Avances en estudios de la Genética Local Paraguay

PARAGUAY

Población: 6.926.100 habitantes.
Superficie: 406, 752 Km2

CONACYT

PROCIENCIA

PROGRAMA PARAGUAYO PARA EL DESARROLLO DE LA CIENCIA Y TECNOLOGÍA

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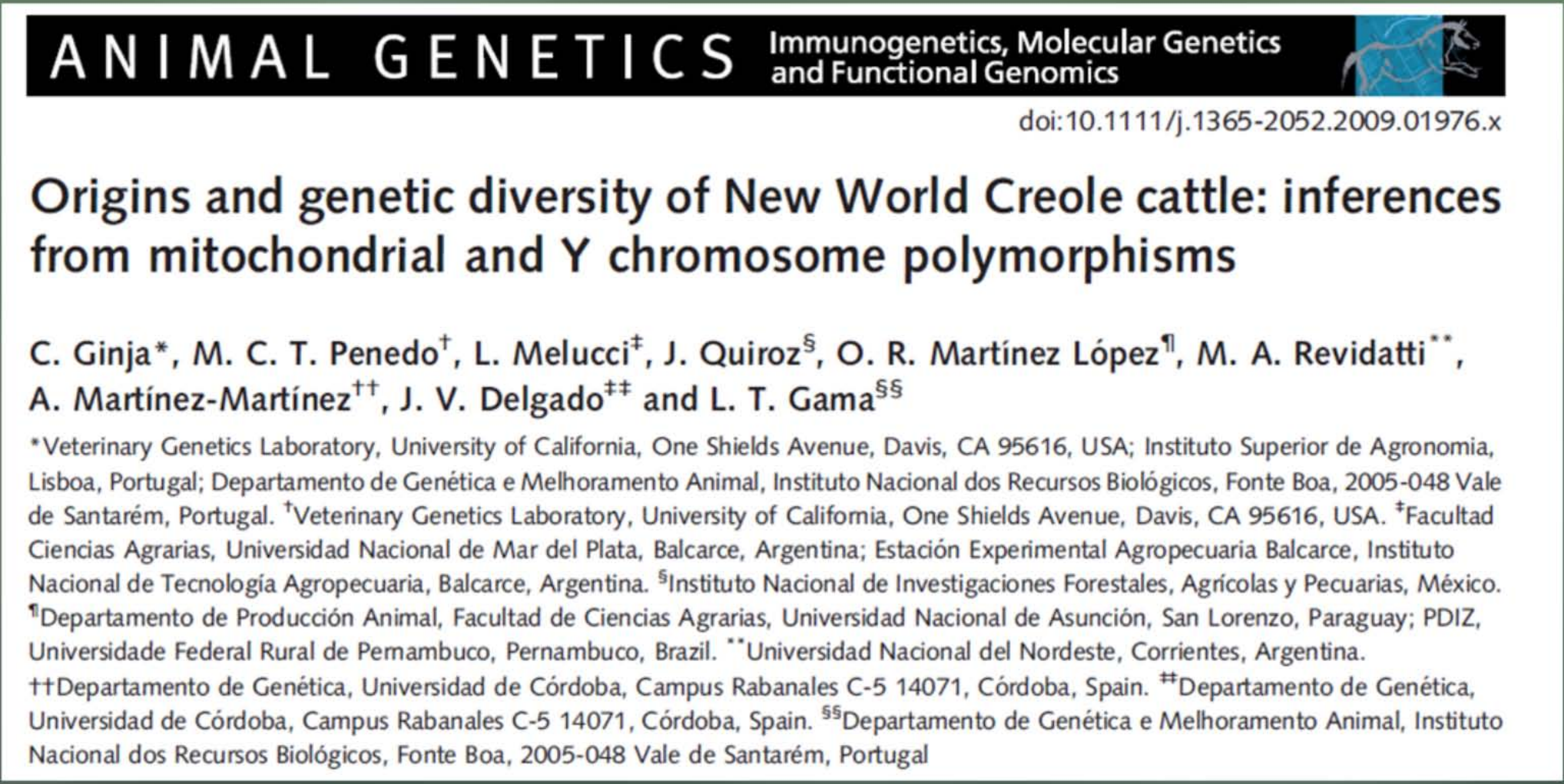
ECOREGIONES DEL PARAGUAY

Peter T. Clark Julio 2012

Gracias por la Atención!!

Especies Zootecnicas estudiadas



ANIMAL GENETICS Immunogenetics, Molecular Genetics and Functional Genomics

doi:10.1111/j.1365-2052.2009.01976.x

Origins and genetic diversity of New World Creole cattle: inferences from mitochondrial and Y chromosome polymorphisms

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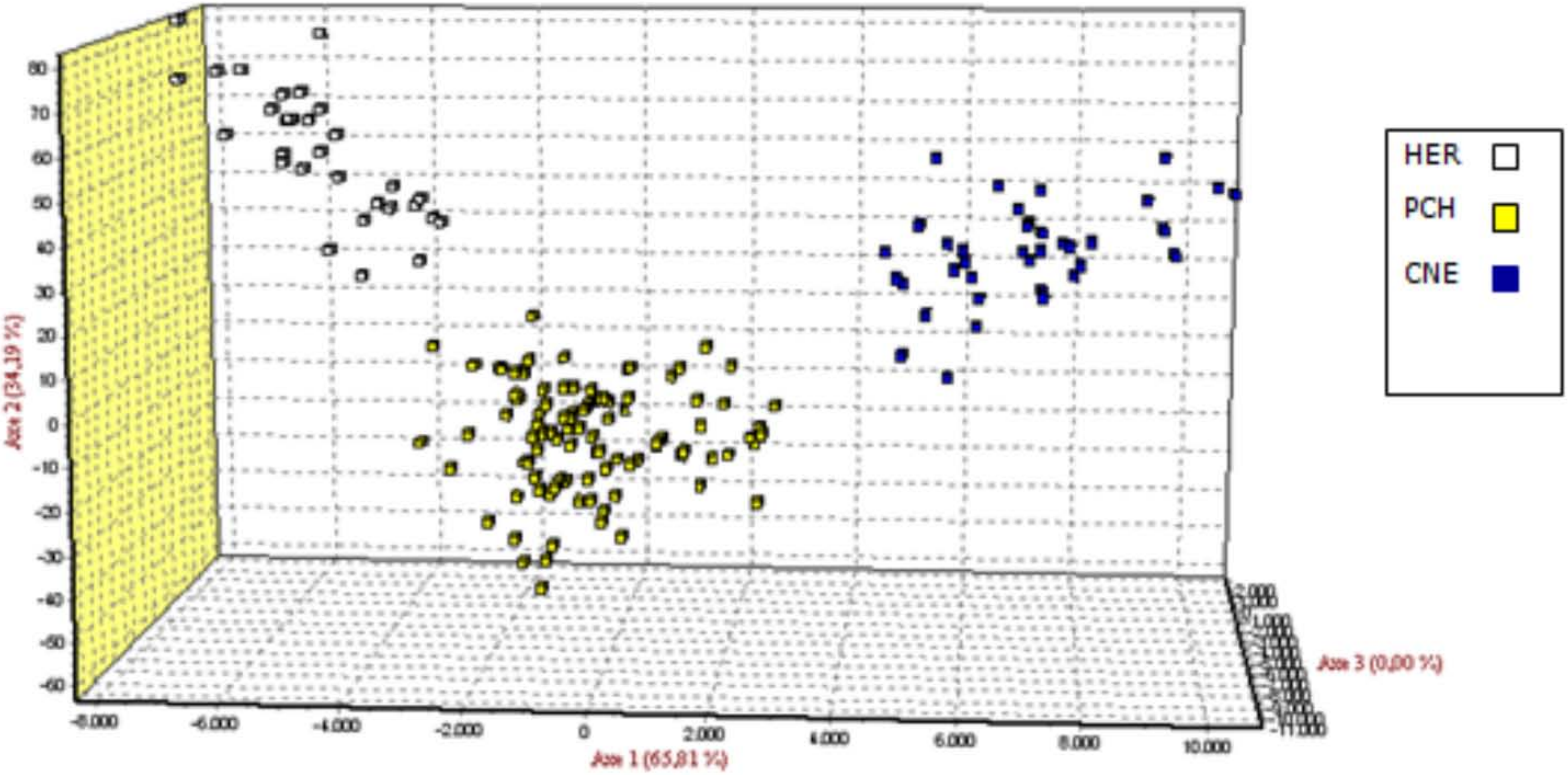
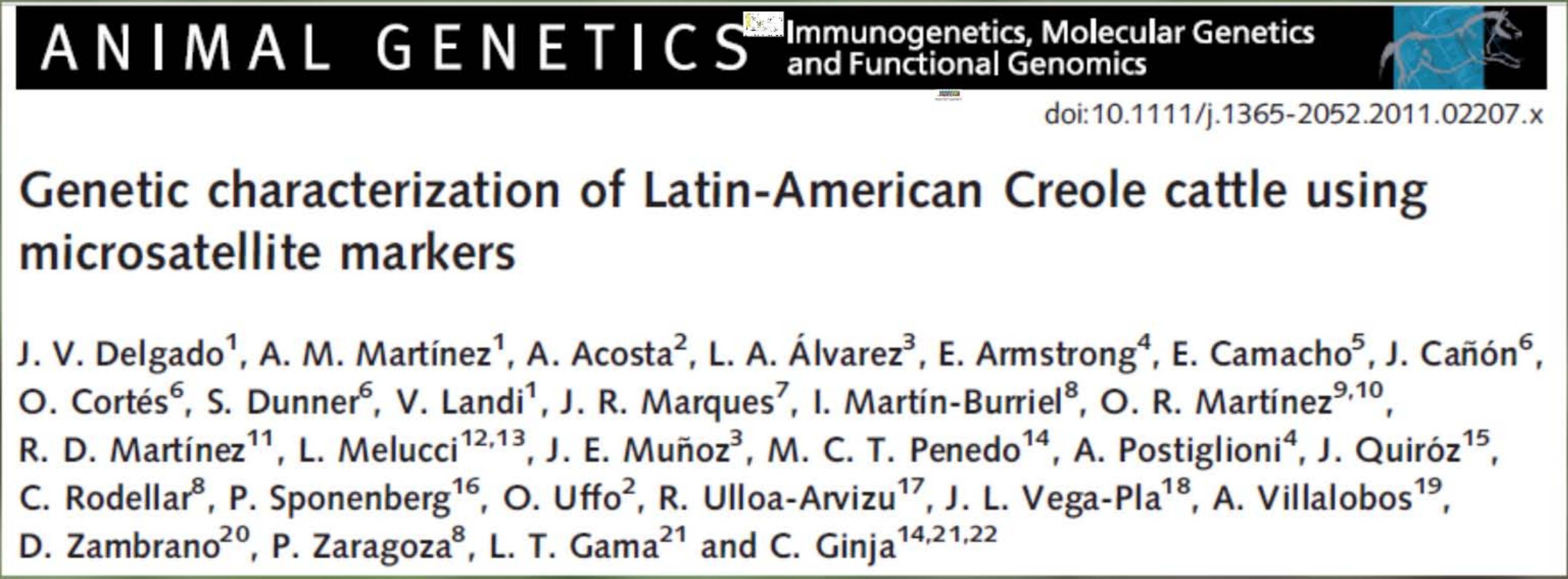


Figura 3. Analise Fatorial de Correspondência para Diferenciação genética individual dos bovinos, Pampa Chaqueño (PCH), Crioulo Pilcomayo (CNE) e Hereford (HER), Versão 3D.



ANIMAL GENETICS Immunogenetics, Molecular Genetics and Functional Genomics

doi:10.1111/j.1365-2052.2011.02207.x

Genetic characterization of Latin-American Creole cattle using microsatellite markers

J. V. Delgado[1], A. M. Martínez[1], A. Acosta[2], L. A. Álvarez[3], E. Armstrong[4], E. Camacho[5], J. Cañón[6], O. Cortés[6], S. Dunner[6], V. Landi[1], J. R. Marques[7], I. Martín-Burriel[8], O. R. Martínez[9,10], R. D. Martínez[11], L. Melucci[12,13], J. E. Muñoz[3], M. C. T. Penedo[14], A. Postiglioni[4], J. Quiróz[15], C. Rodellar[8], P. Sponenberg[16], O. Uffo[2], R. Ulloa-Arvizu[17], J. L. Vega-Pla[18], A. Villalobos[19], D. Zambrano[20], P. Zaragoza[8], L. T. Gama[21] and C. Ginja[14,21,22]

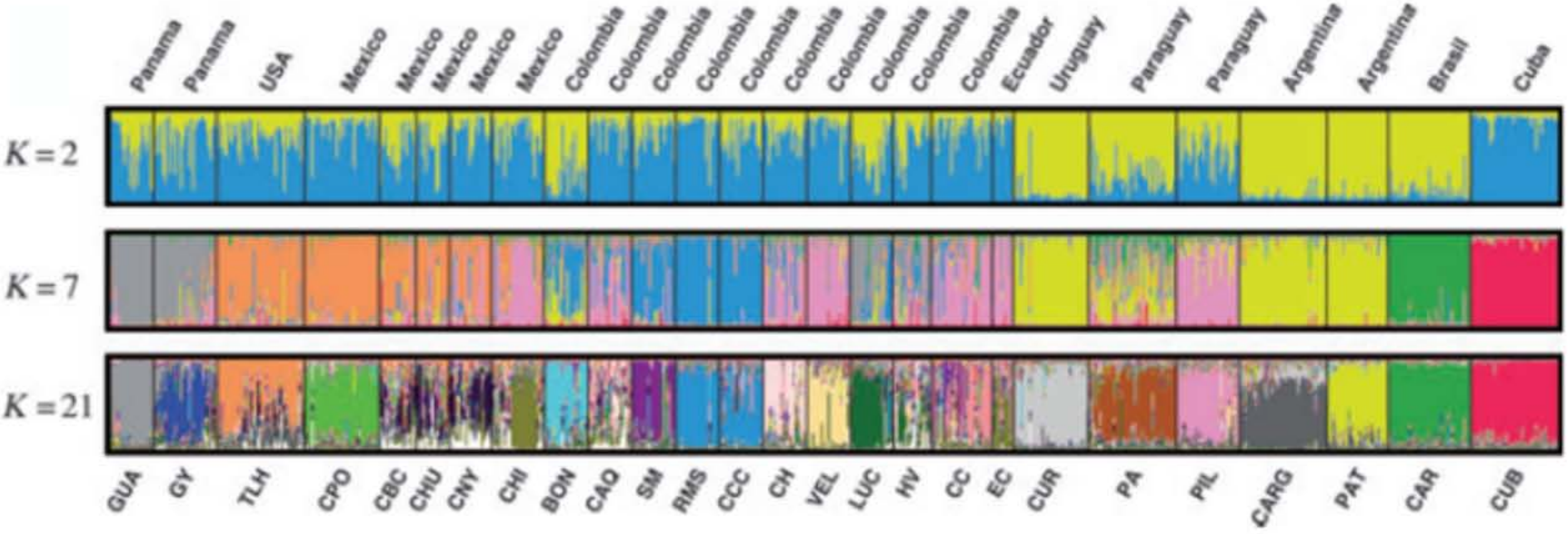


Figure 2 Population structure of 26 cattle populations using the model-based STRUCTURE software. Each animal is represented by a single vertical line divided into *K* colours, where *K* is the number of clusters assumed and the colours show the estimated individual proportions of cluster membership. Results are shown for (a) *K* = 2, (b) *K* = 7 and (c) *K* = 21. Breed abbreviations: GUA, Guabalá; GY, Guaymí; TLH, Texas Longhorn; CPO, Criollo Poblano; CBC, Criollo de Baja California; CHU, Criollo de Chihuahua; CNY, Criollo de Nayarit; CHI, Criollo de Chiapas; BON, Blanco Orejinegro; CAQ, Caqueteño; SM, Sanmartinero; RMS, Romosinuano; CCC, Costeño con Cuernos; CH, Chino Santandereano; VEL, Velásquez; LUC, Lucerna; HV, Hartón del Valle; CC, Criollo Casanareño; EC, Criollo Ecuatoriano; CUR, Criollo Uruguayo; PA, Pampa Chaqueño; PIL, Criollo Pilcomayo; CARG, Criollo Argentino; PAT, Criollo Patagónico; CAR, Caracú; CUB, Criollo Cubano.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diadas.
; BRH,
Nelore,

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REPUBLICA DEL PARAGUAY

ESTUDIO DE LA VARIABILIDAD GENÉTICA DE LOS BOVINOS CON CARACTERÍSTICAS CRIOLLAS EXISTENTES EN LOS HUMEDALES DEL ÑEEMBUCÚ Y ÁREAS DE INFLUENCIA

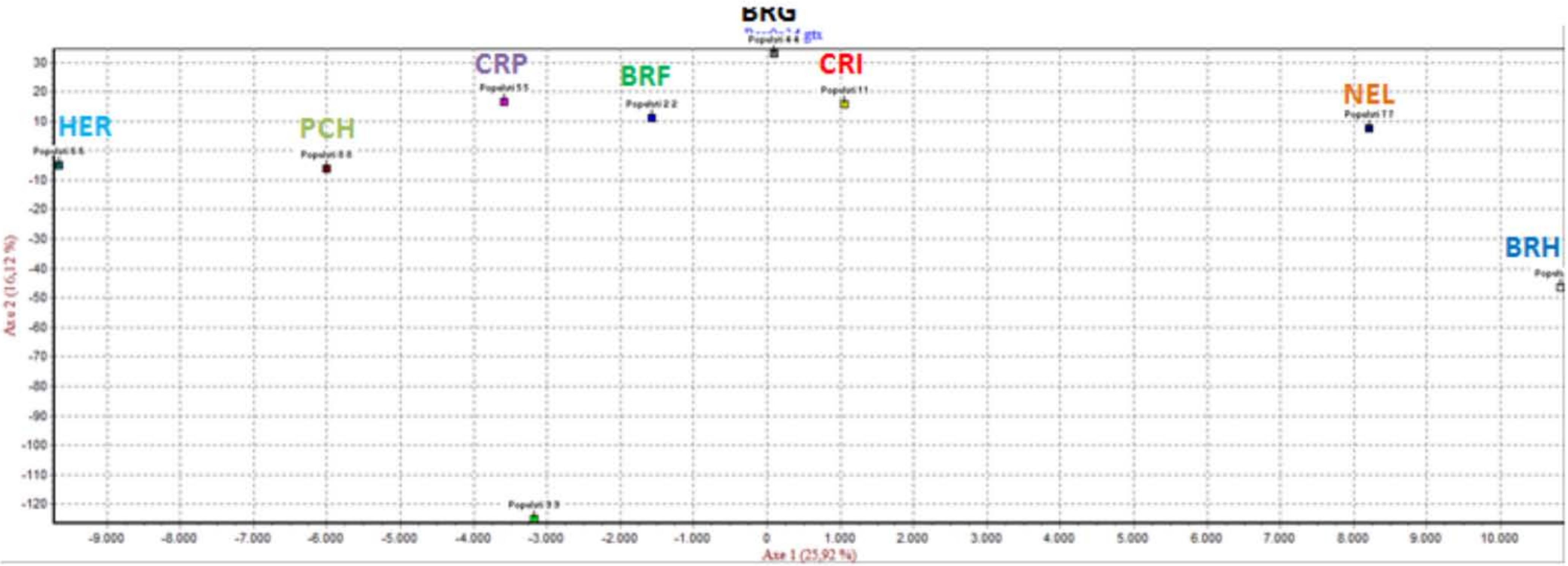

Figura 2. Diferenciación genética de las nueve poblaciones bovinas estudiadas. Imagen en dos dimensiones (2D). CRI, Criollo Ñeembucú; BRF, Braford; BRH, Brahman; BRG, Brangus; CRP, Criollo Pilcomayo; HER, Hereford; NEL, Nelore; PCH, Pampa Chaqueño; SEN, Senepol.

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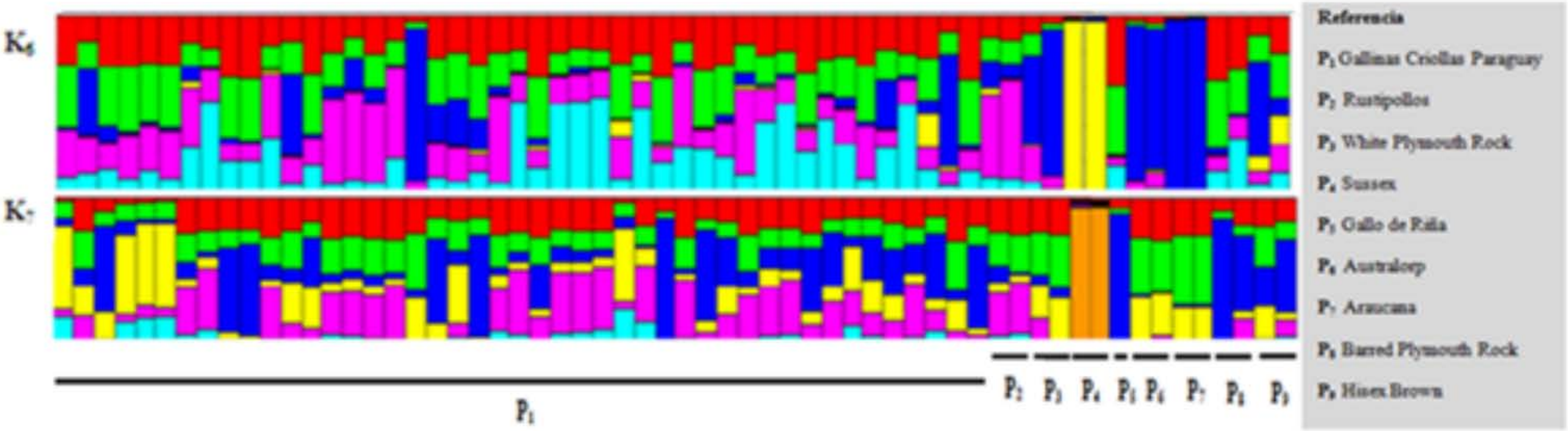
CARACTERIZACIÓN GENÉTICA DE GALLINAS CRIOLLAS EN COMUNIDADES ÍNDIGENAS DEL CHACO CENTRAL Y ZONA DE INFLUENCIA DE LOS HUMEDALES DEL ÑEEMBUCÚ


K_6
K_7
P_1
P_2
P_3
P_4
P_5
P_6
P_7
P_8
P_9
Referencia
P_1 Gallinas Criollas Paraguay
P_2 Rustipollos
P_3 White Plymouth Rock
P_4 Sussex
P_5 Gallo de Riña
P_6 Australorp
P_7 Araucana
P_8 Barred Plymouth Rock
P_9 Hisex Brown

Prezi

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CARACTERIZACION GENETICA DE LOS EQUINOS NATIVOS DE LOS HUMEDALES DEL ÑEEMBUCU Y SU AREA DE INFLUENCIA

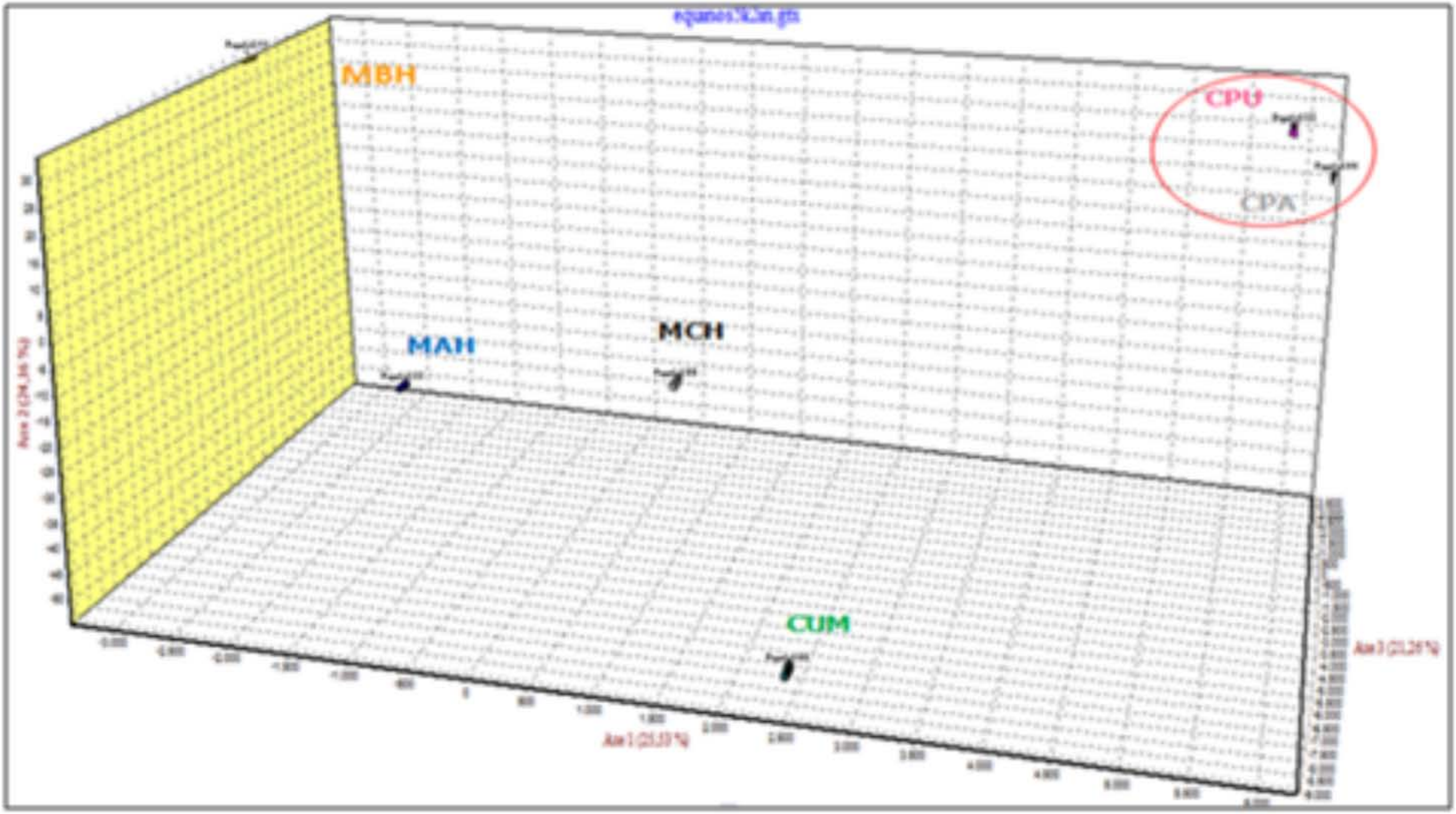
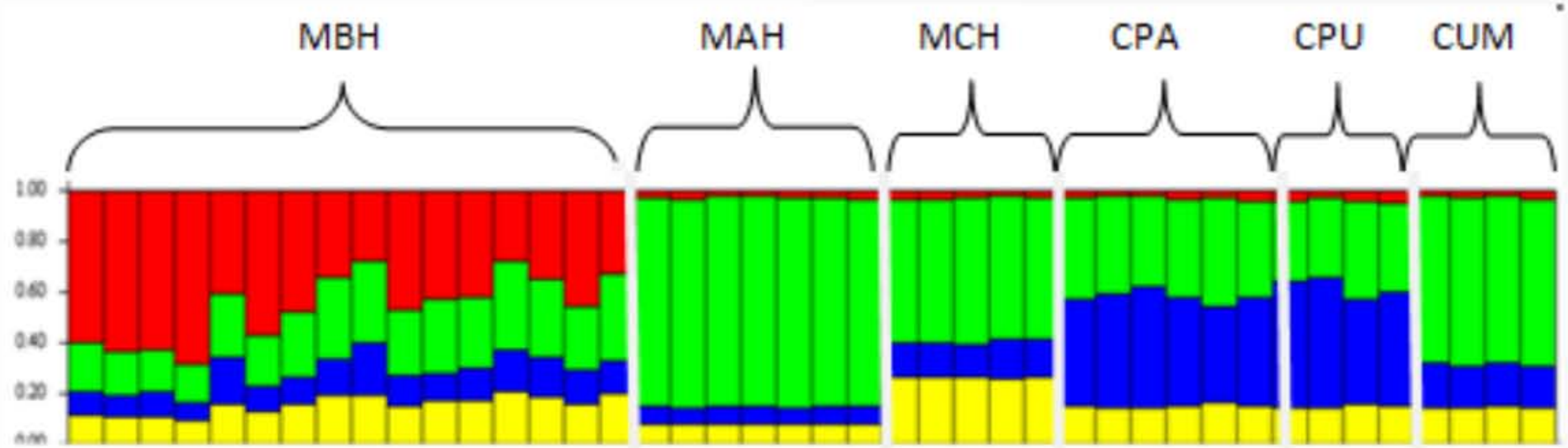
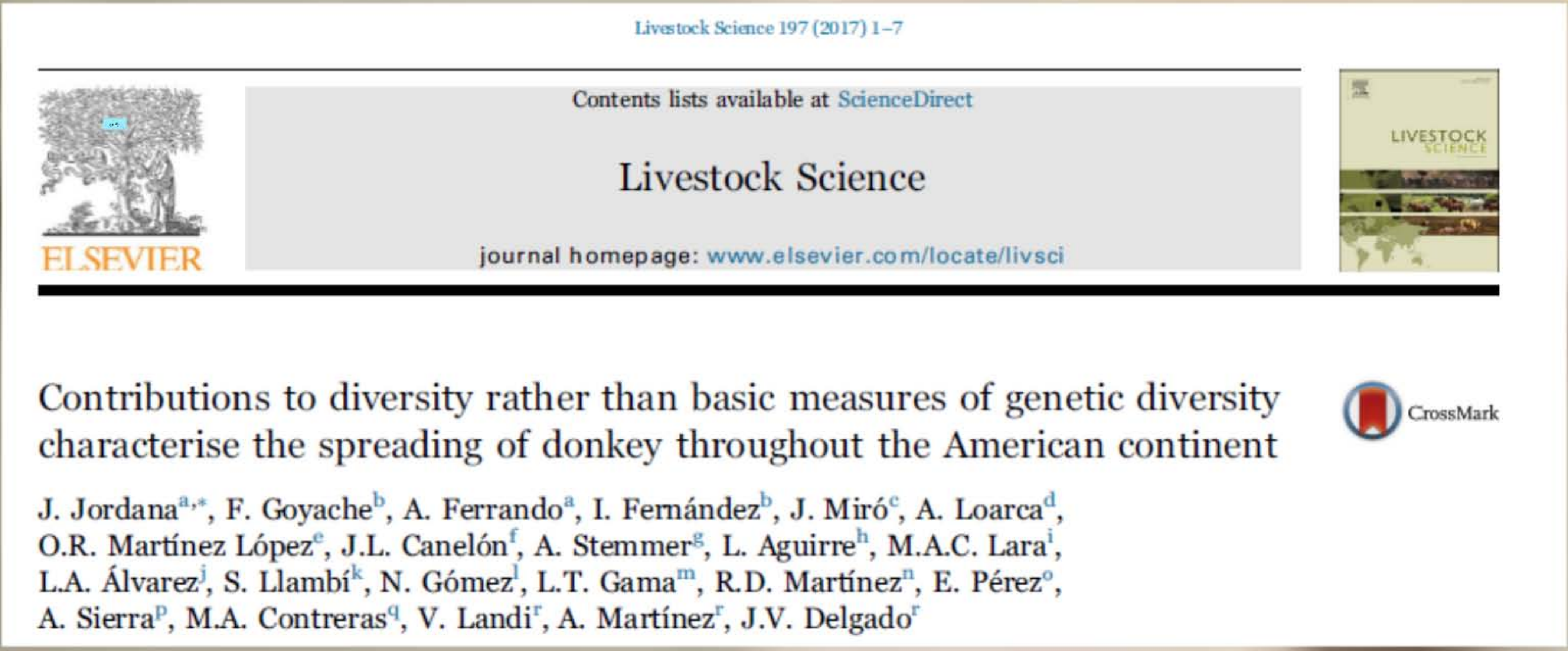


Figura 3. Análisis Factorial de Correspondencia de 6 poblaciones equinas estudiadas. Imagen en tres dimensiones (3D). **MBH**, Mestizo Bajo Humedal; **MAH**, Mestizo Alto Humedal; **MCH**, Mestizo Chaco; **CPA**, Criollo Puro Argentino; **CPU**, Criollo Puro Uruguayo; **CUM**, Cuarto de Milla.


MBH
MAH
MCH
CPA
CPU
CUM
1.00
0.80
0.60
0.40
0.20
0.00



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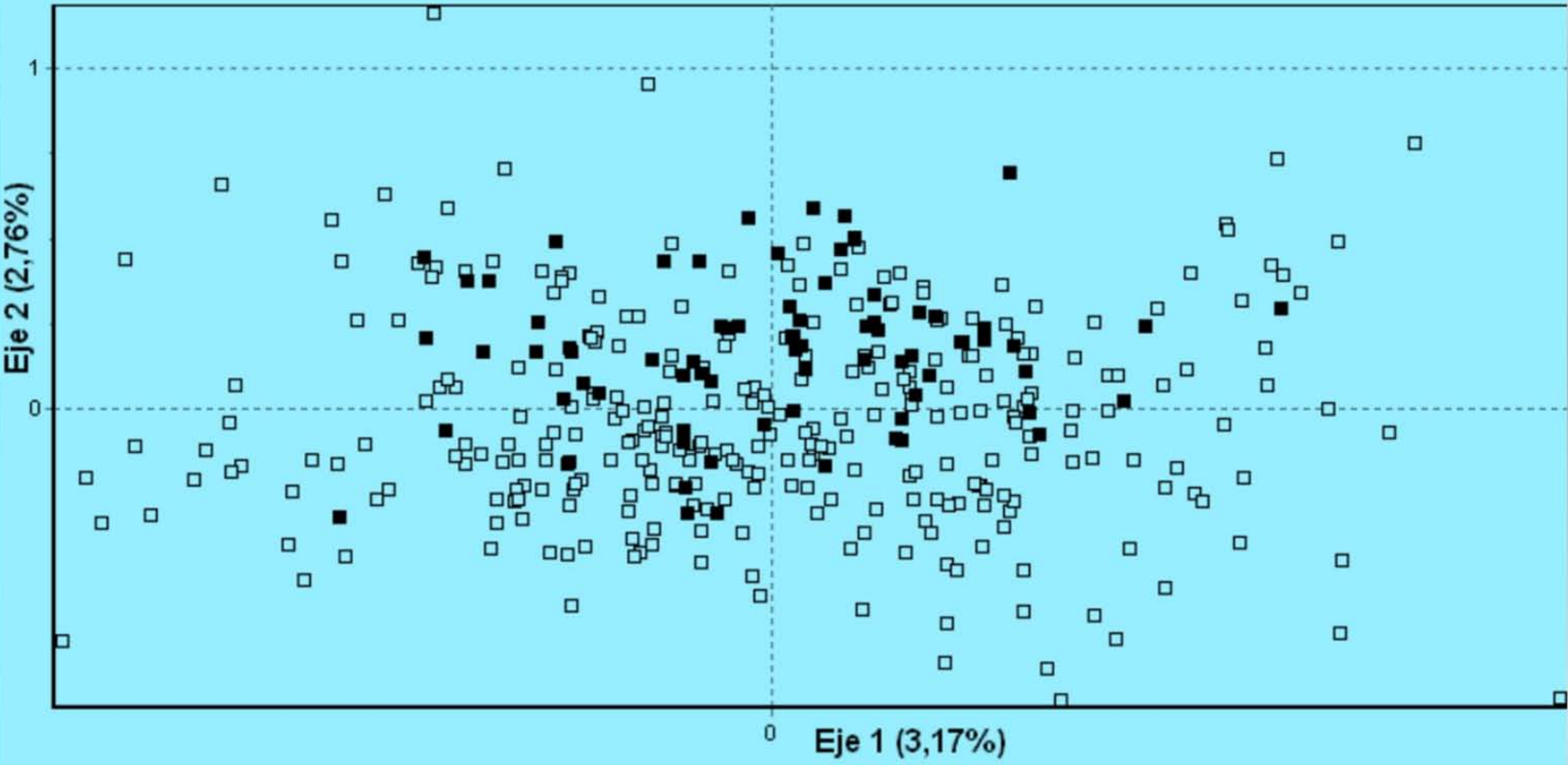
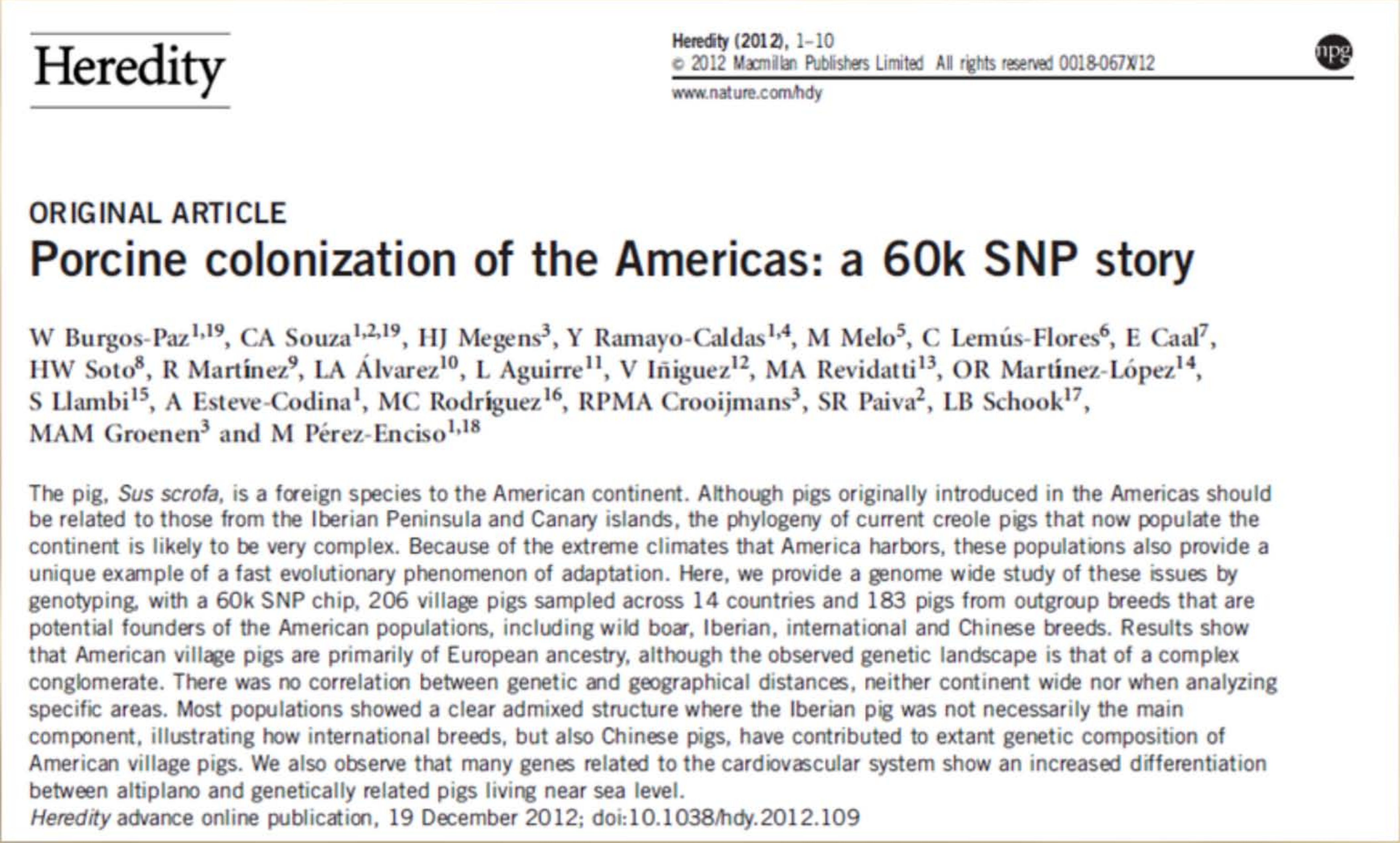
journal homepage: www.elsevier.com/locate/livsci

Contributions to diversity rather than basic measures of genetic diversity characterise the spreading of donkey throughout the American continent

J. Jordana[a,*], F. Goyache[b], A. Ferrando[a], I. Fernández[b], J. Miró[c], A. Loarca[d], O.R. Martínez López[e], J.L. Canelón[f], A. Stemmer[g], L. Aguirre[h], M.A.C. Lara[i], L.A. Álvarez[j], S. Llambí[k], N. Gómez[l], L.T. Gama[m], R.D. Martínez[n], E. Pérez[o], A. Sierra[p], M.A. Contreras[q], V. Landi[r], A. Martínez[r], J.V. Delgado[r]



1
0
Eje 2 (2,76%)
0
Eje 1 (3,17%)



Heredity

Heredity (2012), 1–10

www.nature.com/hdy

ORIGINAL ARTICLE

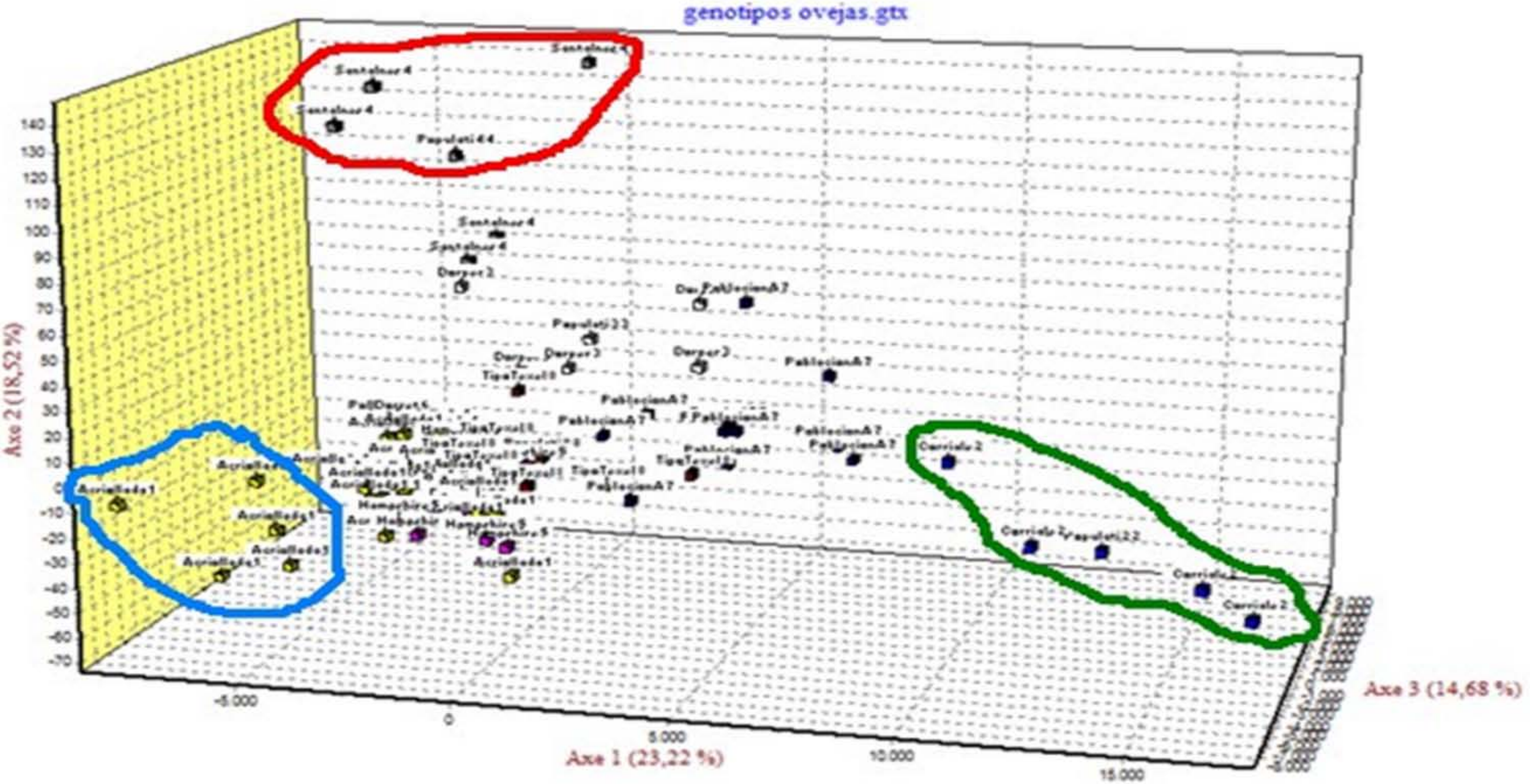
Porcine colonization of the Americas: a 60k SNP story

W Burgos-Paz[1,19], CA Souza[1,2,19], HJ Megens[3], Y Ramayo-Caldas[1,4], M Melo[5], C Lemús-Flores[6], E Caal[7], HW Soto[8], R Martínez[9], LA Álvarez[10], L Aguirre[11], V Iñiguez[12], MA Revidatti[13], OR Martínez-López[14], S Llambi[15], A Esteve-Codina[1], MC Rodríguez[16], RPMA Crooijmans[3], SR Paiva[2], LB Schook[17], MAM Groenen[3] and M Pérez-Enciso[1,18]

The pig, *Sus scrofa*, is a foreign species to the American continent. Although pigs originally introduced in the Americas should be related to those from the Iberian Peninsula and Canary islands, the phylogeny of current creole pigs that now populate the continent is likely to be very complex. Because of the extreme climates that America harbors, these populations also provide a unique example of a fast evolutionary phenomenon of adaptation. Here, we provide a genome wide study of these issues by genotyping, with a 60k SNP chip, 206 village pigs sampled across 14 countries and 183 pigs from outgroup breeds that are potential founders of the American populations, including wild boar, Iberian, international and Chinese breeds. Results show that American village pigs are primarily of European ancestry, although the observed genetic landscape is that of a complex conglomerate. There was no correlation between genetic and geographical distances, neither continent wide nor when analyzing specific areas. Most populations showed a clear admixed structure where the Iberian pig was not necessarily the main component, illustrating how international breeds, but also Chinese pigs, have contributed to extant genetic composition of American village pigs. We also observe that many genes related to the cardiovascular system show an increased differentiation between altiplano and genetically related pigs living near sea level.

Heredity advance online publication, 19 December 2012; doi:10.1038/hdy.2012.109

VARIABILIDAD GENÉTICA DE OVINOS CON CARACTERÍSTICAS CRIOLLAS DE LOS HUMEDALES DE LA REGIÓN ORIENTAL


genotipos ovejas.gtx
Axe 1 (23,22 %)
Axe 2 (18,52 %)
Axe 3 (14,68 %)
140
130
120
110
100
90
80
70
60
50
40
30
20
10
0
-10
-20
-30
-40
-50
-60
-70
-5.000
0
5.000
10.000
15.000
Santalnar 4
Santalnar 4
Santalnar 4
Papulati 4 4
Santalnar 4
Santalnar 4
Dargar 2
Da PablacionA 7
Papulati 2 2
Dargar Dargar 3
Dargar 3
PablacionA 7
TipoTexal 10
PablacionA 7
PallDargar 5
A Acriallada 1
PablacionA 7
PablacionA 7
PablacionA 7
PablacionA 7
PablacionA 7
TipoTexal 10
TipoTexal 10
Acriallada 1
Acriallada 1
Acriallada 1
Acriallada 1
Acriallada 3
Acriallada 1
Hamarbire 5
Hamarbire 5
Hamarbire 5
Acriallada 1
PablacionA 7
Carriala 2
Carriala 2
Papulati 2 2
Carriala 2
Carriala 2

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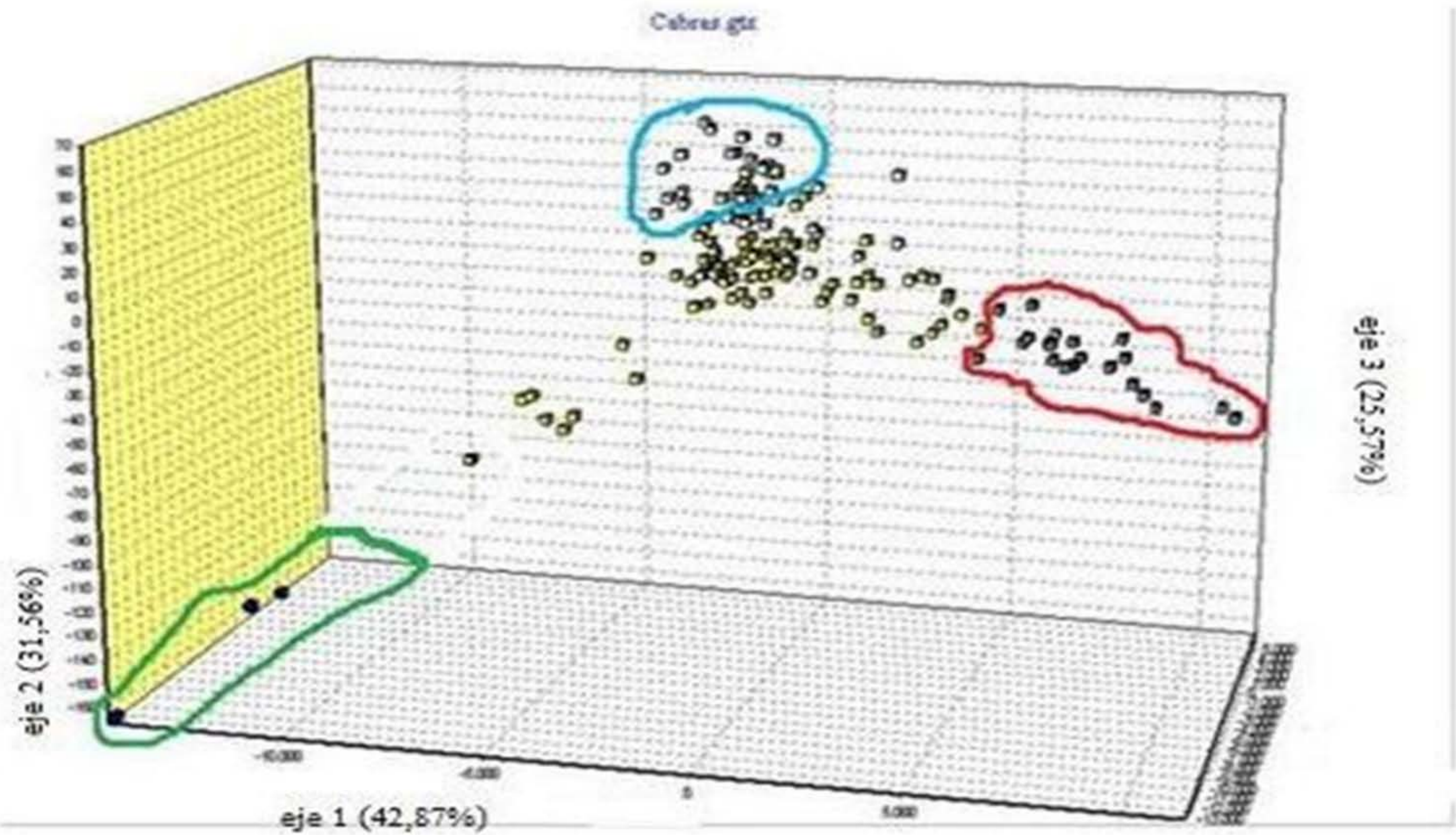
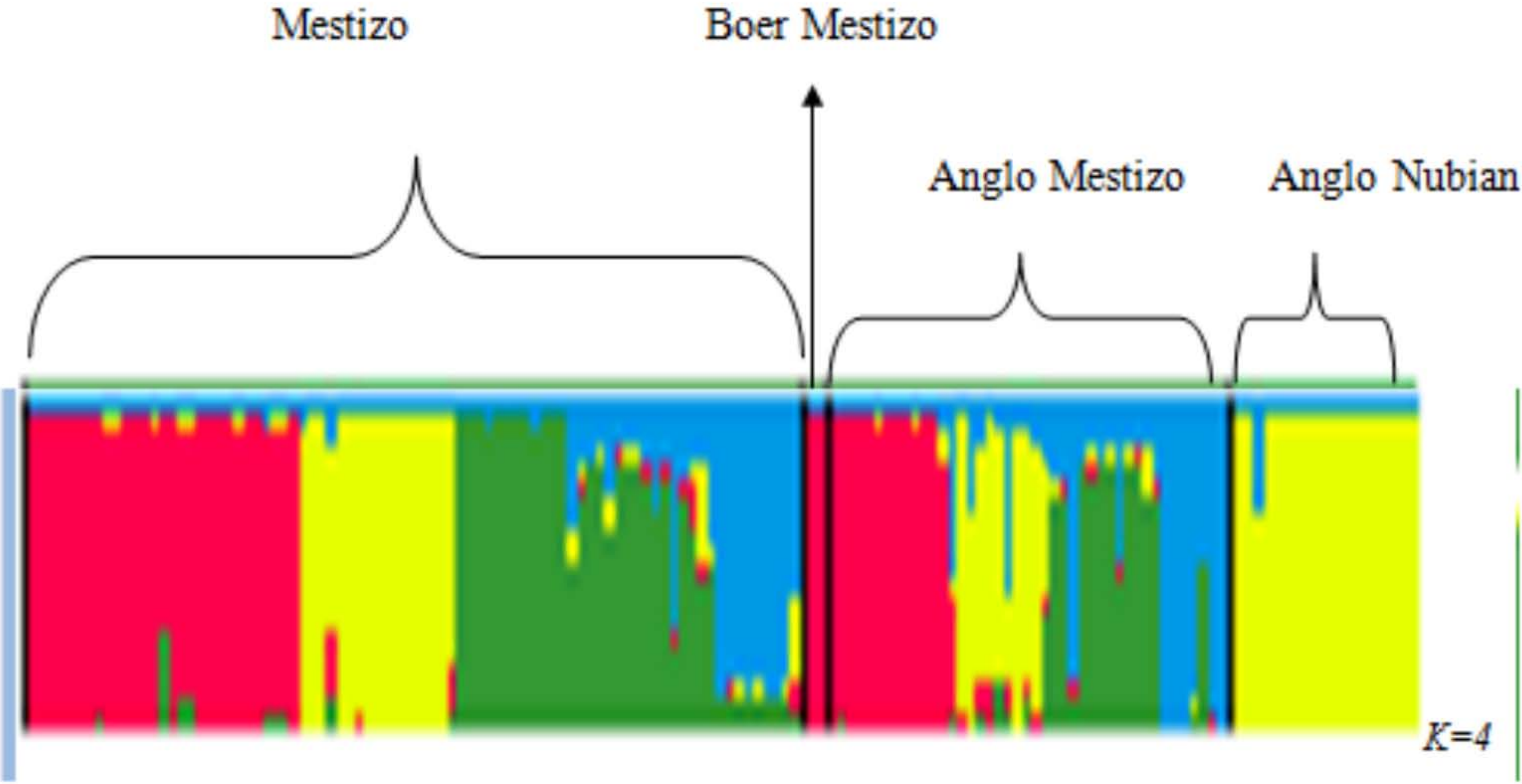
ESTUDIO DE LA VARIABILIDAD GENÉTICA DE POBLACIONES CAPRINAS CRIADOS EN SISTEMAS GANADEROS CONVENCIONALES DENTRO DEL DEPARTAMENTO DE PRESIDENTE HAYES


Cabras gta
eje 3 (25,57%)
eje 2 (31,56%)
eje 1 (42,87%)
-10.000
-5.000
0
5.000


Mestizo
Boer Mestizo
Anglo Mestizo
Anglo Nubian
K=4

CONACYT

PROCIENCIA

PROGRAMA PARAGUAYO PARA EL DESARROLLO DE LA CIENCIA Y TECNOLOGÍA

Gracias por la Atención!!