THE CHALLENGE OF DEFINING CONSERVATION PRIORITIES OF LIVESTOCK BREEDS

Ginja *et al. Genetics Selection Evolution* 2013, **45**:35
http://www.gsejournal.org/content/45/1/35

GSE Genetics Selection Evolution

RESEARCH Open Access

Analysis of conservation priorities of Iberoamerican cattle based on autosomal microsatellite markers

Catarina Ginja

http://biobovis.jimdo.com/

BIOBOVIS CONSORTIUM

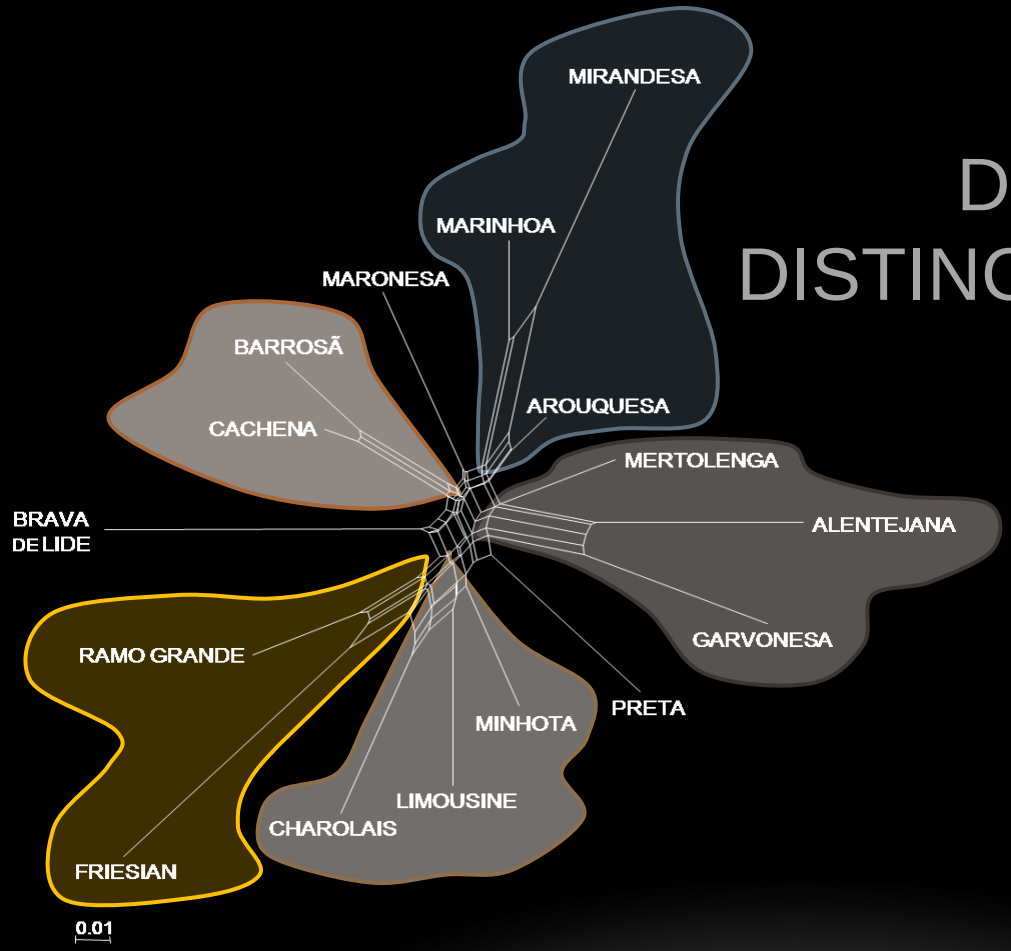
CONSERVATION PRIORITIES

Maximize genetic diversity?

Yakow

Zubron/Cattalo

Conservation priorities



GENETIC DIFFERENTIATION ?
DISTINCT EVOLUTIONARY HISTORIES

Conservation priorities

WHICH SCALE?

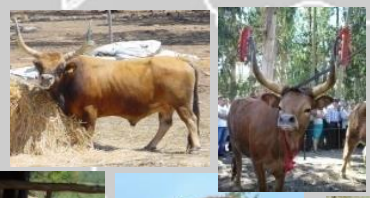
Portugal
Iberia
Europe
Americas

SPECIES

15 Native cattle Breeds
Recent evolutionary History
< 600 years

145 <	**Adult Females**	**< 15,000**
3 <	Mean herd size	< 54

AZORES ARCHIPELAGO













CONTINENTAL PORTUGAL

93,345 Km²
< 11,000,000 population

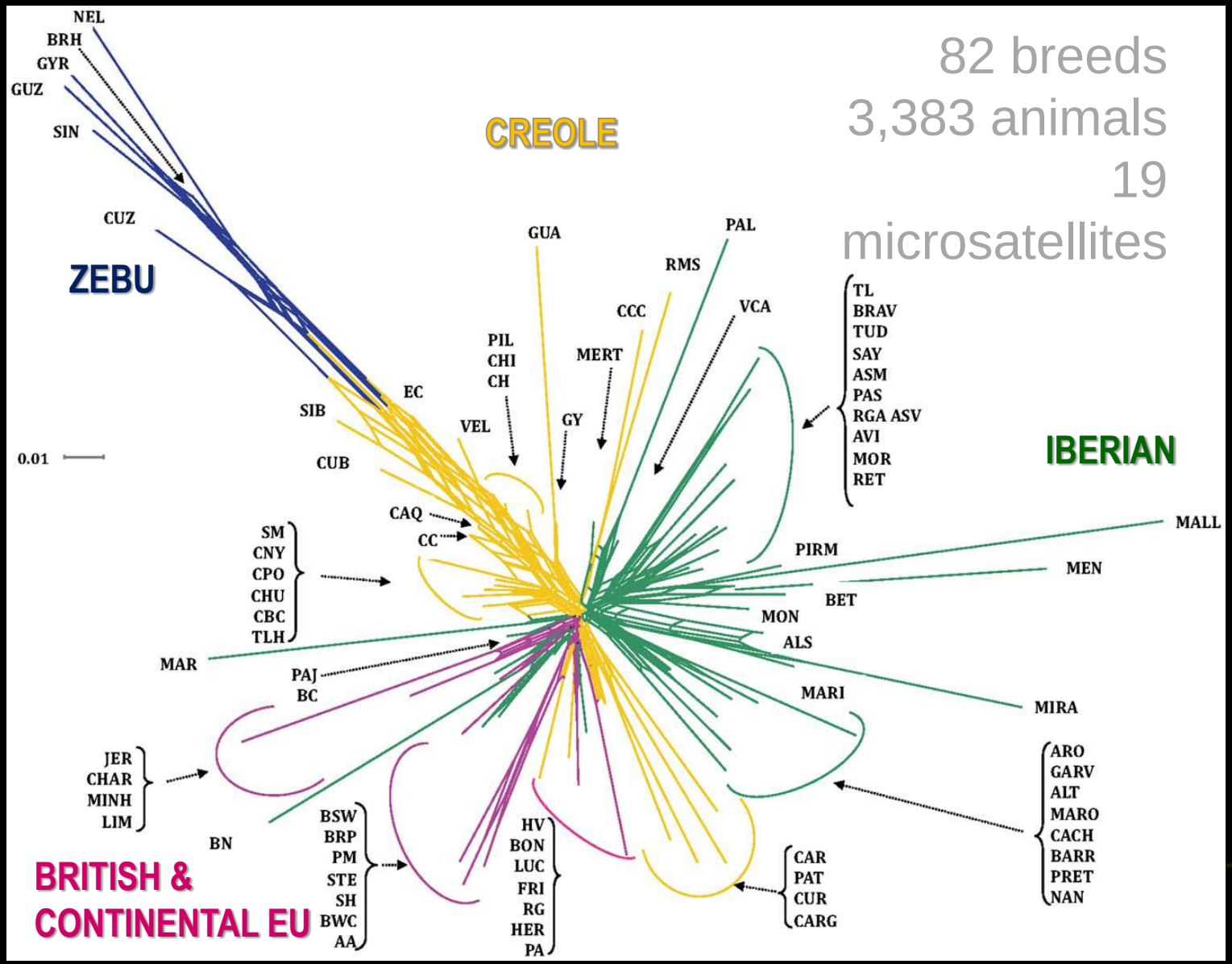
BIODIVERSITY HOTSPOTS

AIM

To analyse the contribution of each breed/geographic breed group to the total genetic diversity – metapopulation

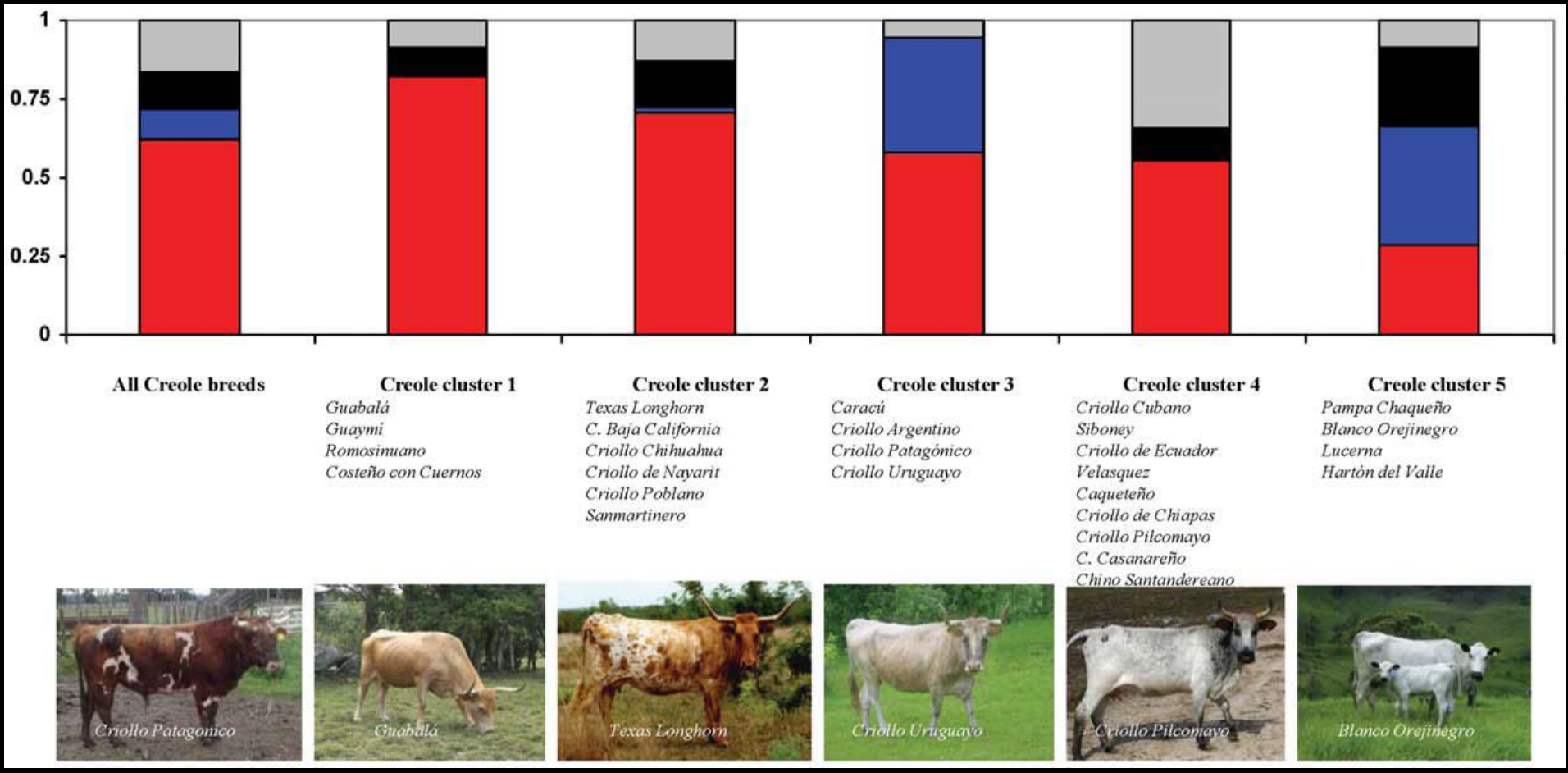
Tools to
- Manage animal genetic resources
- Define conservation programs

POPULATIONS & BREED GROUPS



Martínez, A. *et al.* (2012). PlosONE7 (11): e4906

Contribution of Iberian, U.K., Continental EU & Zebu breeds to Creole cattle



CONSERVATION ANALYSES

- Weitzman approach (PC_{Wei}) – approximation algorithm

  Reflects *only* breed differentiation

  Reynolds genetic distances

- Within-breed genetic diversity assessed directly

  From heterozigosity (PC_{He})

- Combined approach – Ollivier & Foulley ($PC_{Fst}/PC_{5:1}$) – within- & between-breed genetic diversities weighted by Fst or a 5:1 proportion

CONSERVATION ANALYSES

KINSHIP-BASED METHODS

To minimize overall kinship coefficient of the metapopulation

- **Eding & Meuwissen 2001**

  MEKs obtained from individual genotypes

- **Caballero & Toro 2002**

  Average molecular coancestries (*fm*) based on allele frequencies

  Contributions to global coancestry (f) & average Nei's distance

CONSERVATION ANALYSES

2 DIMENSIONS

- **Creole cattle**

  27 populations from 12 countries

- **13 breed groups**

  geographical distributions & types

  e.g. taurine, indicine & crossbred

  6 Creole

  1 U.K.
  1 Zebu

  4 Iberian

  1 Continental EU

rather than a metapopulation of worldwide cattle

RESULTS

PARTIAL CONTRIBUTIONS

IBERIAN

PC_{Wei} (CB)	PC_{He} (CW)	MEKs	PC_{Fst} 0.090*CB+0.910*CW	$PC_{5:1}$ 0.833*CB+0.167*CW
MAL 7.523	STE 0.269	SAY 0.318	MEN 0.482	MAL 6.204
PAL 7.048	RET 0.265	MAL 0.164	SAY 0.451	PAL 5.818
MIR 6.798	SAY 0.251	RET 0.153	BN 0.389	MIR 5.608
MEN 6.401	ASV 0.244	MON 0.131	RET 0.372	MEN 5.317
BN 6.325	MON 0.219	VCA 0.089	MON/NAN 0.368	BN 5.238

- MAL, PAL, MIR, MEN, BN
  >>> genetic distances, distinct evolutionary histori

- STE, RET, SAY, ASV, MON
  >>> within-breed diversity, *i.e.* heterozigosity

Cañon, J. *et al.* (2011). Animal 5(9): 1323-

RESULTS

PARTIAL CONTRIBUTIONS

CREOLE

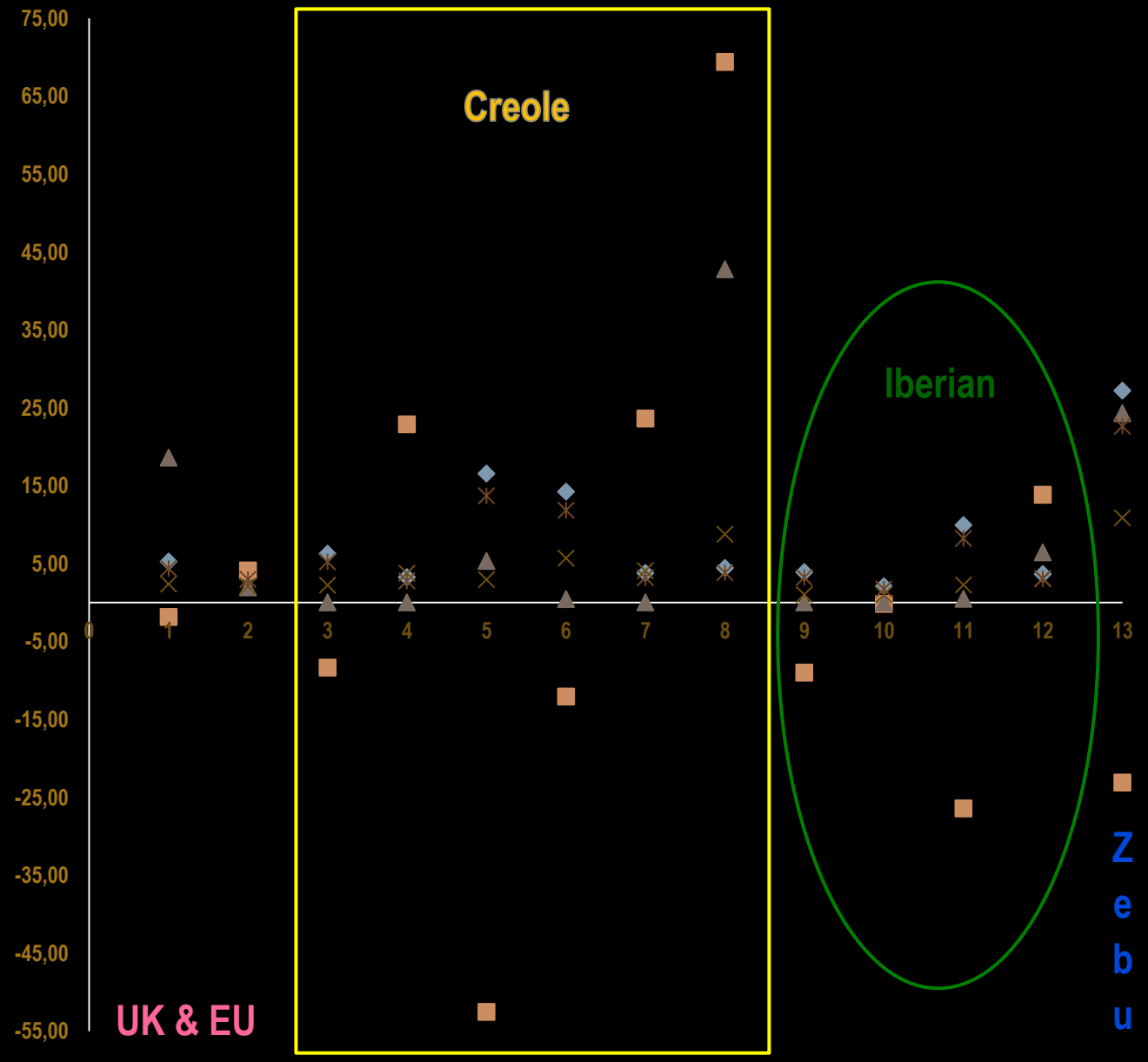
PC_{Wei} (CB)	PC_{He} (CW)	MEKs	PC_{Fst} 0.087*CB+0.913*CW	$PC_{5:1}$ 0.833*CB+0.167*CW
GUA 9.88	CNY 0.252	SIB 0.215	SIB 0.579	GUA 8.161
RMS 6.18	CAQ 0.249	CPO 0.167	GUA 0.484	RMS 5.087
PAT 5.95	HVA 0.226	CUB 0.124	CUB 0.448	PAT 4.896
SIB 5.4	CHI 0.222	PCH 0.109	VEL 0.411	SIB 4.518
CAR 5.39	CHU 0.196	ECU 0.096	CNY 0.385	CAR 4.466

- GUA, RMS, PAT, SIB, CAR
  >>> genetic distances; distinct breeds, Iberian & African influences

- CNY, CAQ, HVA, CHI, CHU
  >>> within-breed diversity, crossbred with EU, UK & Zebu cattle

RESULTS

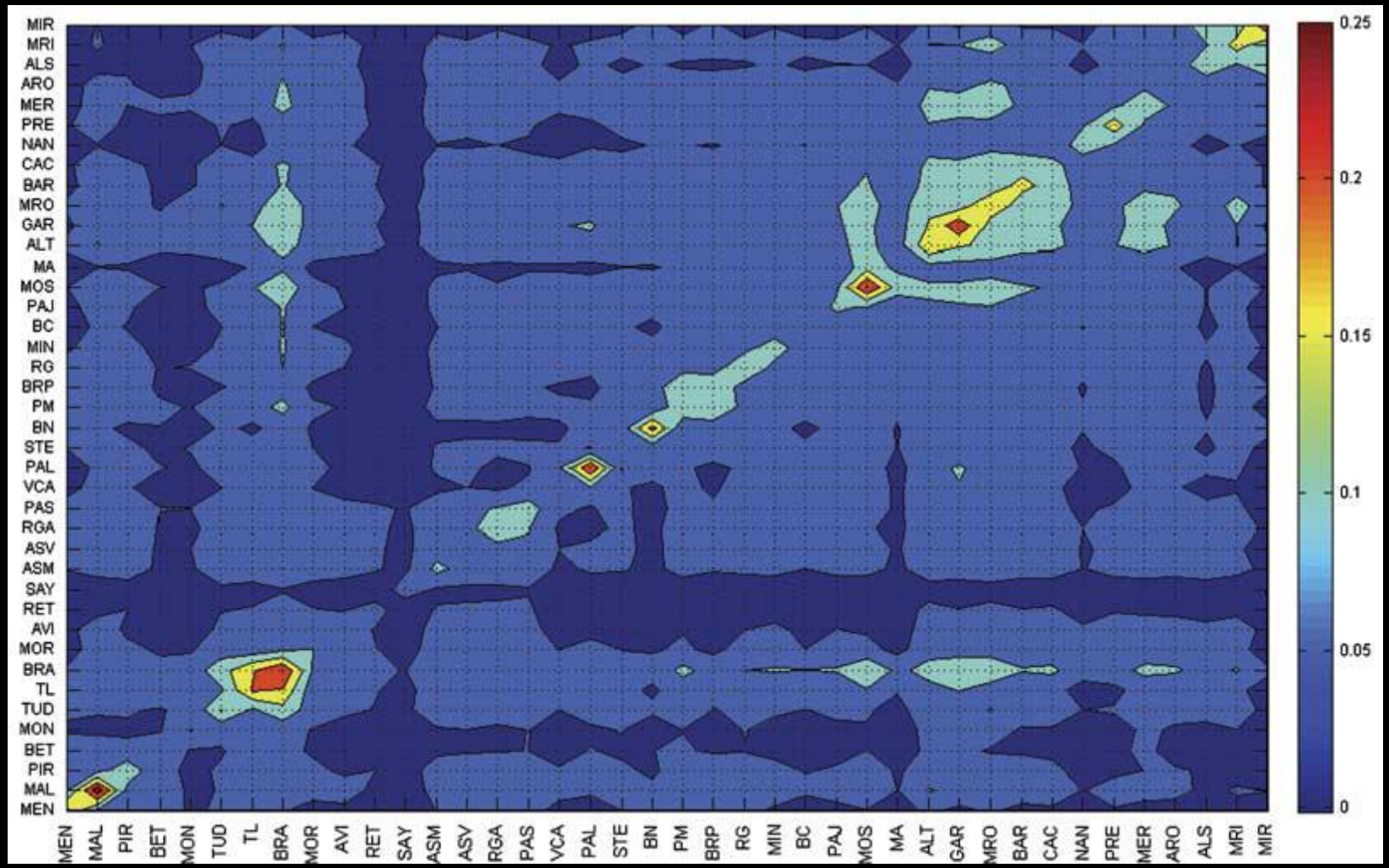
PARTIAL CONTRIBUTIONS



BIG QUESTION?
Which breed-groups represent specific evolutionary processes e.g. ADAPTATION

RESULTS

KINSHIP IBERIA



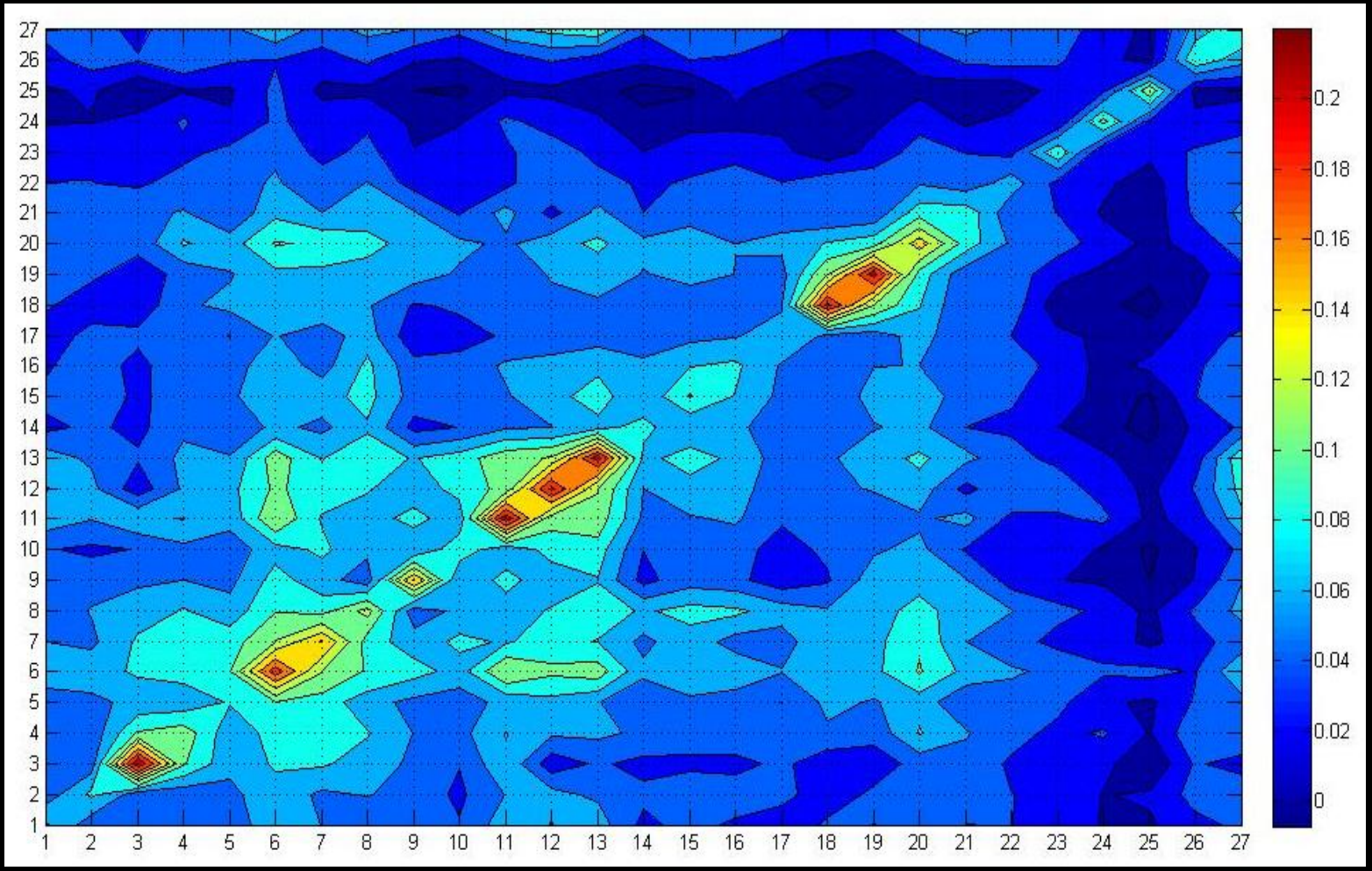
Diagonal: Inbreeding

Genetic structure

Cañon, J. *et al.* (2011). Animal 5(9): 1323-34

RESULTS

KINSHIP CREOLE

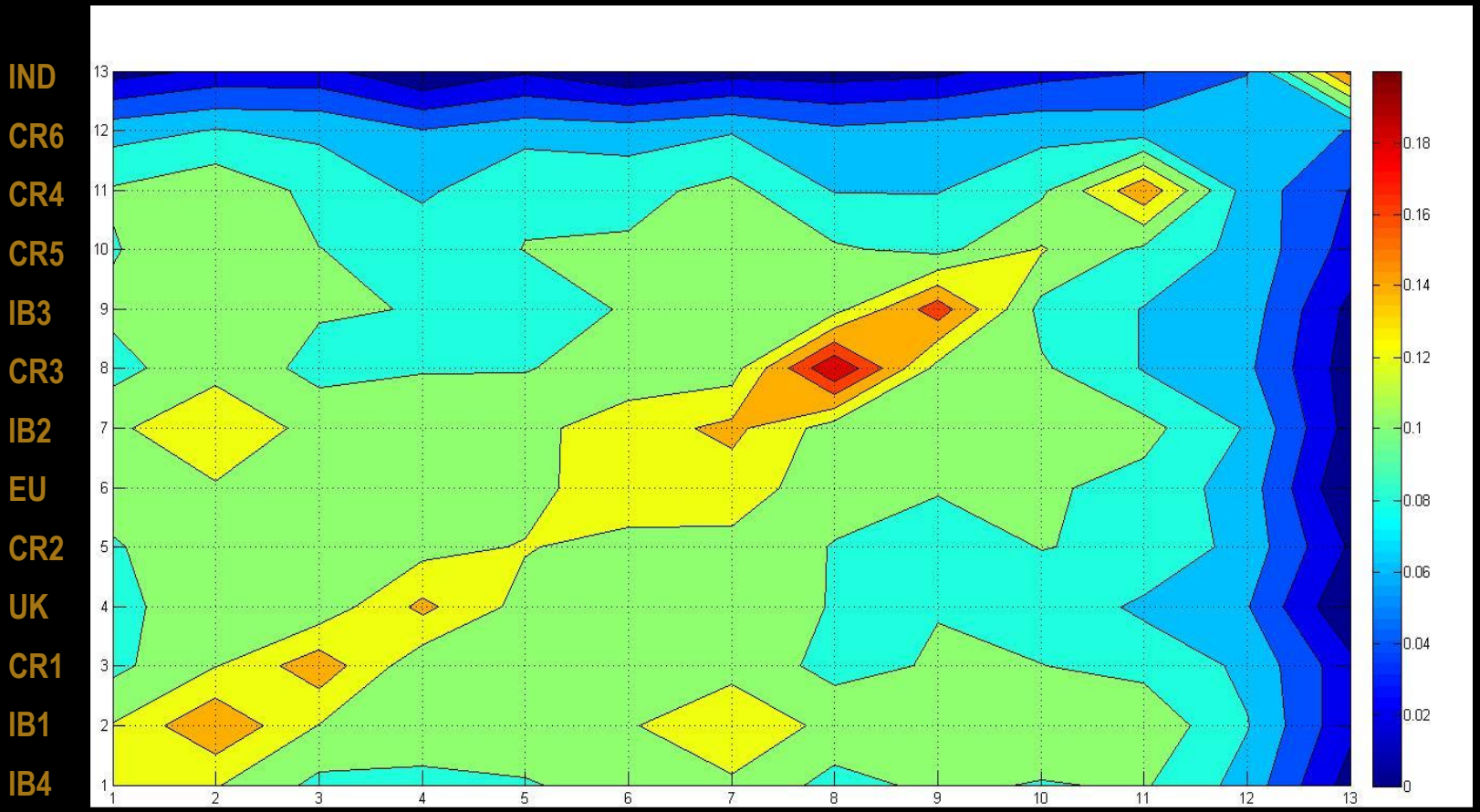


Inbreeding
BON, CHS, CUB, TLH, CAR, CCC, PIL

Zebu influence
Mexico, Cuba, Equador, Panama, Colombia

RESULTS

KINSHIP BREED - GROUPS

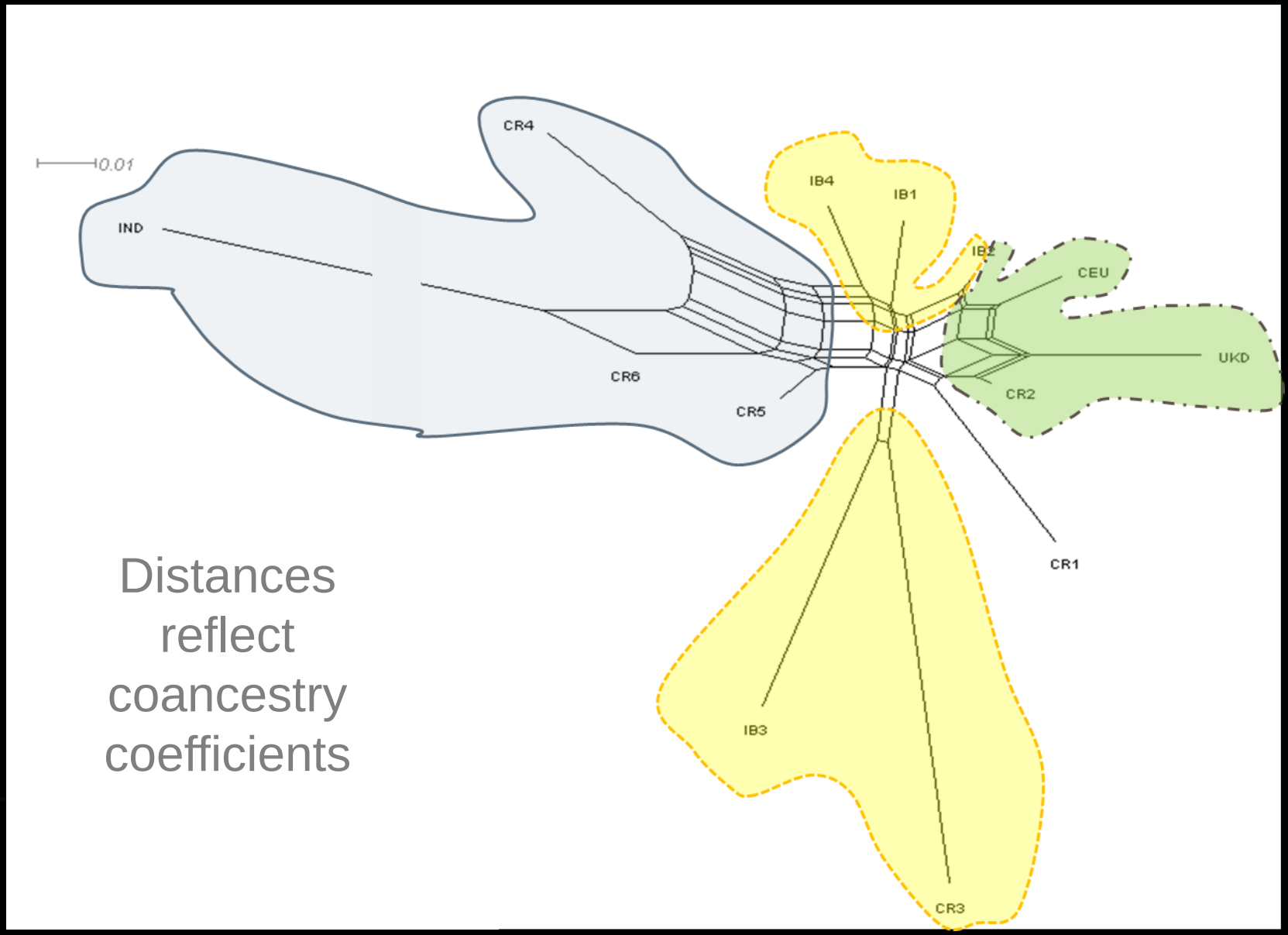


IB1, IB4, IB2 & IB3 (Canary Isl.) , CR3 (Colombia)

IB2, CR2 & UK/EU

CR5, CR4, CR6 & IND

RESULTS KINSHIP DISTANCES



Distances reflect coancestry coefficients

CONCLUSIONS

- **Essential to consider several parameters**
  Within-breed diversity
  Breed differentiation
- **Analyse conservation priorities at several scales**

Recommendation

Information must be shared with Governmental Agencies for integration in conservation & management programs

‘A HANDFUL OF NOTHIN’ ?

- **Identification of genomic regions under selection**

  better estimates of conservation values?

- **Phenotypic information?**

- **Selection for adaptive alleles**

  will it cause further losses of genetic variation?

To preserve the ecosystems – promote sustainable breeding

& added value from certified products

ACKNOWLEDGMENTS

- L Gama, O Cortes, JV Delgado, S Dunner, D García,
- V Landi, I Martín-Burriel,
- A Martínez-Martínez, MCT Penedo, C Rodellar, P. Zaragoza, J. Cañon
- BIOBOVIS Consortium
- CYTED XII-H/CONBIAND networks
- Veterinary Genetics Laboratory, UCDavis

FUNDING

- EU FP7/2007-2013, PCOFUND-GA-2009-246542
- FCT Portugal - Marie Curie/Welcome II fellowship Ref. DFRH/WIIA/15/201
- INIA, Spain

Thank You!

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THERE'S HOPE!