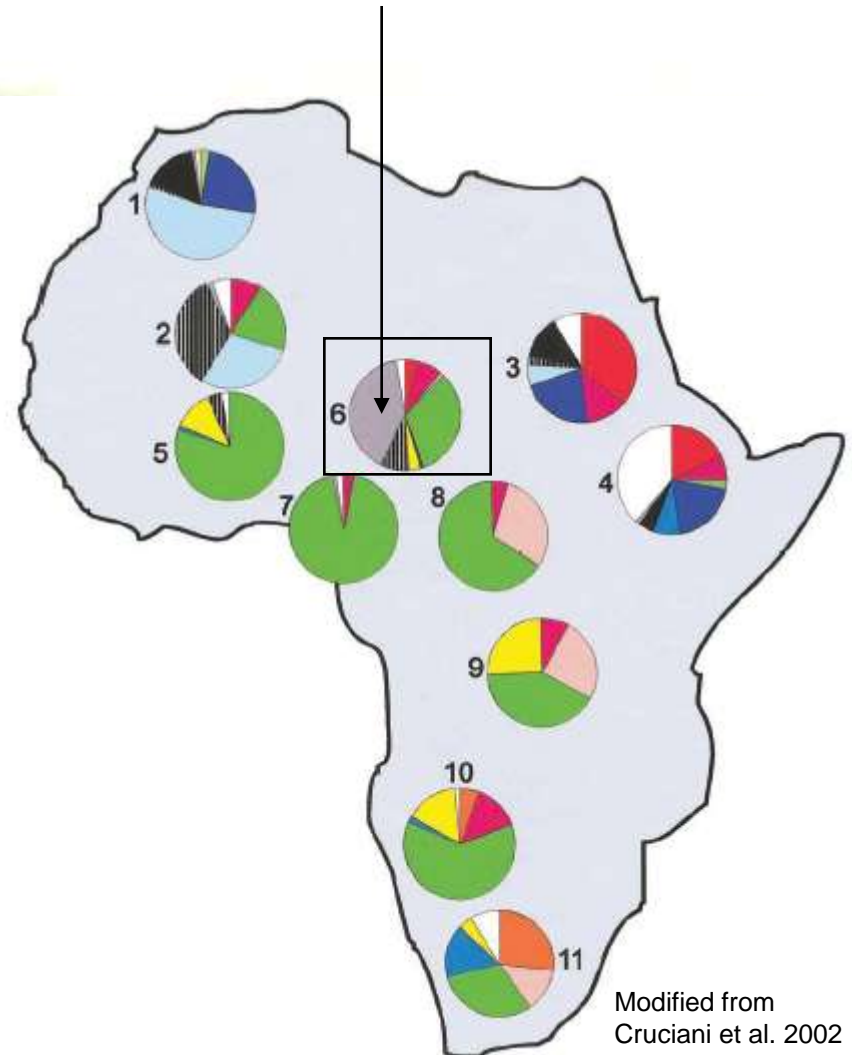
%	Kele	Bekwil	Benga	Duma	Eviya	Fang	Kota	Makina	Ndumu	Nzebi	Obamba	Orungu	Punu	Shake	Teke	Tsogo	Eshira	Galaa	Okande	Bakola	BakaG	BakaC
A				2					3	3						2					9	
B2a	2		4	2	21	2	4	14	3	7	4		7	9		8	17	2		9		
B2b			2	4	4		2					5	2	7						27	64	60
E		20	2						3			5	2					2		5	12	20
E1							2					5										
E2	12		2	9	17		2	2	5	2	11	10	4	9	8	5	12	4				
E3a	84	80	85	80	58	80	85	84	75	84	74	76	74	72	81	85	71	89	100	55	12	20
E3b1																		2				
G			2																			
R1b	2		2	2		19	6		11	3	11		12	2	10					5	3	
Total	50	5	48	46	24	64	53	43	36	57	47	21	58	43	48	60	42	47	6	22	33	5

# Y-chromosome diversity in W-C Africa



**Haplogroup R1b\***  
 North Africa  
 Middle East

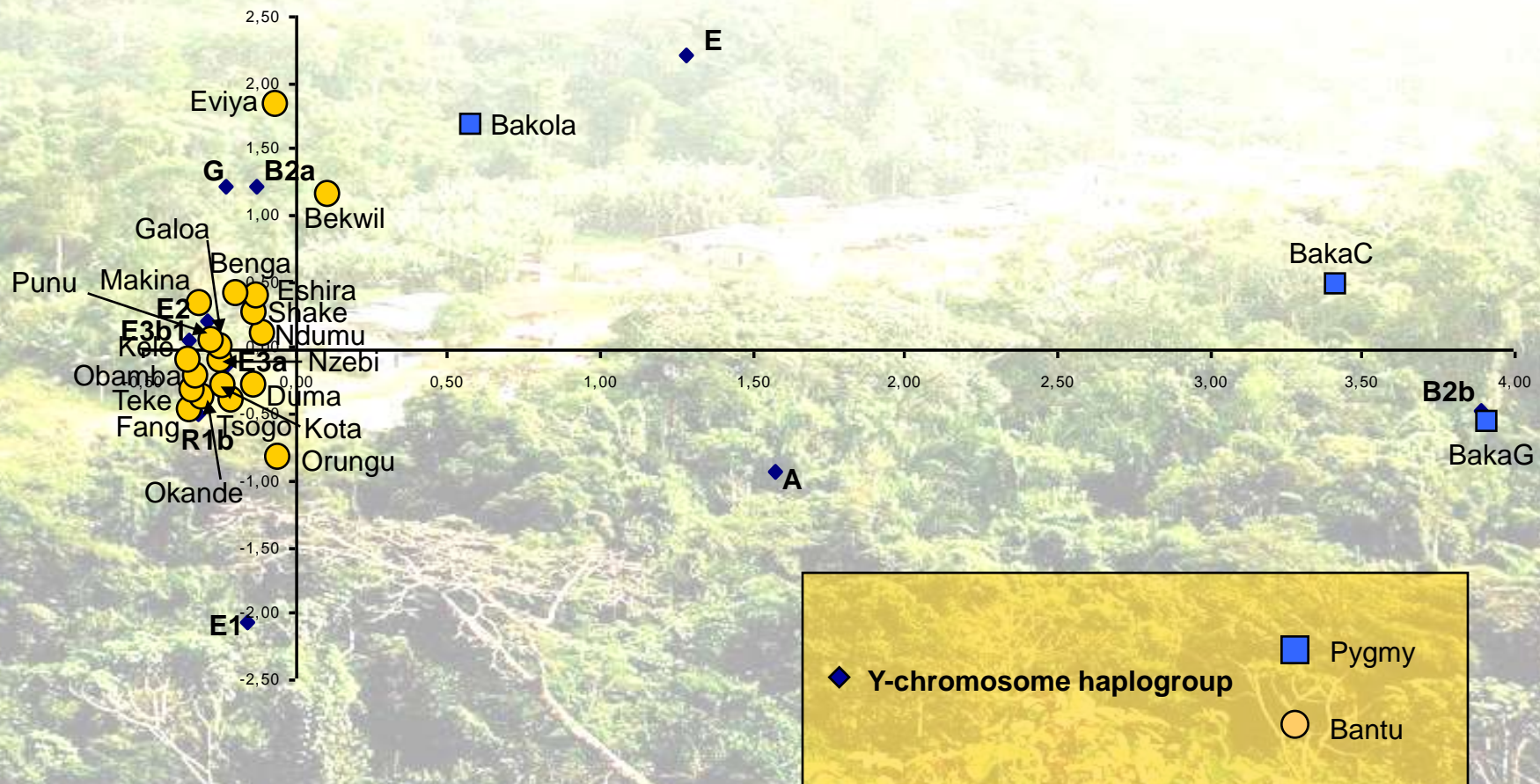
## Haplogroup R1b\*



Modified from  
 Cruciani et al. 2002

# Y-chromosome diversity in W-C Africa

Correspondence analysis: haplogroup composition  
First two dimension plot (75.6% genetic variance)



# Y-chromosome diversity in W-C Africa

Analysis of MOlecular VAriance (AMOVA):  
haplogroup composition

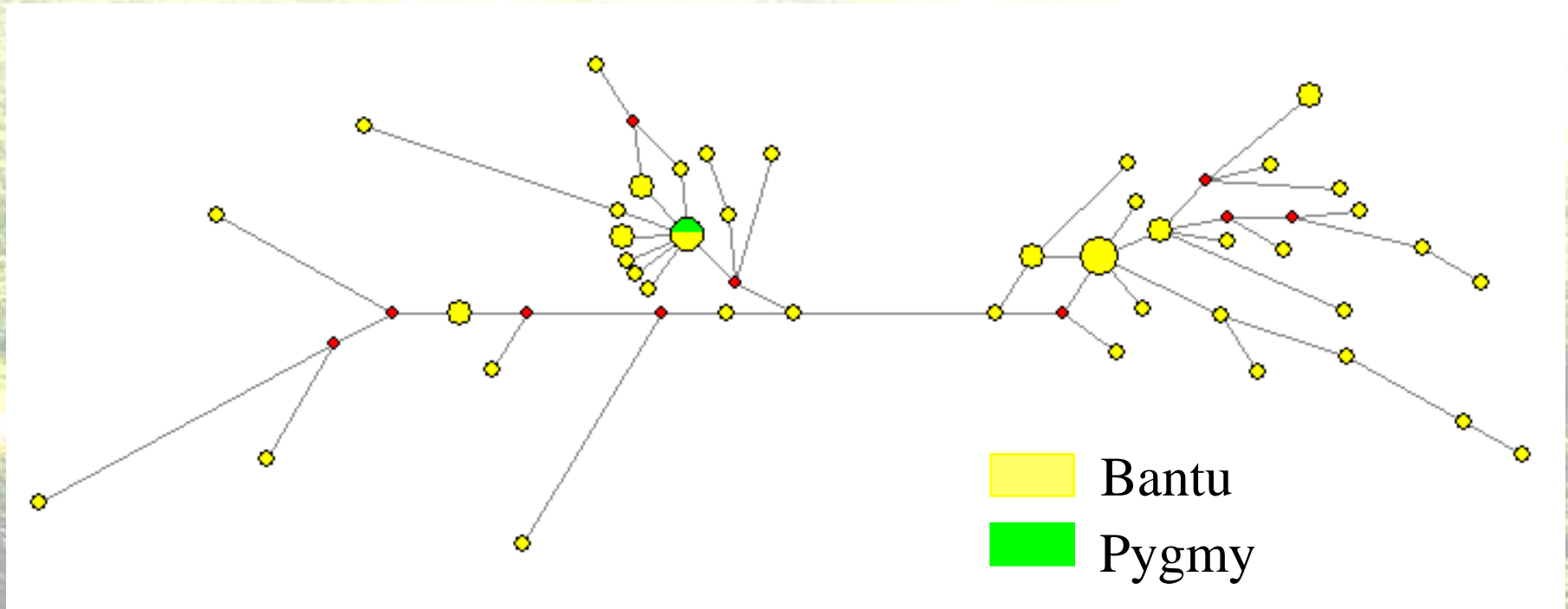
<u>HAPLOGROUPS</u>	Between groups	Among populations	Within Populations
All populations		12%	88%
Bantu agriculturalist		2%	98%
Pygmy		25%	75%
Bantu versus Pygmy	34%	3%	63%

All values are significant ( $p < 0.001$ )

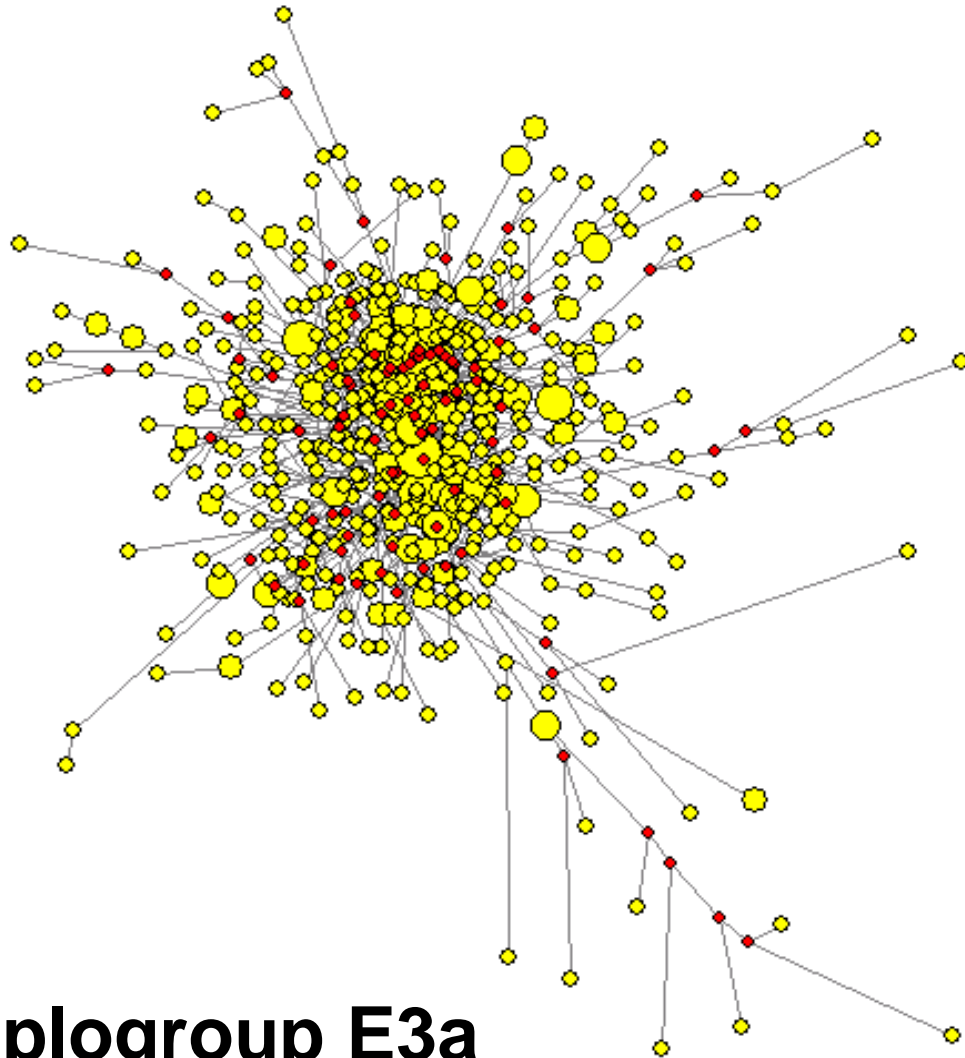


# Y-chromosome diversity in W-C Africa

## Haplogroup B2a



# Y-chromosome diversity in W-C Africa



**Haplogroup E3a**

# Y-chromosome diversity in W-C Africa

Founder Bantu Haplotype (Thomas et al. 2000)

HAPLOGROUP E3a

DYS 391 - DYS 390 - DYS 393 - DYS 392 - DYS 19



10 - 21 - 13 - 11 - 15

One step-neighbours:

11 - 21 - 13 - 11 - 15

10 - 22 - 13 - 11 - 15

10 - 21 - 12 - 11 - 15

10 - 21 - 14 - 11 - 15

10 - 21 - 13 - 10 - 15

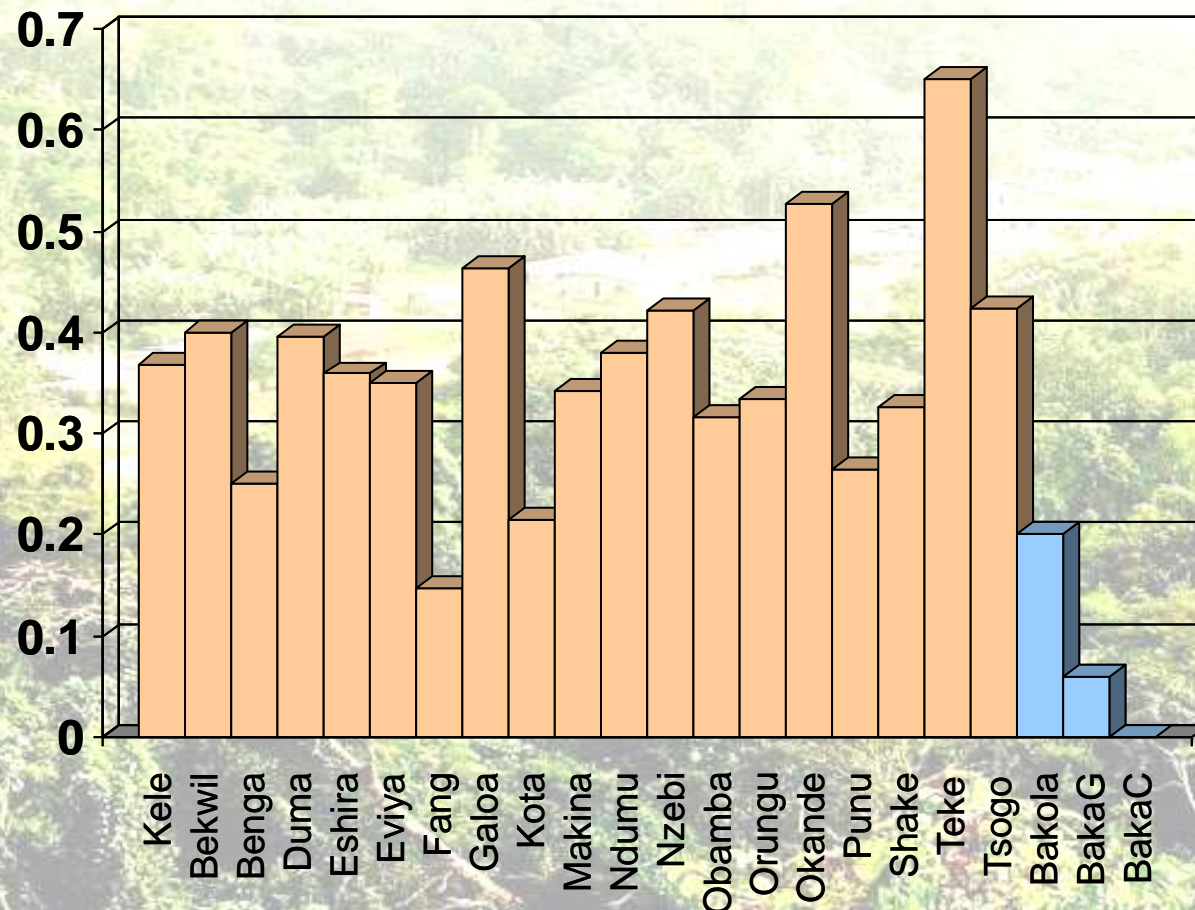
10 - 21 - 13 - 12 - 15

10 - 21 - 13 - 11 - 14

10 - 21 - 13 - 11 - 16

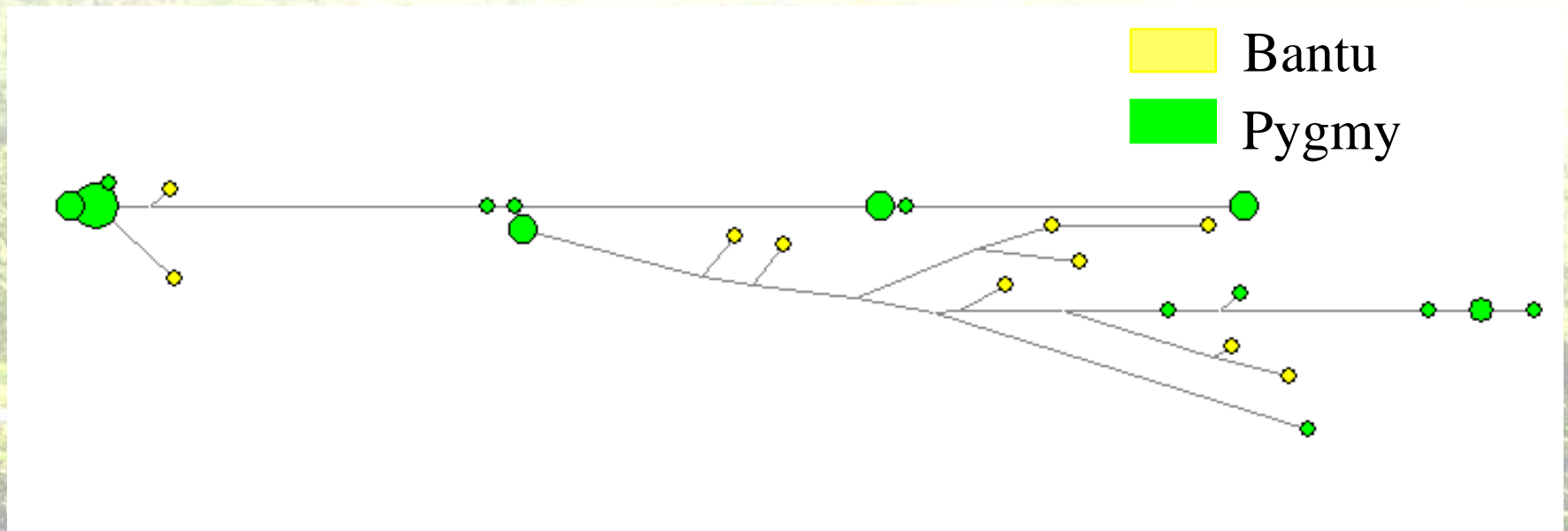
# Y-chromosome diversity in W-C Africa

Founder “Bantu haplotype” frequencies



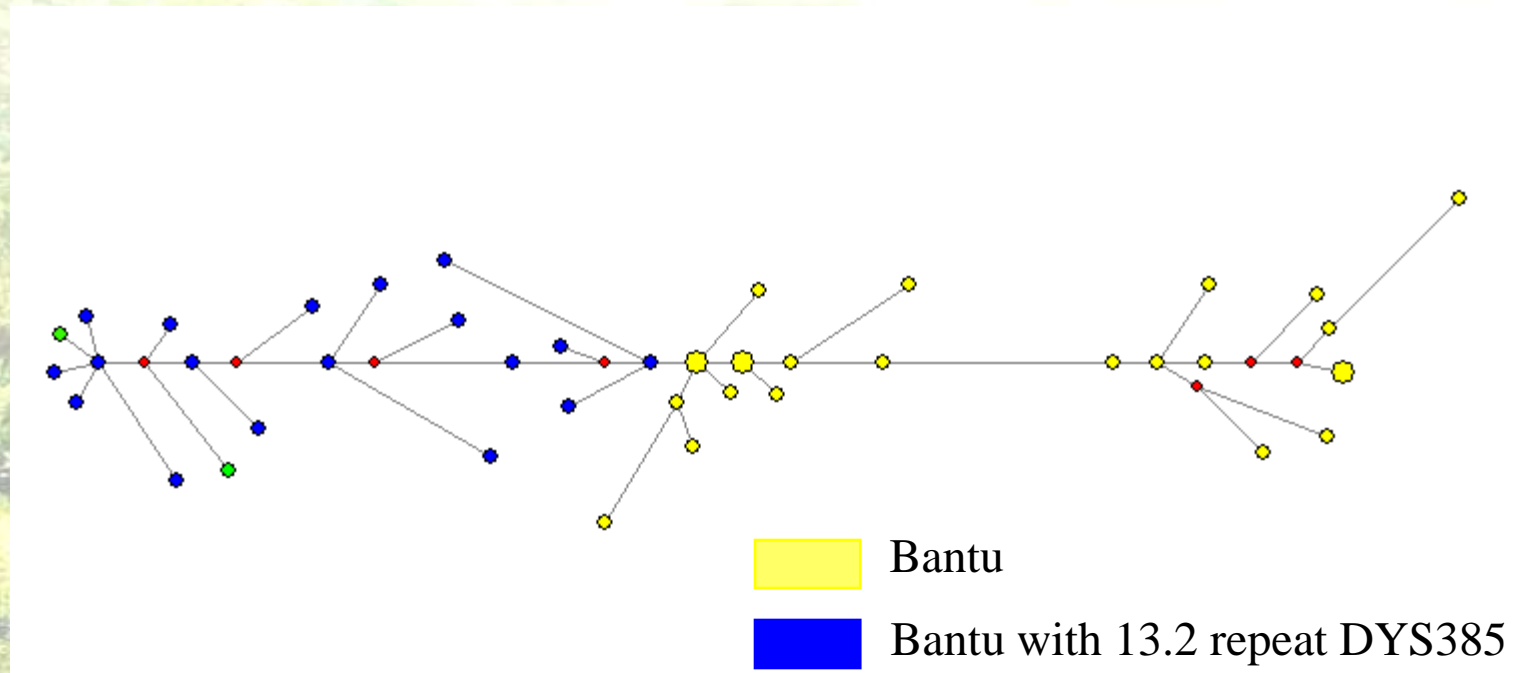
# Y-chromosome diversity in W-C Africa

## Haplogroup B2b

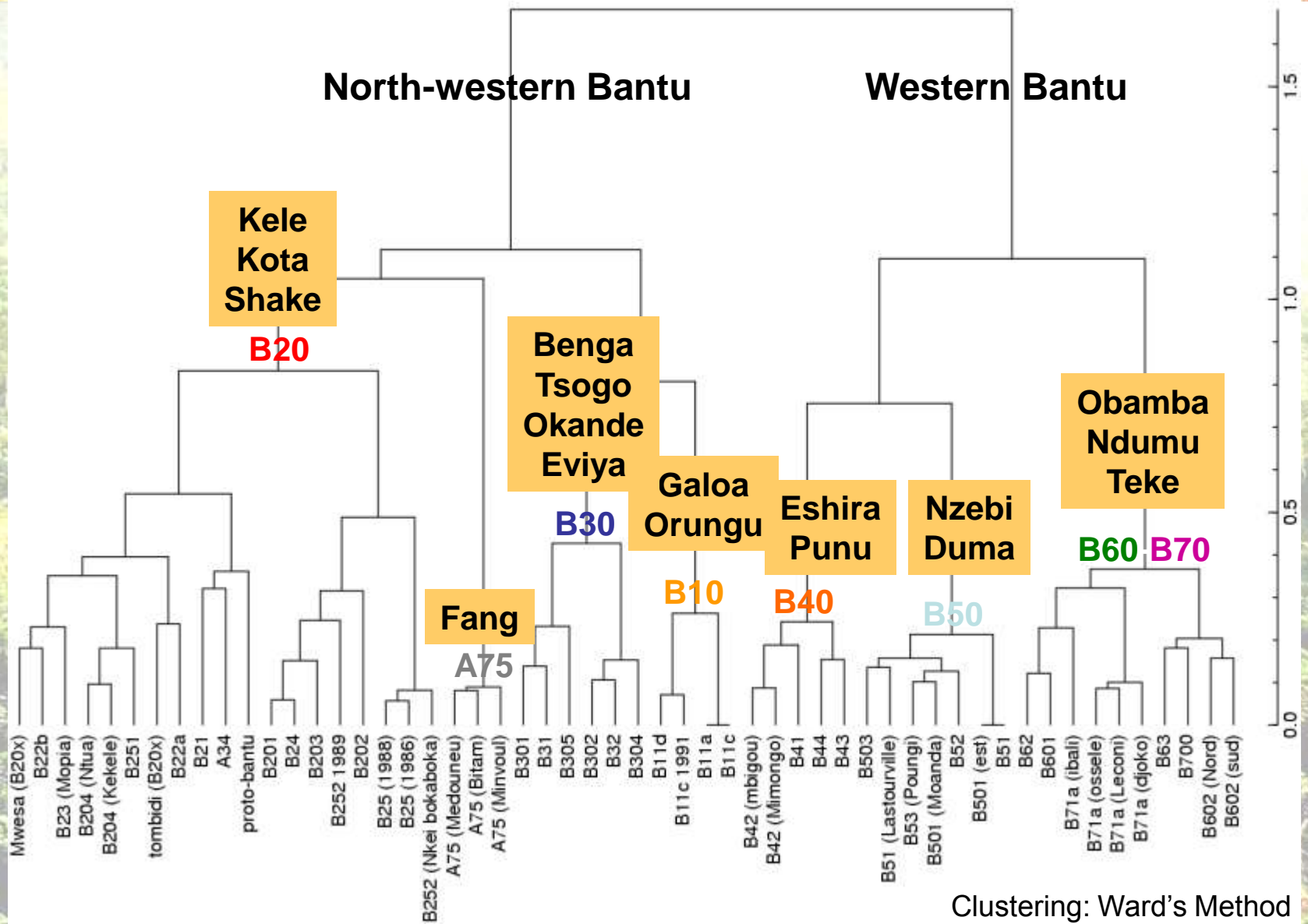


# Y-chromosome diversity in W-C Africa

## Haplogroup R1b\*



# Y-chromosome diversity in W-C Africa



# Y-chromosome diversity in W-C Africa

- **Genetic differentiation between Bantu/Pygmies: common ancestry, differentiation and contacts**
- **Bantu agriculturalist homogeneity/Pygmy heterogeneity: Bantu expansion and Pygmy isolation**
- **Sexual asymmetry: Bantu Y lineages into Pygmy**
- **Presence of non-African haplogroup in Bantu (R1b): contact with northern populations**



# Conclusions and perspectives

- Description of W-C African genetic landscape
- Differentiation between agriculturalists and Pygmies:
  - Common ancestors, isolation and gene flow
- Asymmetrical gene flow:
  - Maternal gene flow from Pygmy to Bantu agriculturalists
  - Paternal gene flow from Bantu agriculturalist to Pygmy
  - The offspring can be assimilated in both groups
- Homogeneity within agriculturalists: common and recent origin: Bantu expansion.
- Lack of correlation between genes and languages
- Ethnic groups or populations socially constructed



**Thank you for your attention!**

