



Alliance



Diversidad de variedades de cacao en el Peru como centro de origen

Evert Thomas, PhD

Patrones de diversidad en cacao resultado de interacción factores naturales y humanos

- Historia natural
 - Biología reproductiva
 - Cambio climático pasado (cacao tiene ~9M de edad!)
- Historia humana:
 - dispersión
 - Cuellos de botella genética
 - Cultivación y selección

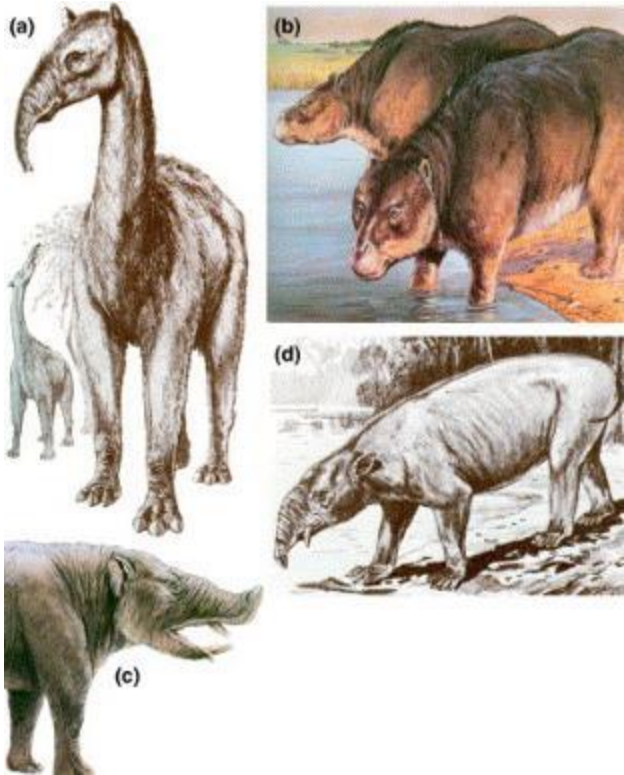
Biología reproductiva - dispersión



Theobroma cacao L.
Image processed by Thomas Schoepke
www.plant-pictures.de

- Frutos escasos e indehiscentes; no se caen naturalmente
- Semillas relacitrantes que germinan en el fruto
- Necesidad de dispersor(es) especializados
- En la realidad: dispersión pocas veces observado y distancias cortas
- Principalmente monos y menos frecuente ardillas, venados, danta, aves

Biología reproductiva - dispersión



- Porque el arbol de cacao invierte tanta energia en frutos tan especializados que parecen ser muy ineficientes para la dispersion?
- Megafauna Pleistocenico extinto?

presente



Manejo y dispersión humano

- Papel importante en dispersión desde hace más de 12.000 años
- Evidencia más antigua domesticación Sur Ecuador – Norte Perú hace 5400 años
- Pulpa alrededor de semillas → fermentación → descubrimiento chocolate?
- Solo en Mesoamérica domesticación para uso de semilla?
- creación de diferentes cultivares: criollo, amelonado/catongo, nacional, chuncho etc

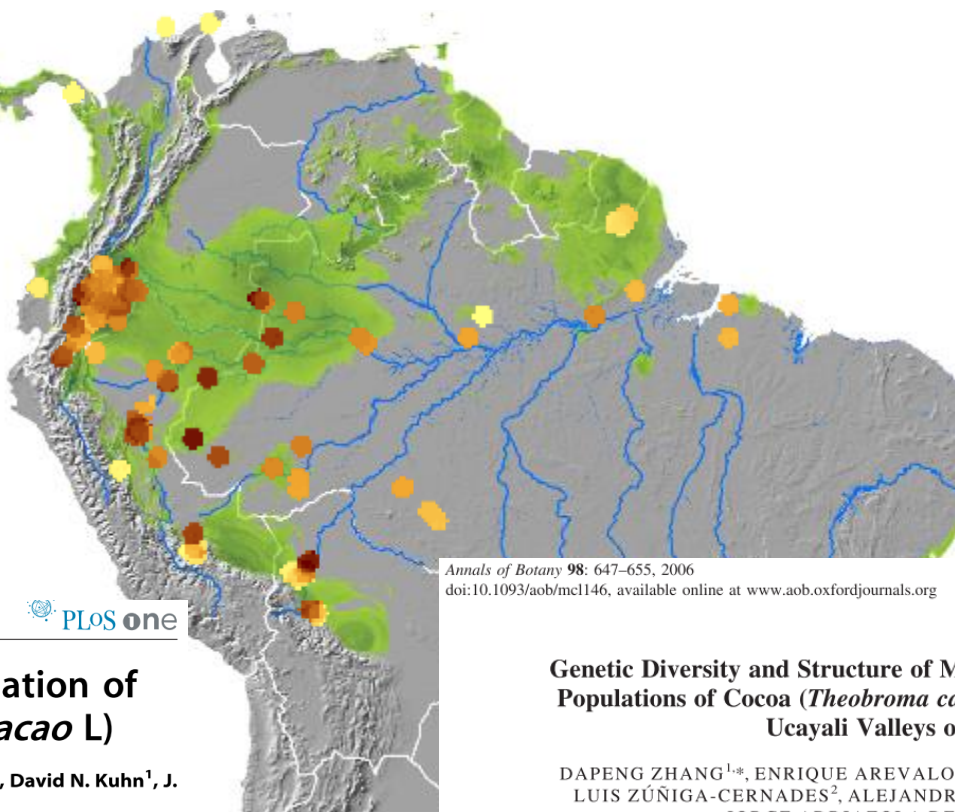
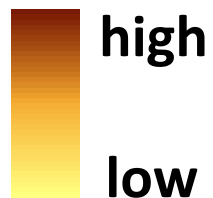




Genetic diversity and spatial structure in a new distinct *Theobroma cacao* L. population in Bolivia

Dapeng Zhang · Windson July Martínez · Elizabeth S. Johnson ·
Eduardo Somarriba · Wilberth Phillips-Mora ·
Carlos Astorga · Sue Mischke · Lyndel W. Meinhardt

Riqueza
alelica



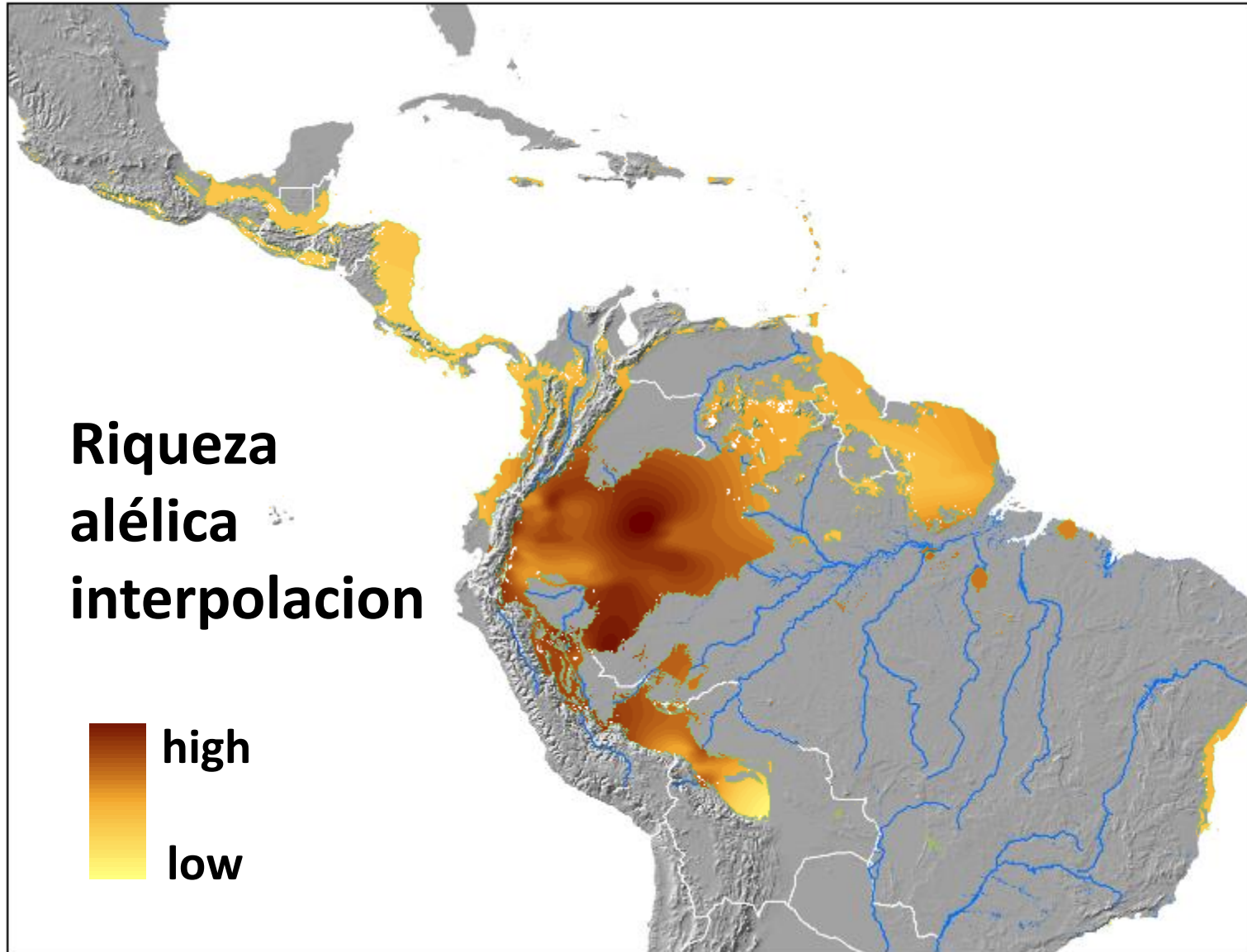
Annals of Botany 98: 647–655, 2006
doi:10.1093/aob/mcl146, available online at www.aob.oxfordjournals.org

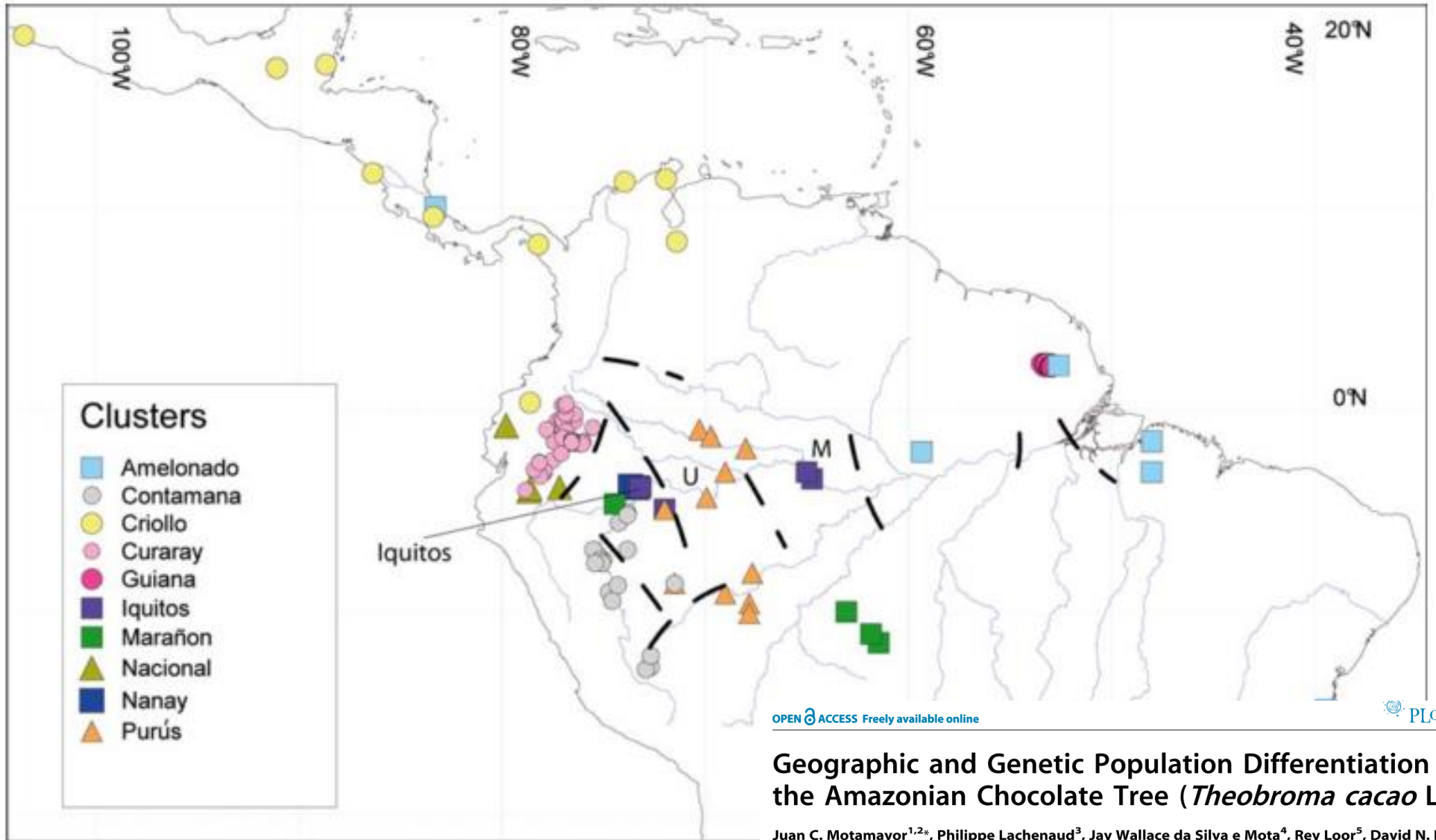
Geographic and Genetic Population Differentiation of the Amazonian Chocolate Tree (*Theobroma cacao* L)

Juan C. Motamayor^{1,2*}, Philippe Lachenaud³, Jay Wallace da Silva e Mota⁴, Rey Loor⁵, David N. Kuhn¹, J. Steven Brown¹, Raymond J. Schnell¹

Genetic Diversity and Structure of Managed and Semi-natural Populations of Cocoa (*Theobroma cacao*) in the Huallaga and Ucayali Valleys of Peru

DAPENG ZHANG^{1*}, ENRIQUE AREVALO-GARDINI², SUE MISCHKE¹,
LUIS ZÚÑIGA-CERNADES², ALEJANDRO BARRETO-CHAVEZ² and
JORGE ADRIAZOLA DEL AGUILA²





OPEN ACCESS Freely available online

PLOS ONE

Geographic and Genetic Population Differentiation of the Amazonian Chocolate Tree (*Theobroma cacao* L)

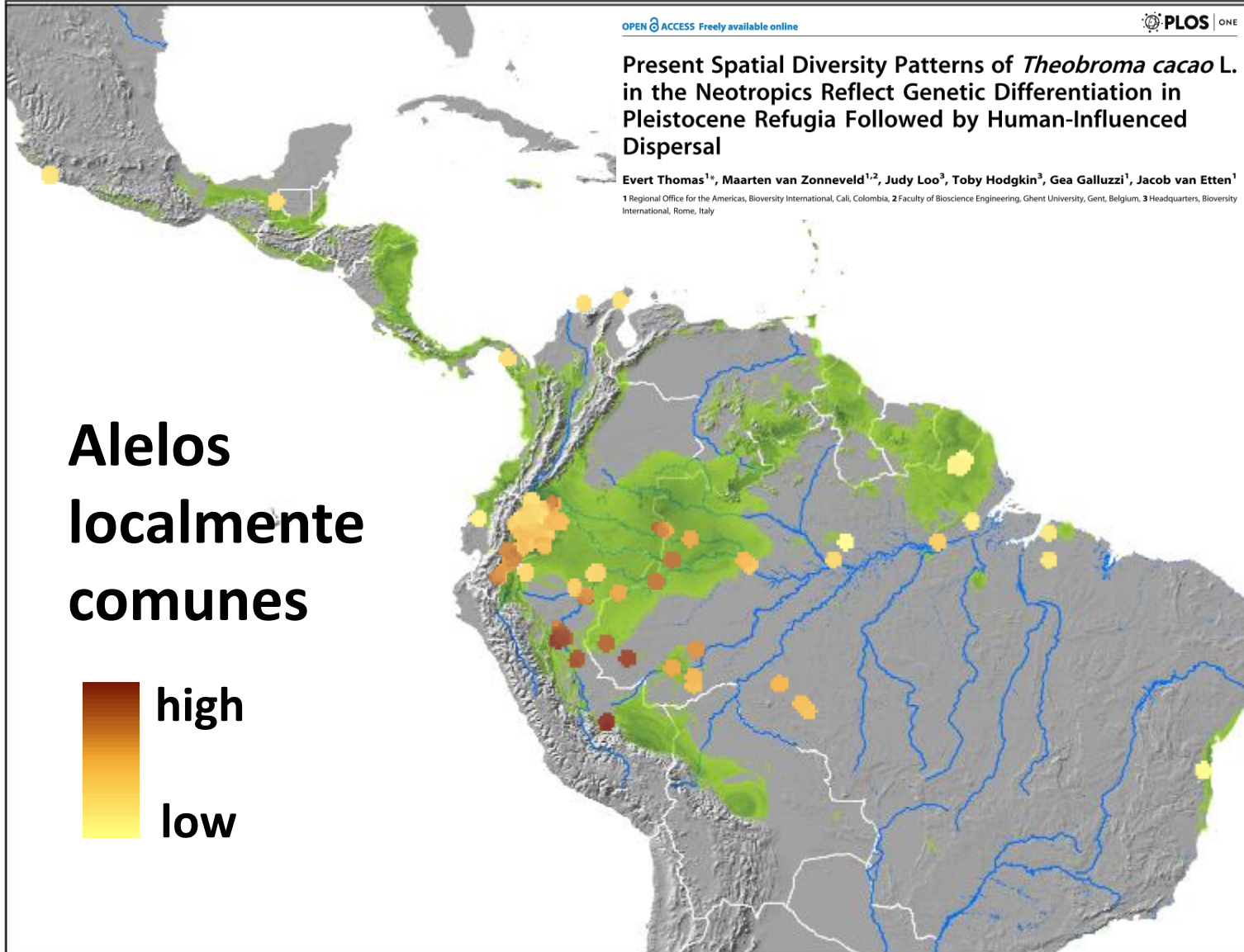
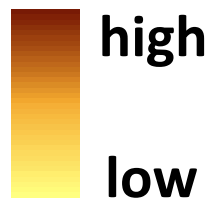
Juan C. Motamayor^{1,2*}, Philippe Lachenaud³, Jay Wallace da Silva e Mota⁴, Rey Loo⁵, David N. Kuhn¹, J. Steven Brown¹, Raymond J. Schnell¹

Present Spatial Diversity Patterns of *Theobroma cacao* L. in the Neotropics Reflect Genetic Differentiation in Pleistocene Refugia Followed by Human-Influenced Dispersal

Evert Thomas^{1*}, Maarten van Zonneveld^{1,2}, Judy Loo³, Toby Hodgkin³, Gea Galluzzi¹, Jacob van Etten¹

¹ Regional Office for the Americas, Bioversity International, Cali, Colombia, ² Faculty of Bioscience Engineering, Ghent University, Ghent, Belgium, ³ Headquarters, Bioversity International, Rome, Italy

Alelos
localmente
comunes

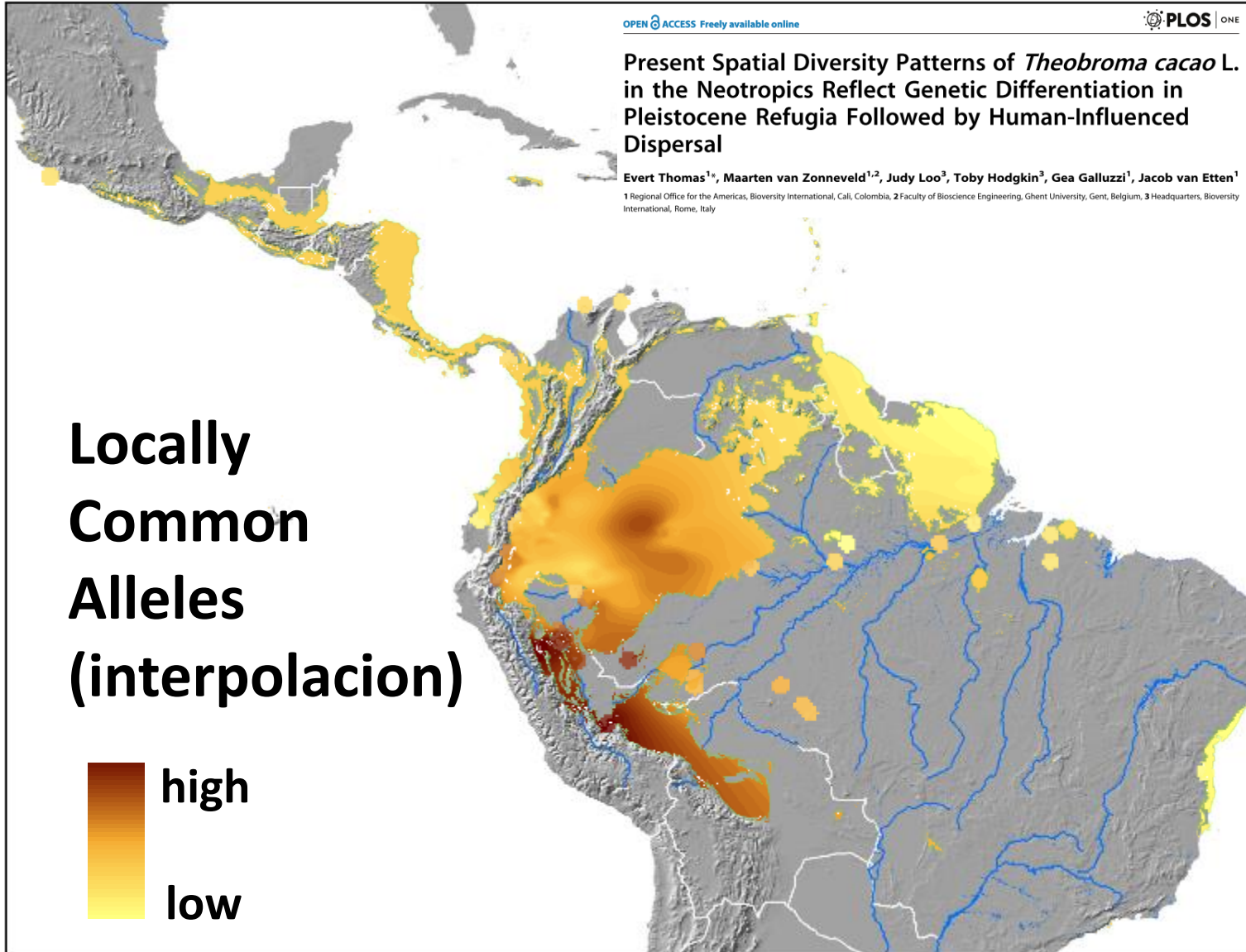


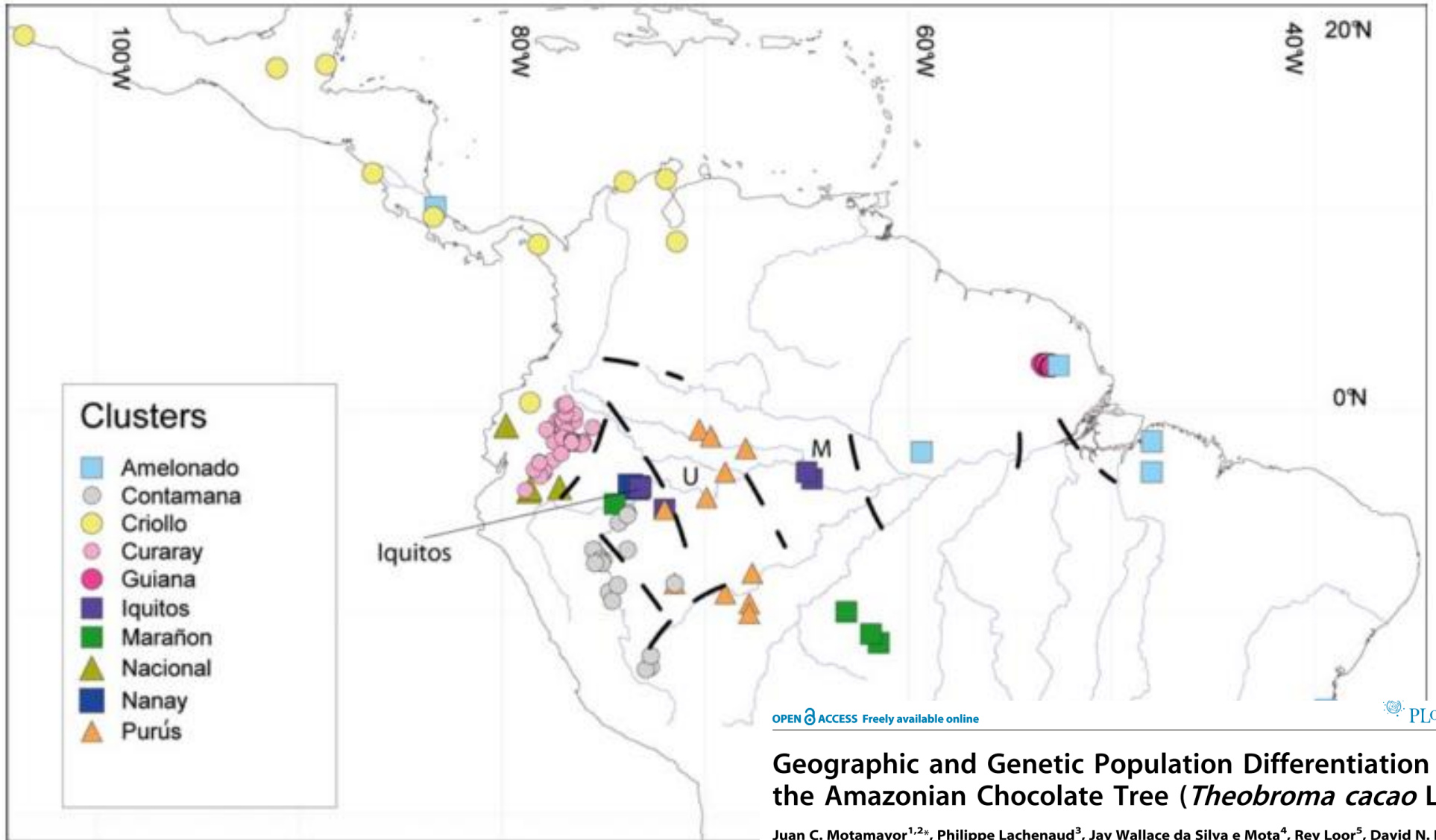
Present Spatial Diversity Patterns of *Theobroma cacao* L. in the Neotropics Reflect Genetic Differentiation in Pleistocene Refugia Followed by Human-Influenced Dispersal

Evert Thomas^{1*}, Maarten van Zonneveld^{1,2}, Judy Loo³, Toby Hodgkin³, Gea Galluzzi¹, Jacob van Etten¹

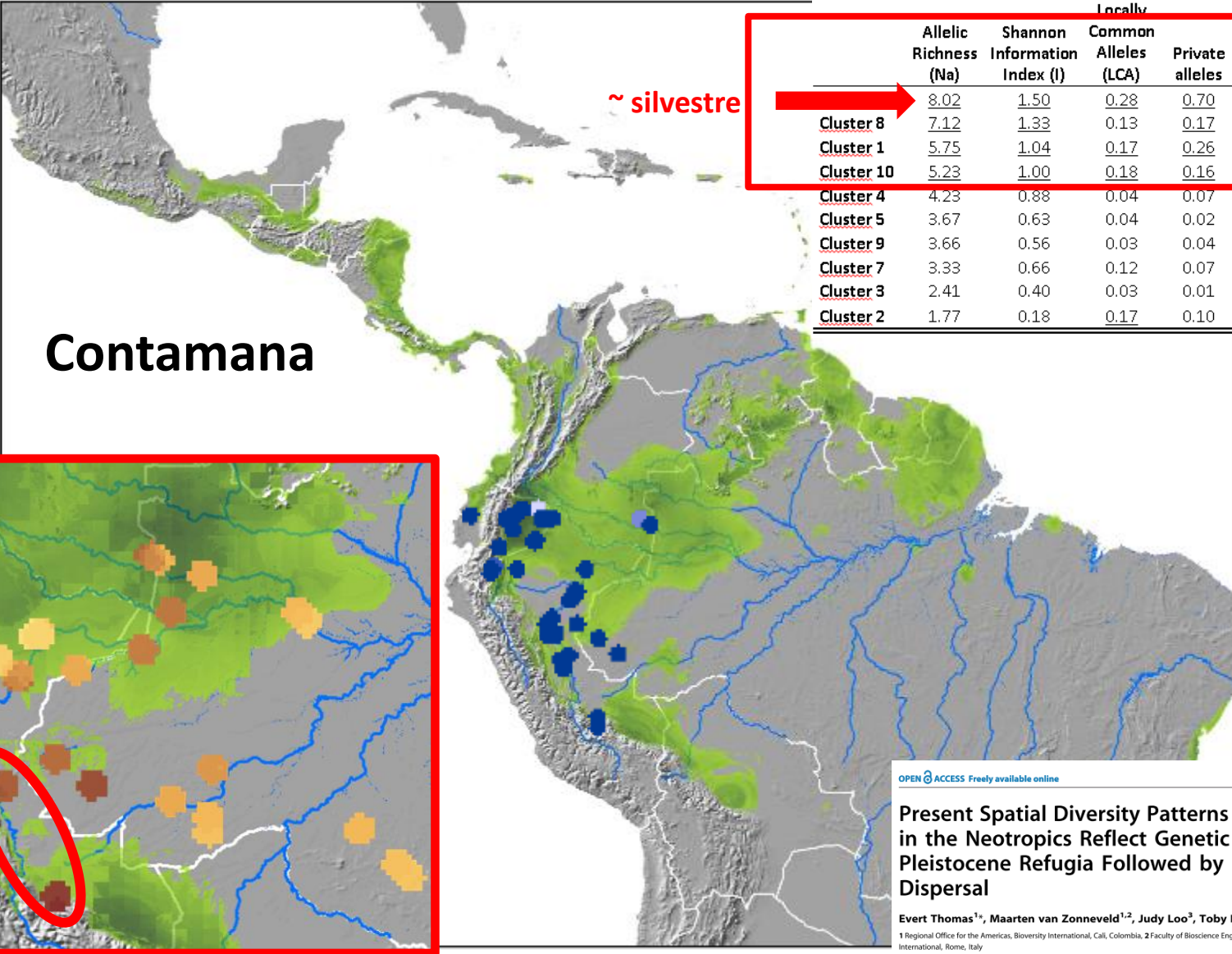
¹ Regional Office for the Americas, Bioversity International, Cali, Colombia, ² Faculty of Bioscience Engineering, Ghent University, Ghent, Belgium, ³ Headquarters, Bioversity International, Rome, Italy

**Locally
Common
Alleles
(interpolacion)**





clusters



~ silvestre

Table 1. Averages of genetic parameters per locus for clusters 1 to 10, based on 1,000 bootstrap samples of 35 trees (i.e. the size of the smallest cluster). Four highest values for each of the parameter are underlined. For the fixation index the four lowest values are underlined

	Allelic Richness (Na)	Shannon Information Index (I)	Common Alleles (LCA)	Private alleles	Ho	He	Fixation index (F)
	<u>8.02</u>	<u>1.50</u>	<u>0.28</u>	<u>0.70</u>	<u>0.40</u>	<u>0.68</u>	0.41
Cluster 8	<u>7.12</u>	<u>1.33</u>	0.13	<u>0.17</u>	<u>0.55</u>	<u>0.63</u>	<u>0.12</u>
Cluster 1	<u>5.75</u>	<u>1.04</u>	<u>0.17</u>	<u>0.26</u>	<u>0.40</u>	<u>0.51</u>	0.21
Cluster 10	<u>5.23</u>	<u>1.00</u>	<u>0.18</u>	<u>0.16</u>	0.36	<u>0.50</u>	0.28
Cluster 4	4.23	0.88	0.04	0.07	<u>0.45</u>	0.47	<u>0.04</u>
Cluster 5	3.67	0.63	0.04	0.02	0.15	0.33	0.54
Cluster 9	3.66	0.56	0.03	0.04	0.25	0.29	<u>0.13</u>
Cluster 7	3.33	0.66	0.12	0.07	0.30	0.36	<u>0.18</u>
Cluster 3	2.41	0.40	0.03	0.01	0.11	0.23	0.49
Cluster 2	1.77	0.18	<u>0.17</u>	0.10	0.02	0.10	0.77

OPEN ACCESS Freely available online

PLOS ONE

Present Spatial Diversity Patterns of *Theobroma cacao* L. in the Neotropics Reflect Genetic Differentiation in Pleistocene Refugia Followed by Human-Influenced Dispersal

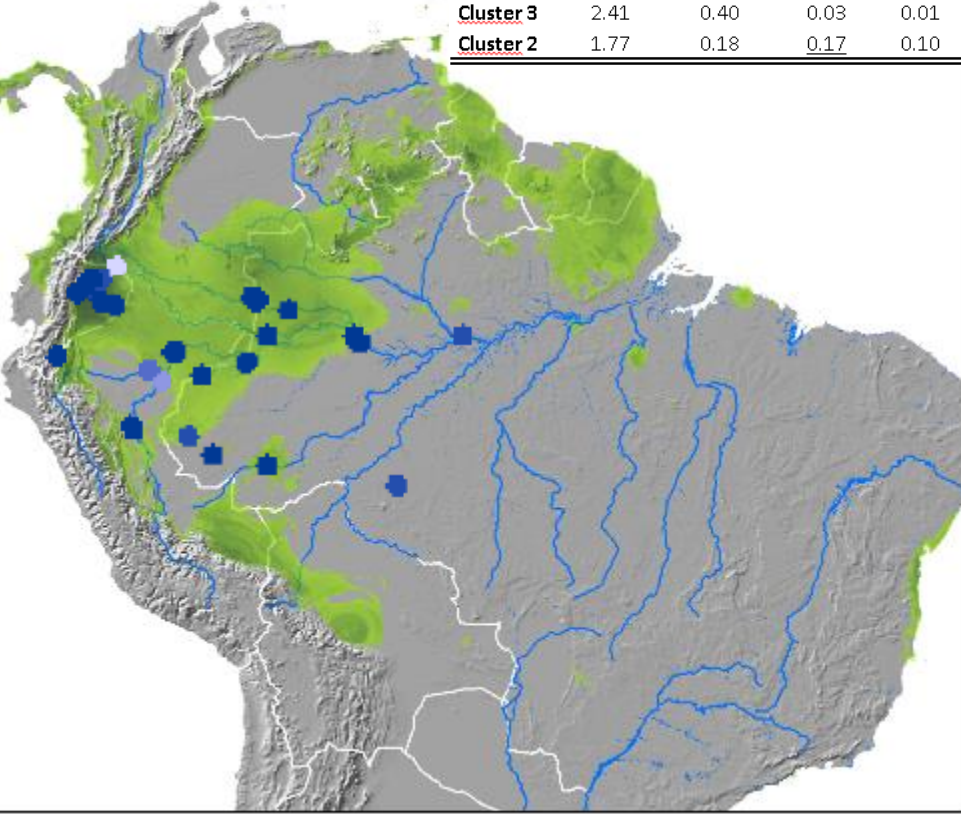
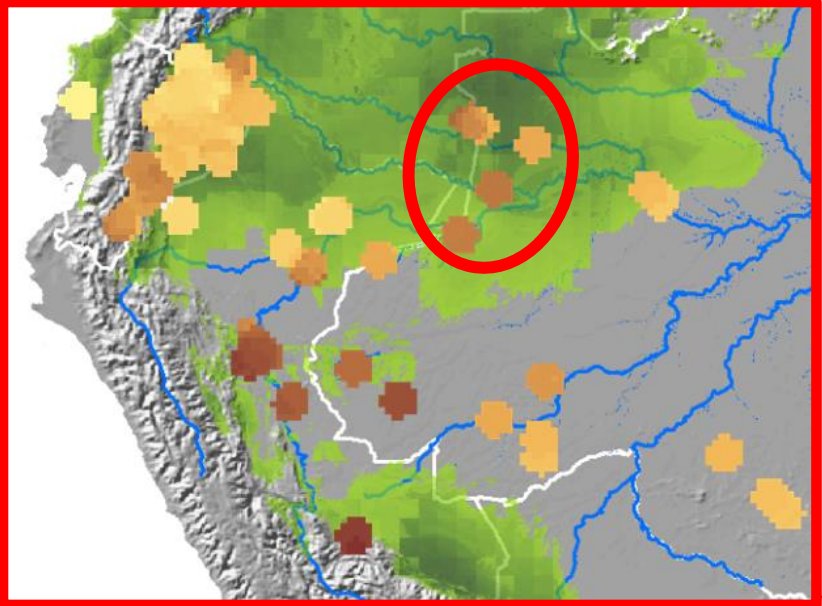
Evert Thomas^{1*}, Maarten van Zonneveld^{1,2}, Judy Loo³, Toby Hodgkin³, Gea Galluzzi¹, Jacob van Etten¹
¹ Regional Office for the Americas, Bioversity International, Cali, Colombia, ² Faculty of Bioscience Engineering, Ghent University, Gent, Belgium, ³ Headquarters, Bioversity International, Rome, Italy

clusters



Table 1. Averages of genetic parameters per locus for clusters 1 to 10, based on 1,000 bootstrap samples of 35 trees (i.e. the size of the smallest cluster). Four highest values for each of the parameter are underlined. For the fixation index the four lowest values are underlined

	Allelic Richness (Na)	Shannon Information Index (I)	Common Alleles (LCA)	Private alleles	Ho	He	Fixation index (F)
Cluster 6	<u>8.02</u> <u>7.12</u>	<u>1.50</u> <u>1.33</u>	0.28 0.13	0.70 <u>0.17</u>	<u>0.40</u> <u>0.55</u>	<u>0.68</u> <u>0.63</u>	0.41 0.12
Cluster 1	5.75	<u>1.04</u>	<u>0.17</u>	<u>0.26</u>	<u>0.40</u>	<u>0.51</u>	0.21
Cluster 10	<u>5.23</u>	<u>1.00</u>	<u>0.18</u>	<u>0.16</u>	0.36	<u>0.50</u>	0.28
Cluster 4	4.23	0.88	0.04	0.07	<u>0.45</u>	0.47	<u>0.04</u>
Cluster 5	3.67	0.63	0.04	0.02	0.15	0.33	0.54
Cluster 9	3.66	0.56	0.03	0.04	0.25	0.29	<u>0.13</u>
Cluster 7	3.33	0.66	0.12	0.07	0.30	0.36	<u>0.18</u>
Cluster 3	2.41	0.40	0.03	0.01	0.11	0.23	0.49
Cluster 2	1.77	0.18	<u>0.17</u>	0.10	0.02	0.10	0.77



clusters

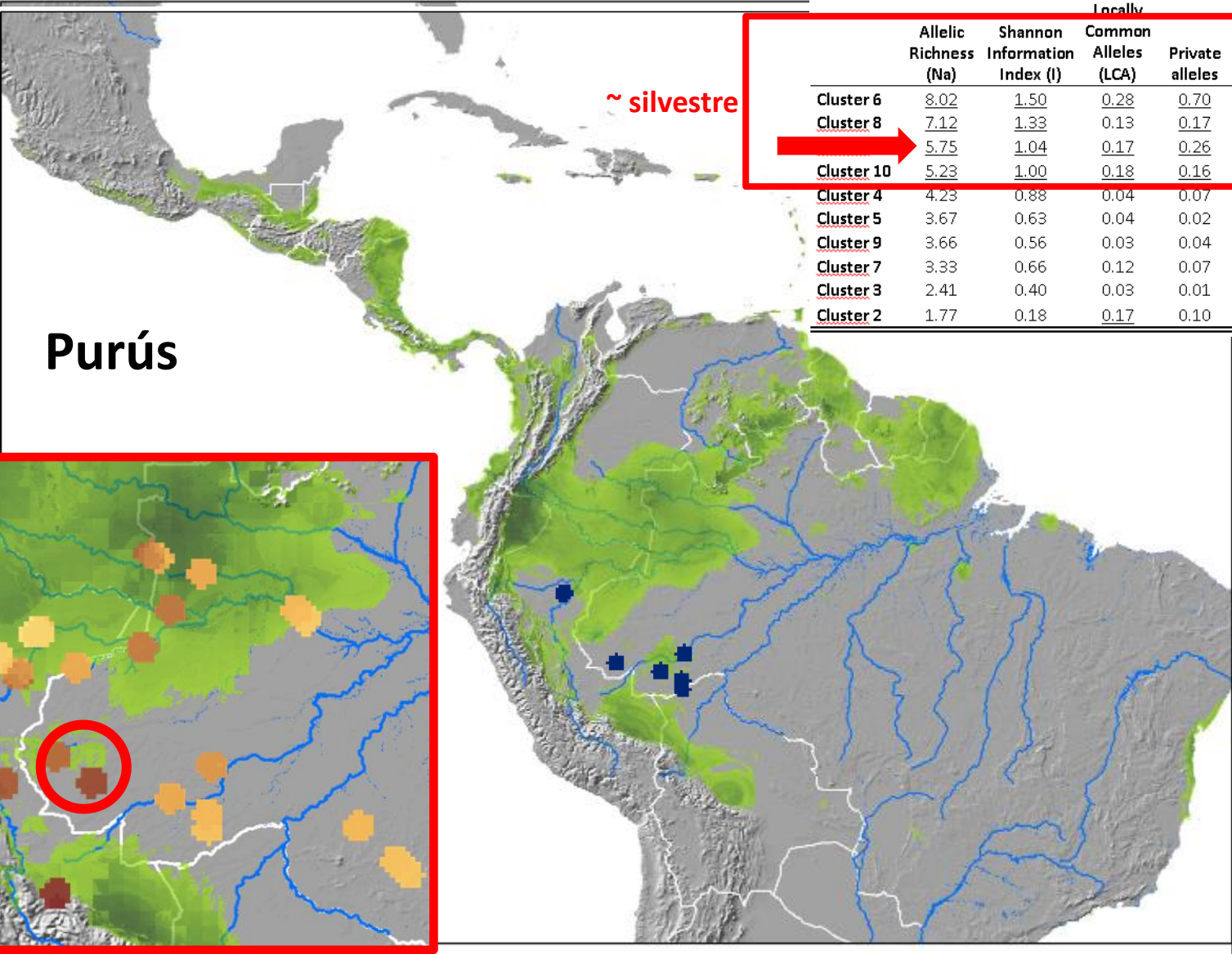
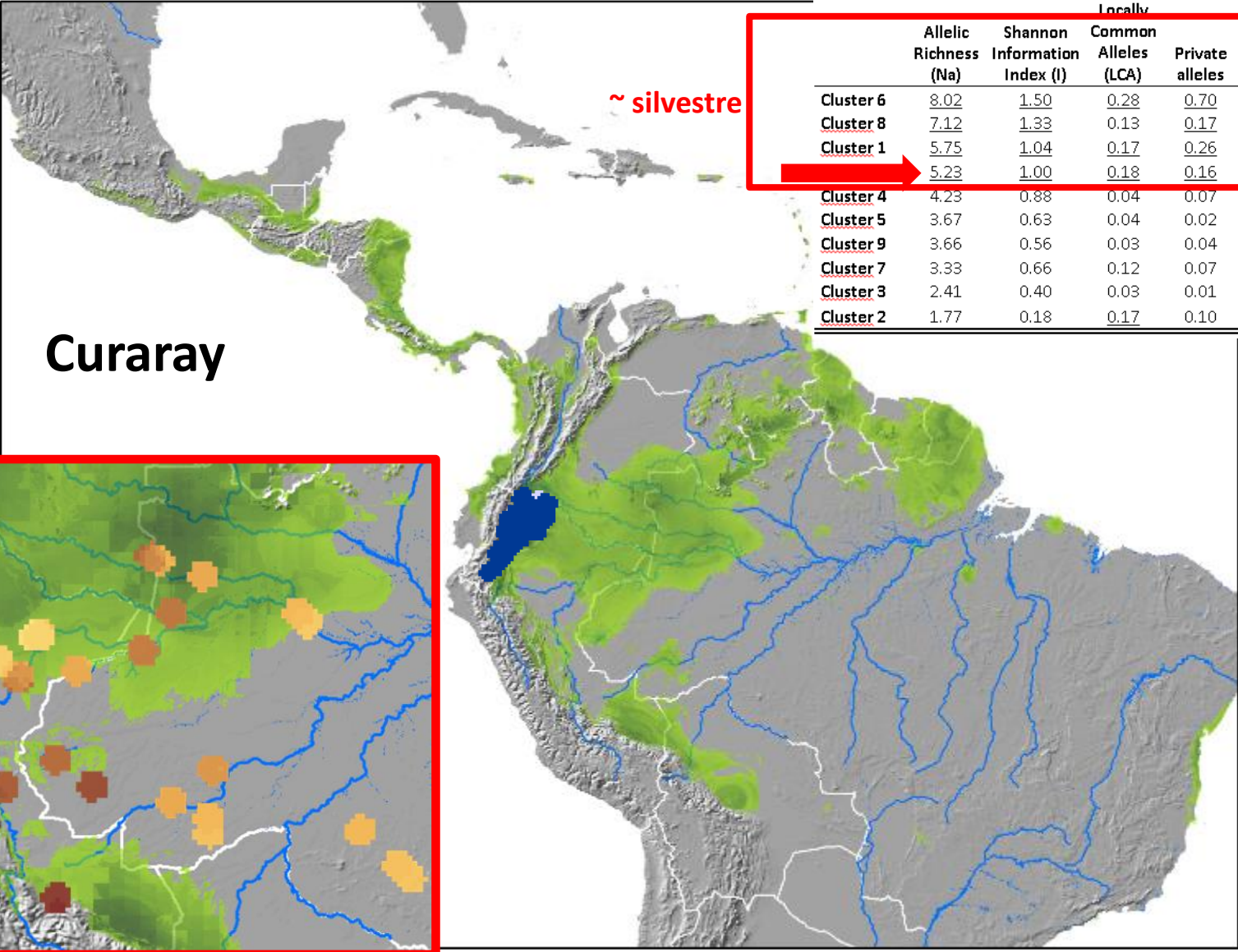


Table 1. Averages of genetic parameters per locus for clusters 1 to 10, based on 1,000 bootstrap samples of 35 trees (i.e. the size of the smallest cluster). Four highest values for each of the parameter are underlined. For the fixation index the four lowest values are underlined

	Allelic Richness (Na)	Shannon Information Index (I)	Common Alleles (LCA)	Private alleles	Ho	He	Fixation index (F)
Cluster 6	<u>8.02</u>	<u>1.50</u>	<u>0.28</u>	<u>0.70</u>	<u>0.40</u>	<u>0.68</u>	0.41
Cluster 8	<u>7.12</u>	<u>1.33</u>	0.13	<u>0.17</u>	<u>0.55</u>	<u>0.63</u>	<u>0.12</u>
Cluster 10	<u>5.75</u>	<u>1.04</u>	<u>0.17</u>	<u>0.26</u>	<u>0.40</u>	<u>0.51</u>	0.21
Cluster 10	<u>5.23</u>	<u>1.00</u>	<u>0.18</u>	<u>0.16</u>	0.36	<u>0.50</u>	0.28
Cluster 4	4.23	0.88	0.04	0.07	0.45	0.47	<u>0.04</u>
Cluster 5	3.67	0.63	0.04	0.02	0.15	0.33	0.54
Cluster 9	3.66	0.56	0.03	0.04	0.25	0.29	<u>0.13</u>
Cluster 7	3.33	0.66	0.12	0.07	0.30	0.36	<u>0.18</u>
Cluster 3	2.41	0.40	0.03	0.01	0.11	0.23	0.49
Cluster 2	1.77	0.18	<u>0.17</u>	0.10	0.02	0.10	0.77

clusters

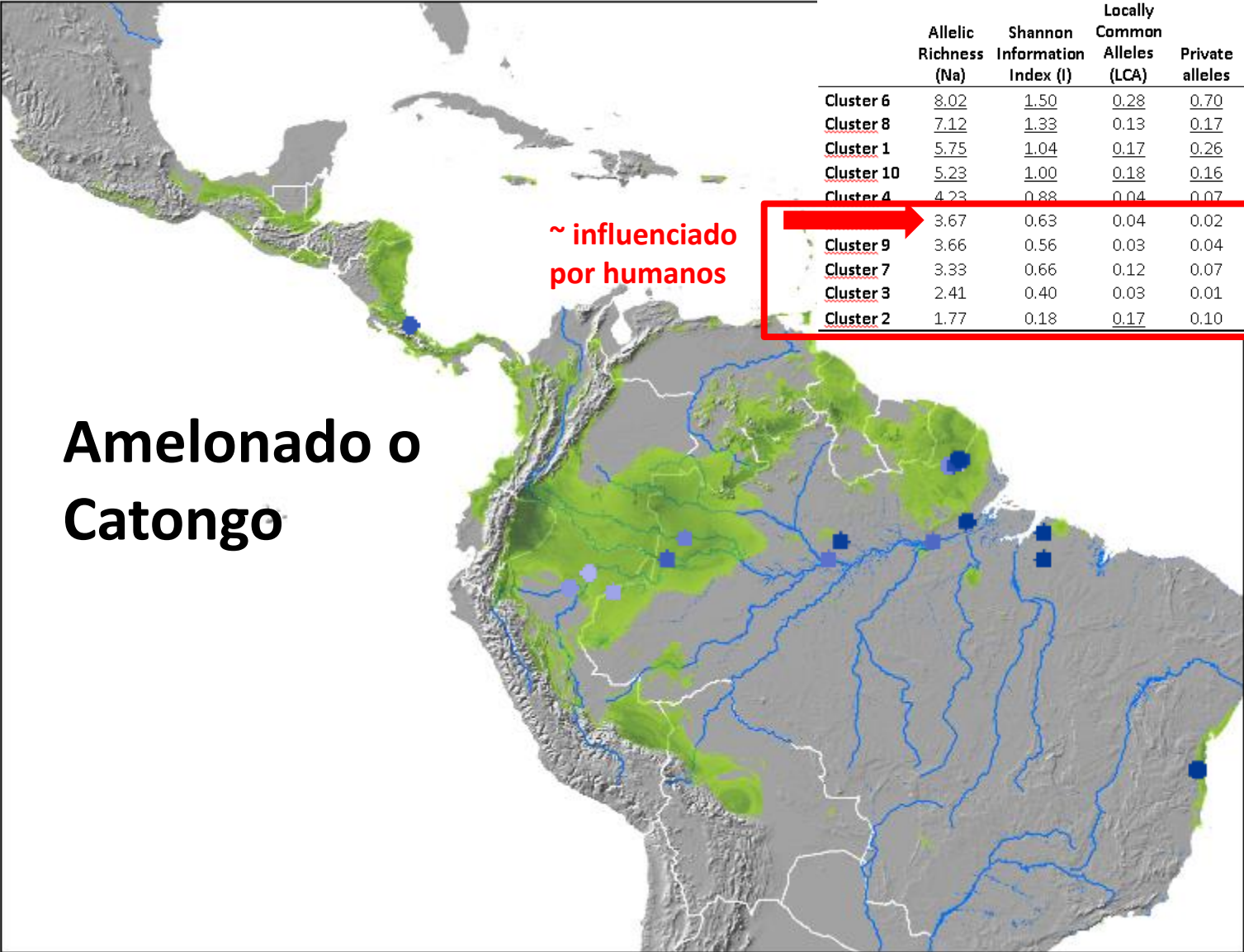


Curaray

Table 1. Averages of genetic parameters per locus for clusters 1 to 10, based on 1,000 bootstrap samples of 35 trees (i.e. the size of the smallest cluster). Four highest values for each of the parameter are underlined. For the fixation index the four lowest values are underlined

	Allelic Richness (Na)	Shannon Information Index (I)	Common Alleles (LCA)	Private alleles	Ho	He	Fixation index (F)
Cluster 6	<u>8.02</u>	<u>1.50</u>	<u>0.28</u>	<u>0.70</u>	<u>0.40</u>	<u>0.68</u>	0.41
Cluster 8	<u>7.12</u>	<u>1.33</u>	0.13	<u>0.17</u>	<u>0.55</u>	<u>0.63</u>	<u>0.12</u>
Cluster 1	<u>5.75</u>	<u>1.04</u>	<u>0.17</u>	<u>0.26</u>	<u>0.40</u>	<u>0.51</u>	0.21
Cluster 1	<u>5.23</u>	<u>1.00</u>	<u>0.18</u>	<u>0.16</u>	0.36	<u>0.50</u>	0.28
Cluster 4	<u>4.23</u>	0.88	0.04	0.07	<u>0.45</u>	0.47	<u>0.04</u>
Cluster 5	3.67	0.63	0.04	0.02	0.15	0.33	0.54
Cluster 9	3.66	0.56	0.03	0.04	0.25	0.29	<u>0.13</u>
Cluster 7	3.33	0.66	0.12	0.07	0.30	0.36	<u>0.18</u>
Cluster 3	2.41	0.40	0.03	0.01	0.11	0.23	0.49
Cluster 2	1.77	0.18	<u>0.17</u>	0.10	0.02	0.10	0.77

clusters



Amelonado o
Catongo

~ influenciado por humanos

Table 1. Averages of genetic parameters per locus for clusters 1 to 10, based on 1,000 bootstrap samples of 35 trees (i.e. the size of the smallest cluster). Four highest values for each of the parameter are underlined. For the fixation index the four lowest values are underlined

	Allelic Richness (Na)	Shannon Information Index (I)	Locally Common Alleles (LCA)	Private alleles	Ho	He	Fixation index (F)
Cluster 6	<u>8.02</u>	<u>1.50</u>	0.28	0.70	<u>0.40</u>	<u>0.68</u>	0.41
Cluster 8	<u>7.12</u>	<u>1.33</u>	0.13	<u>0.17</u>	<u>0.55</u>	<u>0.63</u>	<u>0.12</u>
Cluster 1	<u>5.75</u>	<u>1.04</u>	<u>0.17</u>	<u>0.26</u>	<u>0.40</u>	<u>0.51</u>	0.21
Cluster 10	<u>5.23</u>	<u>1.00</u>	<u>0.18</u>	<u>0.16</u>	0.36	<u>0.50</u>	0.28
Cluster 4	<u>4.23</u>	<u>0.88</u>	0.04	0.07	0.45	0.47	0.04
Cluster 9	3.67	0.63	0.04	0.02	0.15	0.33	0.54
Cluster 7	3.66	0.56	0.03	0.04	0.25	0.29	<u>0.13</u>
Cluster 3	3.33	0.66	0.12	0.07	0.30	0.36	<u>0.18</u>
Cluster 5	2.41	0.40	0.03	0.01	0.11	0.23	0.49
Cluster 2	<u>1.77</u>	<u>0.18</u>	<u>0.17</u>	0.10	0.02	0.10	0.77

clusters

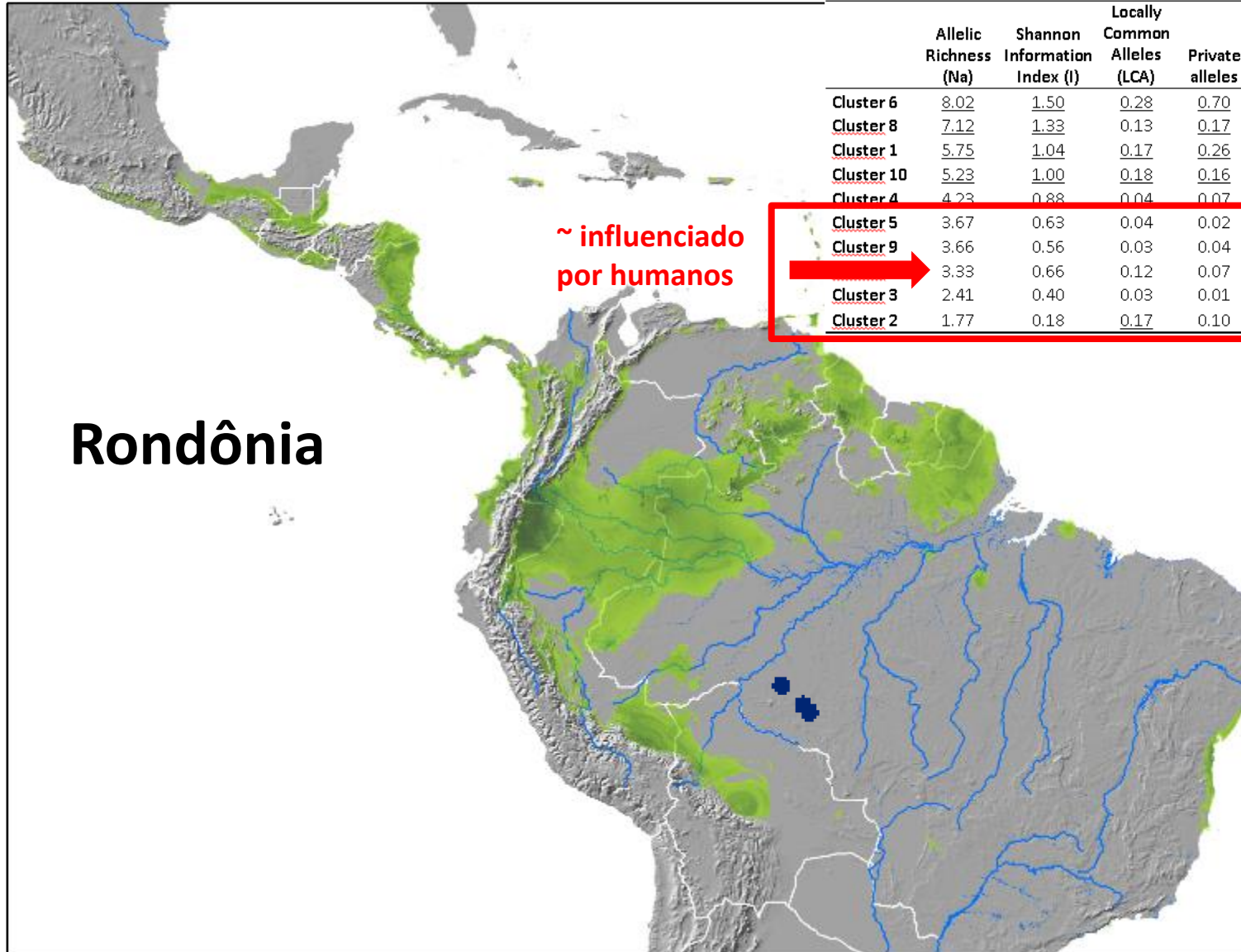
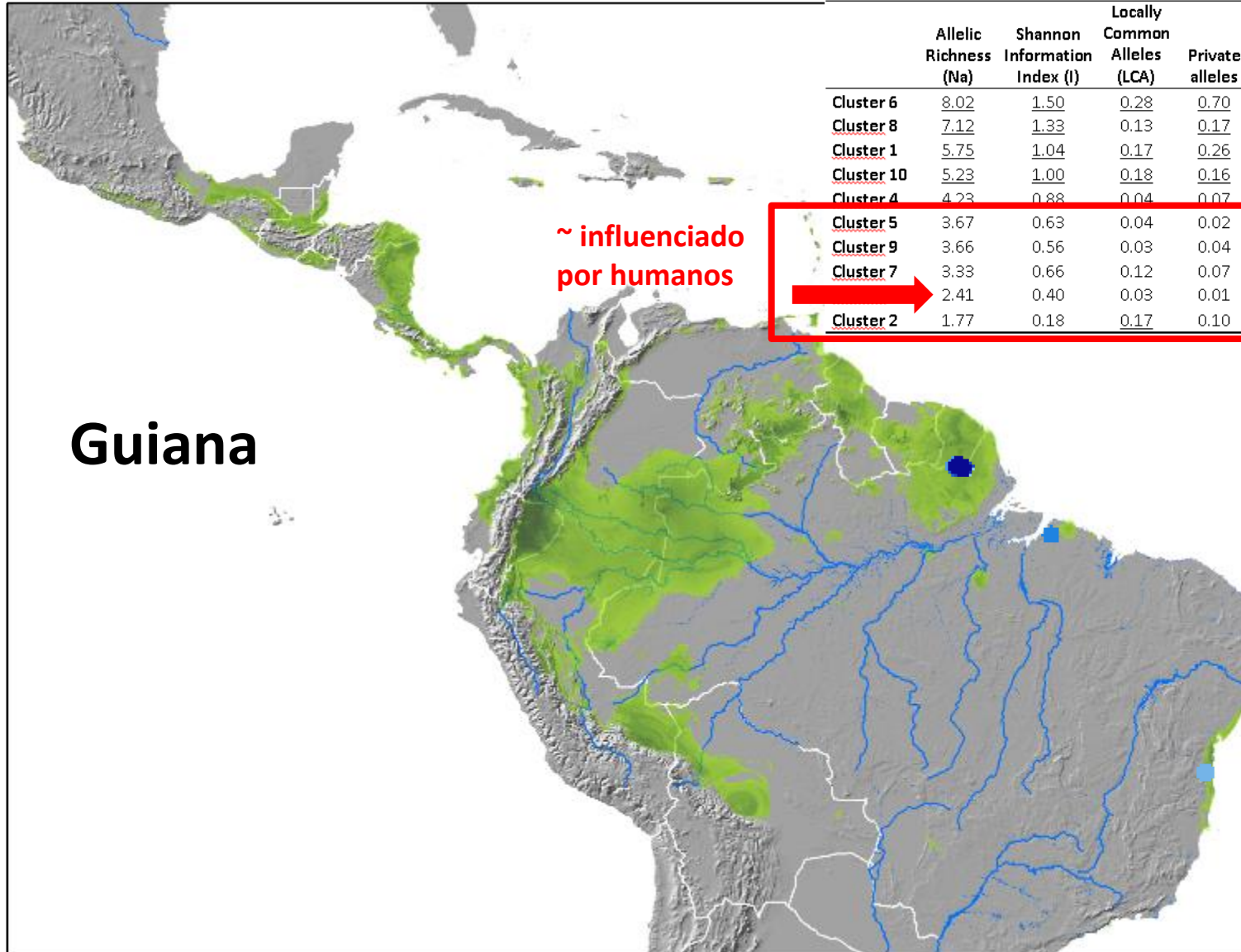


Table 1. Averages of genetic parameters per locus for clusters 1 to 10, based on 1,000 bootstrap samples of 35 trees (i.e. the size of the smallest cluster). Four highest values for each of the parameter are underlined. For the fixation index the four lowest values are underlined

	Allelic Richness (Na)	Shannon Information Index (I)	Locally Common Alleles (LCA)	Private alleles	Ho	He	Fixation index (F)
Cluster 6	<u>8.02</u>	<u>1.50</u>	0.28	<u>0.70</u>	<u>0.40</u>	<u>0.68</u>	0.41
Cluster 8	<u>7.12</u>	<u>1.33</u>	0.13	<u>0.17</u>	<u>0.55</u>	<u>0.63</u>	<u>0.12</u>
Cluster 1	<u>5.75</u>	<u>1.04</u>	<u>0.17</u>	<u>0.26</u>	<u>0.40</u>	<u>0.51</u>	0.21
Cluster 10	<u>5.23</u>	<u>1.00</u>	<u>0.18</u>	<u>0.16</u>	0.36	<u>0.50</u>	0.28
Cluster 4	<u>4.23</u>	<u>0.88</u>	0.04	0.07	0.45	0.47	0.04
Cluster 5	3.67	0.63	0.04	0.02	0.15	0.33	0.54
Cluster 9	3.66	0.56	0.03	0.04	0.25	0.29	<u>0.13</u>
Cluster 3	2.41	0.40	0.03	0.01	0.11	0.23	0.49
Cluster 2	1.77	0.18	<u>0.17</u>	0.10	0.02	0.10	0.77

cluster
s



Guiana

~ influenciado por humanos

Table 1. Averages of genetic parameters per locus for clusters 1 to 10, based on 1,000 bootstrap samples of 35 trees (i.e. the size of the smallest cluster). Four highest values for each of the parameter are underlined. For the fixation index the four lowest values are underlined

	Allelic Richness (Na)	Shannon Information Index (I)	Locally Common Alleles (LCA)	Private alleles	Ho	He	Fixation index (F)
Cluster 6	<u>8.02</u>	<u>1.50</u>	0.28	<u>0.70</u>	<u>0.40</u>	<u>0.68</u>	0.41
Cluster 8	<u>7.12</u>	<u>1.33</u>	0.13	<u>0.17</u>	<u>0.55</u>	<u>0.63</u>	<u>0.12</u>
Cluster 1	<u>5.75</u>	<u>1.04</u>	<u>0.17</u>	<u>0.26</u>	<u>0.40</u>	<u>0.51</u>	0.21
Cluster 10	<u>5.23</u>	<u>1.00</u>	<u>0.18</u>	<u>0.16</u>	0.36	<u>0.50</u>	0.28
Cluster 4	<u>4.23</u>	<u>0.88</u>	0.04	0.07	0.45	0.47	0.04
Cluster 5	3.67	0.63	0.04	0.02	0.15	0.33	0.54
Cluster 9	3.66	0.56	0.03	0.04	0.25	0.29	<u>0.13</u>
Cluster 7	3.33	0.66	0.12	0.07	0.30	0.36	<u>0.18</u>
Cluster 2	2.41	0.40	0.03	0.01	0.11	0.23	0.49
Cluster 2	<u>1.77</u>	<u>0.18</u>	<u>0.17</u>	0.10	0.02	0.10	0.77

cluster
s

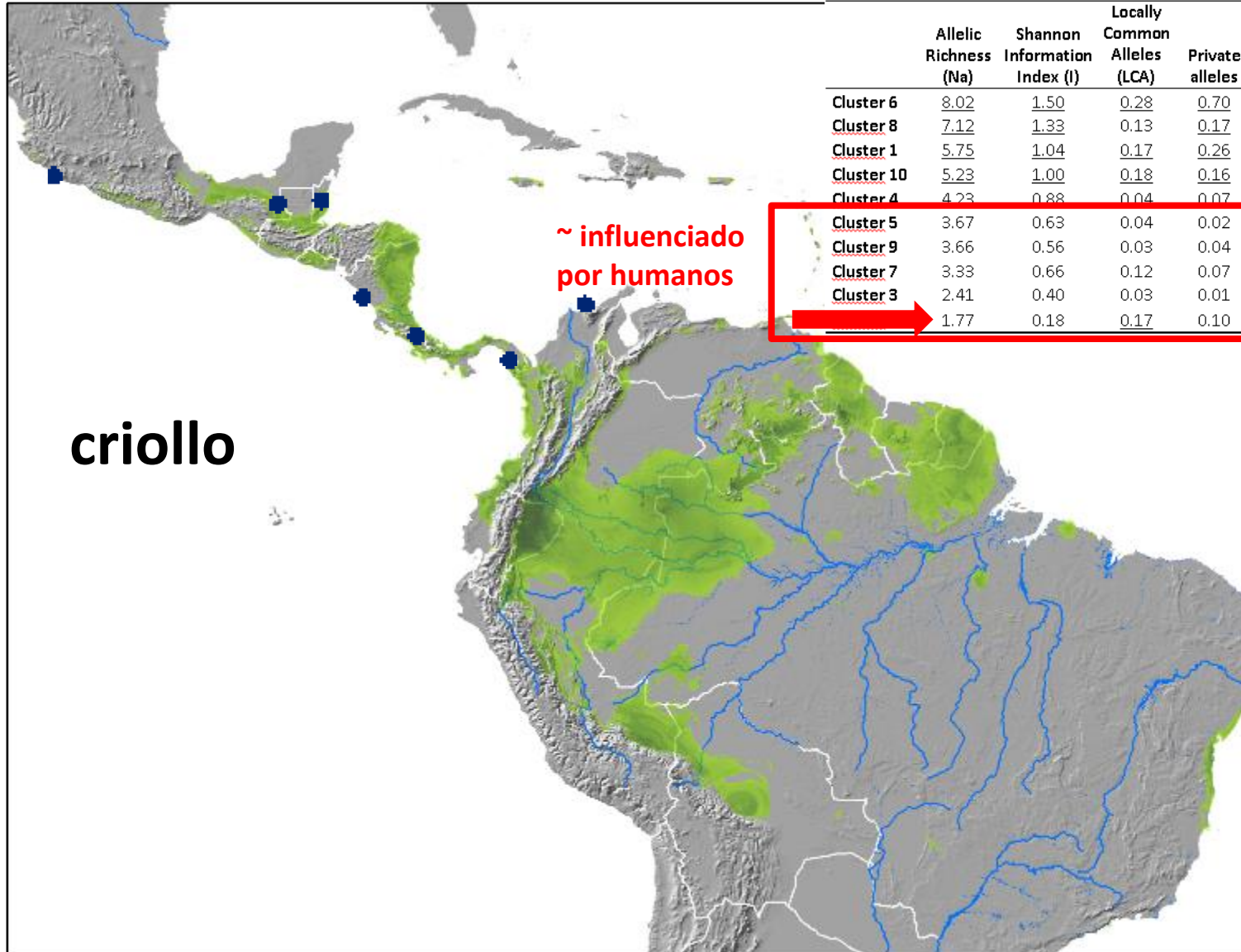
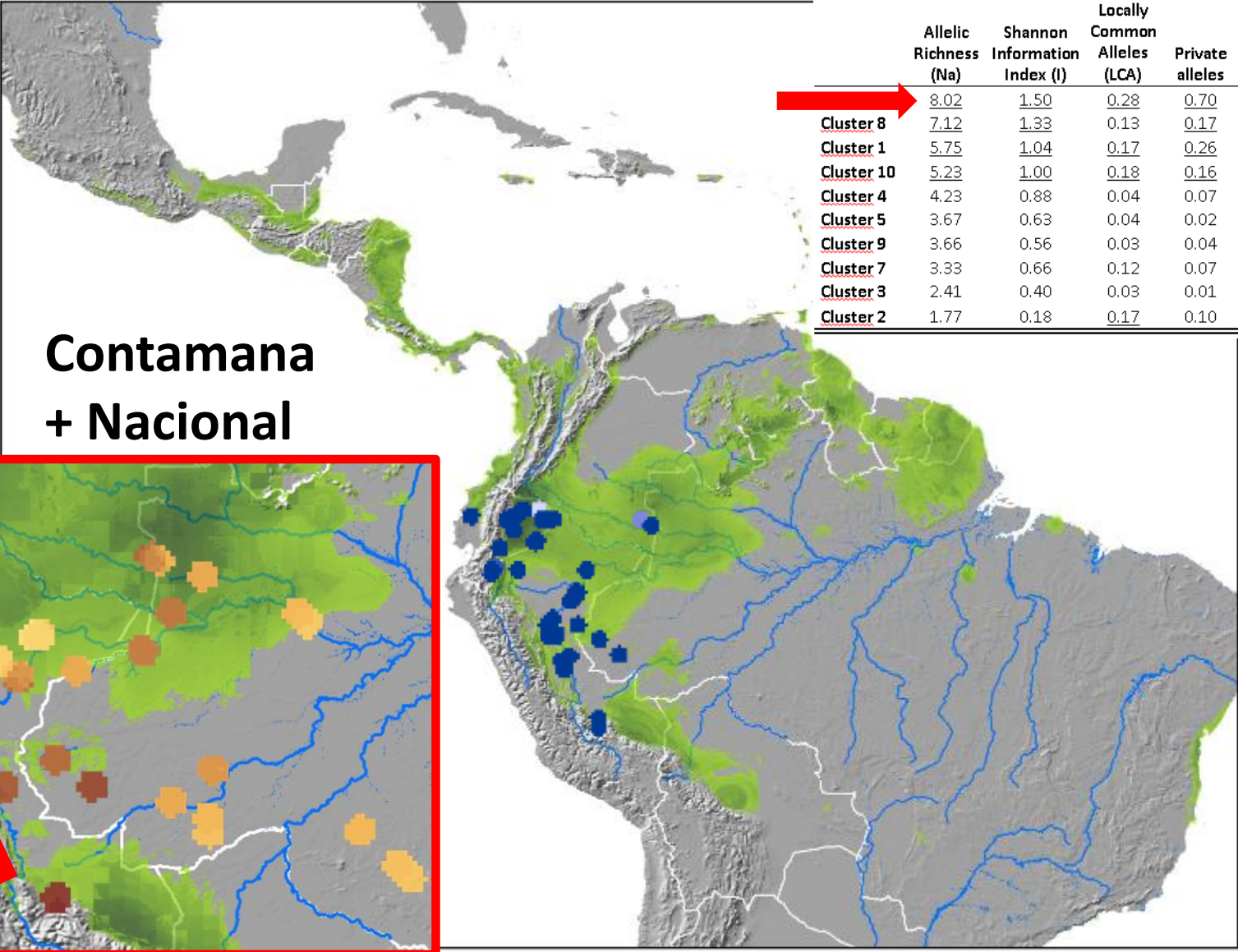


Table 1. Averages of genetic parameters per locus for clusters 1 to 10, based on 1,000 bootstrap samples of 35 trees (i.e. the size of the smallest cluster). Four highest values for each of the parameter are underlined. For the fixation index the four lowest values are underlined

	Allelic Richness (Na)	Shannon Information Index (I)	Locally Common Alleles (LCA)	Private alleles	Ho	He	Fixation index (F)
Cluster 6	<u>8.02</u>	<u>1.50</u>	0.28	<u>0.70</u>	<u>0.40</u>	<u>0.68</u>	0.41
Cluster 8	<u>7.12</u>	<u>1.33</u>	0.13	<u>0.17</u>	<u>0.55</u>	<u>0.63</u>	<u>0.12</u>
Cluster 1	<u>5.75</u>	<u>1.04</u>	<u>0.17</u>	<u>0.26</u>	<u>0.40</u>	<u>0.51</u>	0.21
Cluster 10	<u>5.23</u>	<u>1.00</u>	<u>0.18</u>	<u>0.16</u>	0.36	<u>0.50</u>	0.28
Cluster 4	<u>4.23</u>	<u>0.88</u>	0.04	0.07	0.45	0.47	0.04
Cluster 5	3.67	0.63	0.04	0.02	0.15	0.33	0.54
Cluster 9	3.66	0.56	0.03	0.04	0.25	0.29	<u>0.13</u>
Cluster 7	3.33	0.66	0.12	0.07	0.30	0.36	<u>0.18</u>
Cluster 3	2.41	0.40	0.03	0.01	0.11	0.23	0.49
	1.77	0.18	<u>0.17</u>	0.10	0.02	0.10	0.77

Y el cacao Nacional de Ecuador/blanco de Piura?

clusters



Contamana
+ Nacional

Table 1. Averages of genetic parameters per locus for clusters 1 to 10, based on 1,000 bootstrap samples of 35 trees (i.e. the size of the smallest cluster). Four highest values for each of the parameter are underlined. For the fixation index the four lowest values are underlined

	Allelic Richness (Na)	Shannon Information Index (I)	Locally Common Alleles (LCA)	Private alleles	Ho	He	Fixation index (F)
Cluster 8	<u>8.02</u>	<u>1.50</u>	<u>0.28</u>	<u>0.70</u>	<u>0.40</u>	<u>0.68</u>	0.41
Cluster 1	<u>7.12</u>	<u>1.33</u>	0.13	<u>0.17</u>	<u>0.55</u>	<u>0.63</u>	<u>0.12</u>
Cluster 10	<u>5.75</u>	<u>1.04</u>	<u>0.17</u>	<u>0.26</u>	<u>0.40</u>	<u>0.51</u>	0.21
Cluster 4	<u>5.23</u>	<u>1.00</u>	<u>0.18</u>	<u>0.16</u>	0.36	<u>0.50</u>	0.28
Cluster 5	4.23	0.88	0.04	0.07	<u>0.45</u>	0.47	<u>0.04</u>
Cluster 9	3.67	0.63	0.04	0.02	0.15	0.33	0.54
Cluster 7	3.66	0.56	0.03	0.04	0.25	0.29	<u>0.13</u>
Cluster 3	3.33	0.66	0.12	0.07	0.30	0.36	<u>0.18</u>
Cluster 2	2.41	0.40	0.03	0.01	0.11	0.23	0.49
Cluster 2	1.77	0.18	<u>0.17</u>	0.10	0.02	0.10	0.77

Table 1. Averages of genetic parameters per locus for clusters 1 to 10, based on 1,000 bootstrap samples of 35 trees (i.e. the size of the smallest cluster). Four highest values for each of the parameter are underlined. For the fixation index the four lowest values are underlined

	Allelic Richness (Na)	Shannon Information Index (I)	Locally Common Alleles (LCA)	Private alleles	Ho	He	Fixation index (F)
Cluster 8	<u>8.02</u>	<u>1.50</u>	<u>0.28</u>	<u>0.70</u>	<u>0.40</u>	<u>0.68</u>	0.41
Cluster 1	<u>7.12</u>	<u>1.33</u>	0.13	<u>0.17</u>	<u>0.55</u>	<u>0.63</u>	<u>0.12</u>
Cluster 10	<u>5.75</u>	<u>1.04</u>	<u>0.17</u>	<u>0.26</u>	<u>0.40</u>	<u>0.51</u>	0.21
Cluster 4	<u>5.23</u>	<u>1.00</u>	<u>0.18</u>	<u>0.16</u>	0.36	<u>0.50</u>	0.28
Cluster 5	4.23	0.88	0.04	0.07	<u>0.45</u>	0.47	<u>0.04</u>
Cluster 9	3.67	0.63	0.04	0.02	0.15	0.33	0.54
Cluster 7	3.66	0.56	0.03	0.04	0.25	0.29	<u>0.13</u>
Cluster 3	3.33	0.66	0.12	0.07	0.30	0.36	<u>0.18</u>
Cluster 2	2.41	0.40	0.03	0.01	0.11	0.23	0.49
Cluster 2	<u>1.77</u>	<u>0.18</u>	<u>0.17</u>	0.10	0.02	0.10	<u>0.77</u>



Subcluster 1

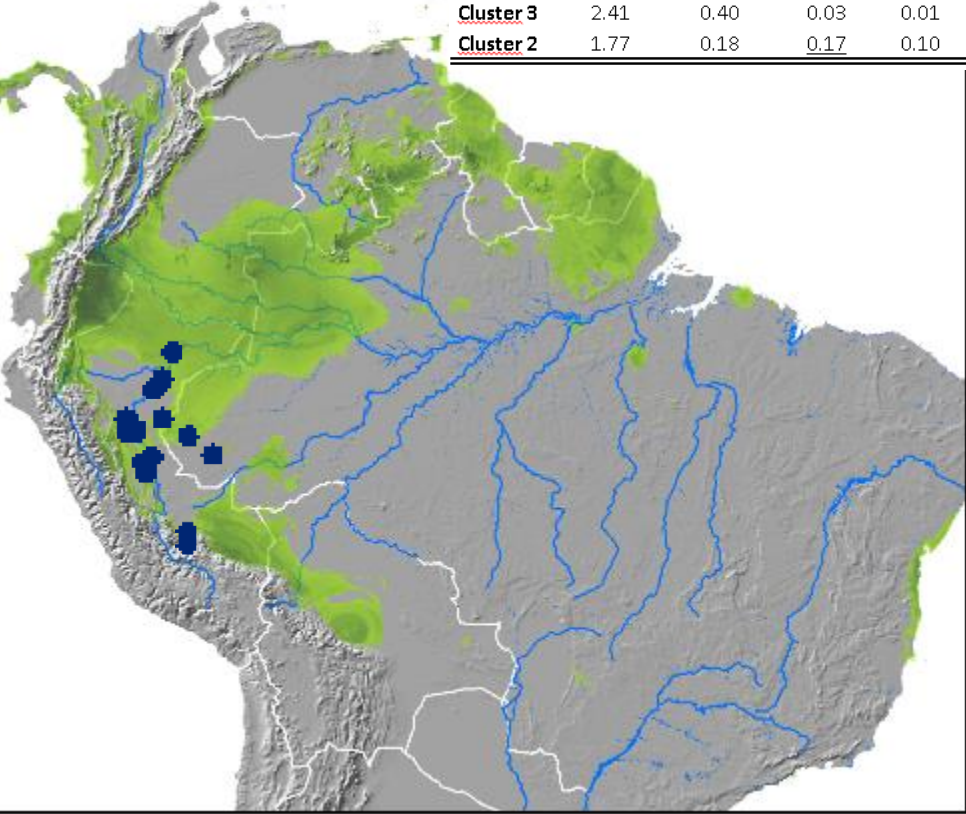
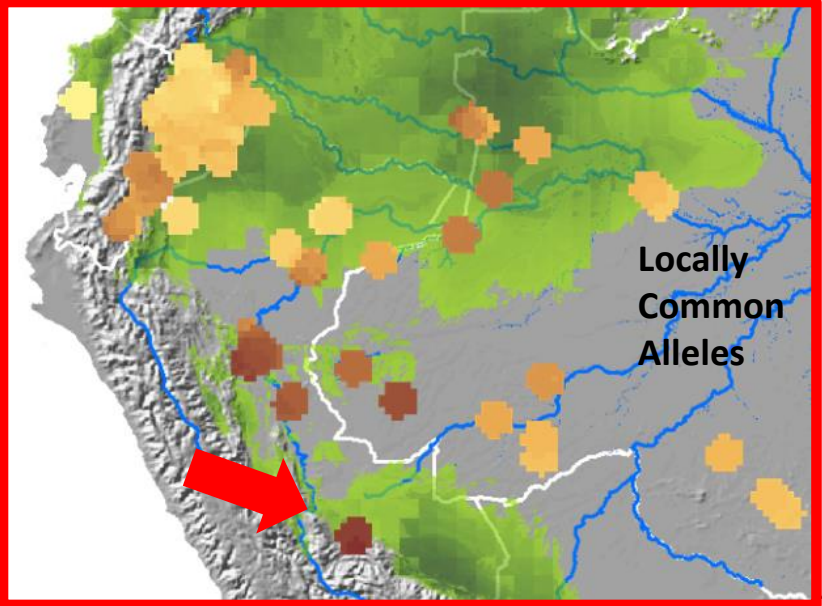
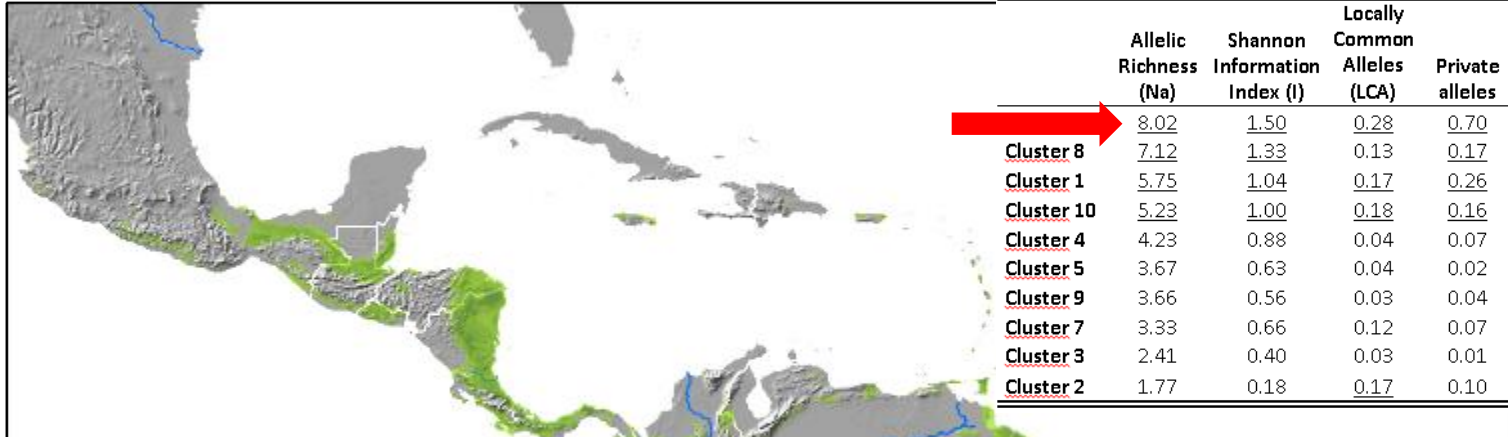


Table 1. Averages of genetic parameters per locus for clusters 1 to 10, based on 1,000 bootstrap samples of 35 trees (i.e. the size of the smallest cluster). Four highest values for each of the parameter are underlined. For the fixation index the four lowest values are underlined

	Allelic Richness (Na)	Shannon Information Index (I)	Locally Common Alleles (LCA)	Private alleles	Ho	He	Fixation index (F)
Cluster 8	<u>8.02</u>	<u>1.50</u>	0.28	0.70	<u>0.40</u>	<u>0.68</u>	0.41
Cluster 1	<u>7.12</u>	<u>1.33</u>	0.13	<u>0.17</u>	<u>0.55</u>	<u>0.63</u>	<u>0.12</u>
Cluster 10	<u>5.75</u>	<u>1.04</u>	<u>0.17</u>	<u>0.26</u>	0.40	<u>0.51</u>	0.21
Cluster 4	<u>5.23</u>	<u>1.00</u>	<u>0.18</u>	<u>0.16</u>	0.36	<u>0.50</u>	0.28
Cluster 5	4.23	0.88	0.04	0.07	<u>0.45</u>	0.47	<u>0.04</u>
Cluster 9	3.67	0.63	0.04	0.02	0.15	0.33	0.54
Cluster 7	3.66	0.56	0.03	0.04	0.25	0.29	<u>0.13</u>
Cluster 3	3.33	0.66	0.12	0.07	0.30	0.36	<u>0.18</u>
Cluster 2	2.41	0.40	0.03	0.01	0.11	0.23	0.49
Cluster 2	<u>1.77</u>	<u>0.18</u>	<u>0.17</u>	0.10	0.02	0.10	0.77



Subclusters 1+2

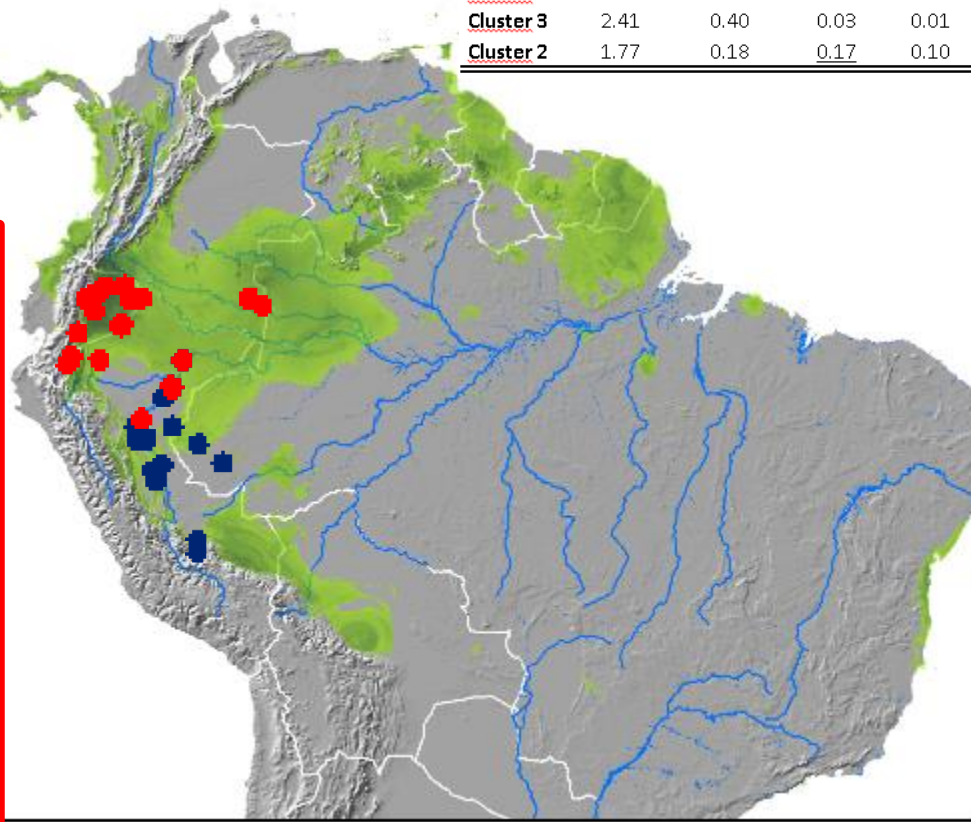
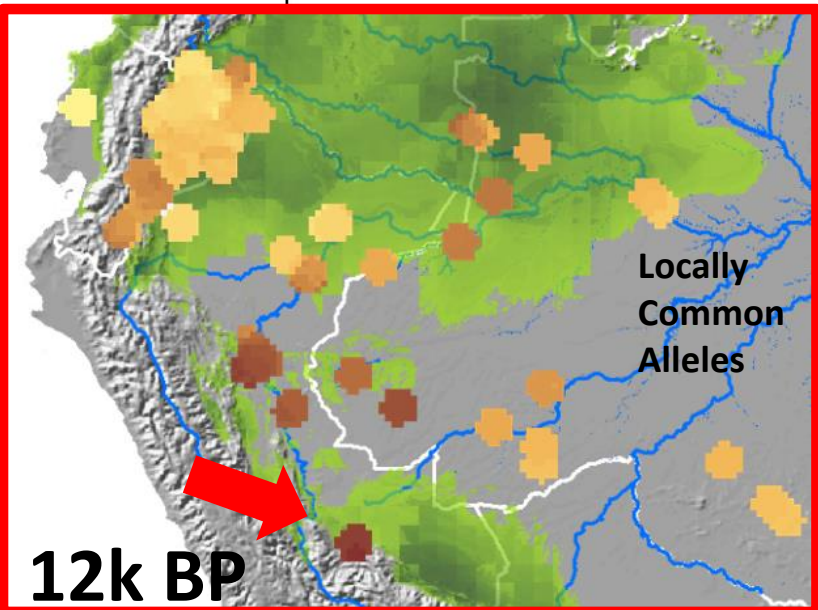
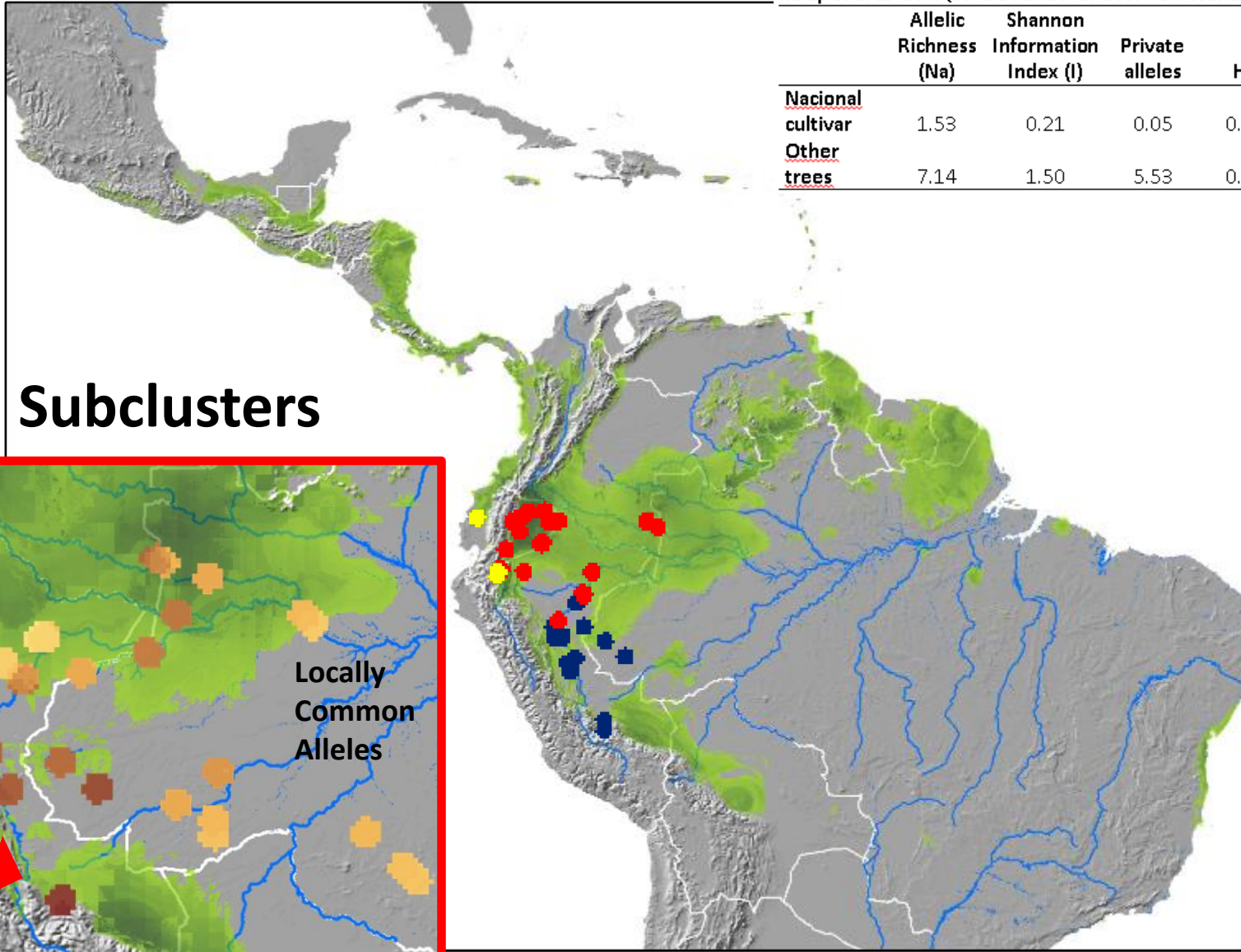


Table 2 Averages of genetic parameters per locus for trees from coastal Ecuador (Nacional cultivar) and the remaining trees from cluster 6, based on 1,000 bootstrap samples of 20 trees (i.e. the number of trees from coastal Ecuador).

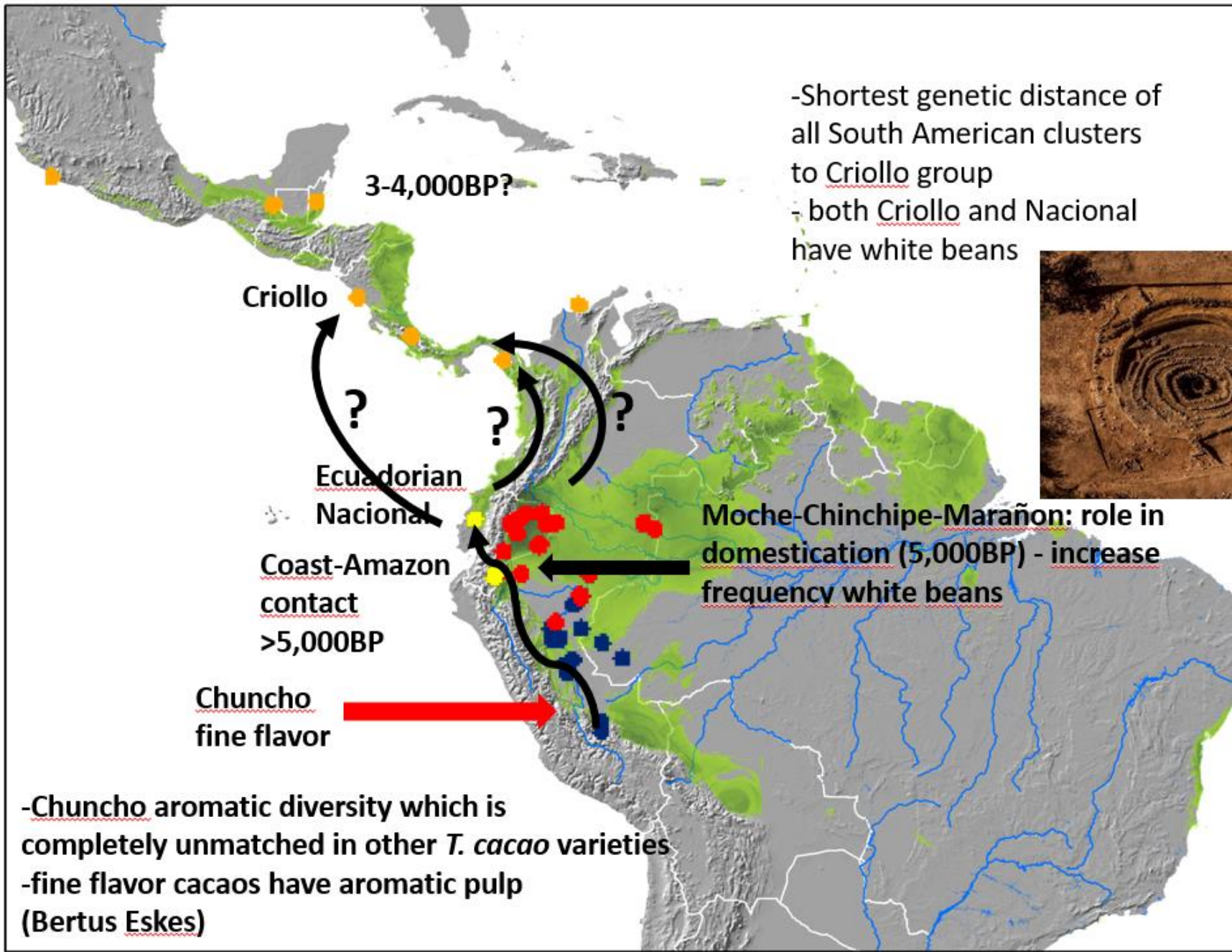
	Allelic Richness (Na)	Shannon Information Index (I)	Private alleles	Ho	He	Fixation index (F)
<u>Nacional cultivar</u>	1.53	0.21	0.05	0.12	0.13	0.08
<u>Other trees</u>	7.14	1.50	5.53	0.44	0.69	0.36



Subclusters

12k BP

Locally
Common
Alleles



- Shortest genetic distance of all South American clusters to Criollo group
- both Criollo and Nacional have white beans

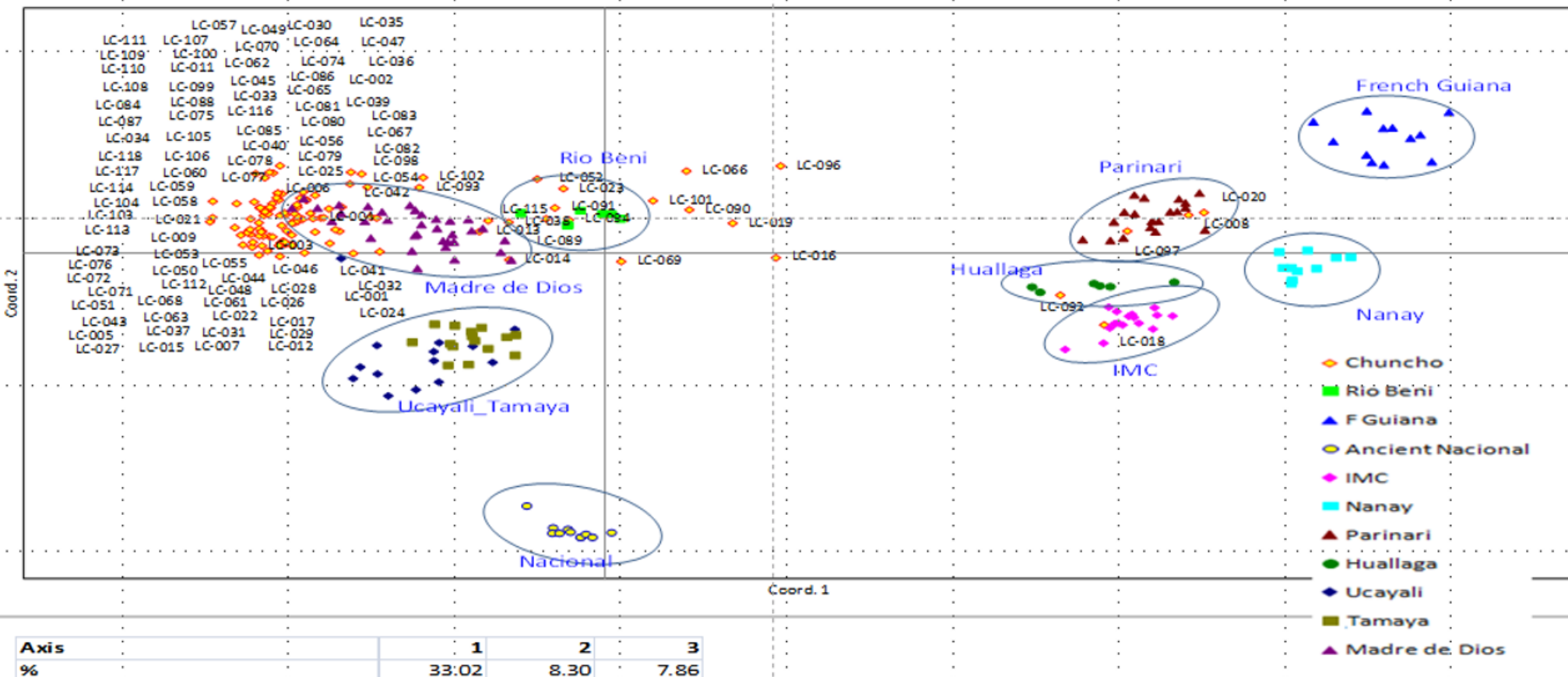


- Chuncho aromatic diversity which is completely unmatched in other *T. cacao* varieties
- fine flavor cacaos have aromatic pulp (Bertus Eskes)

Grupos geneticos datos mas recientes

(Zhang et al unpublished)

Principal Coordinates (PCoA)



-Shortest genetic distance of
all South American clusters
to Criollo group
- both Criollo and Nacional
have white beans

3-4,000BP?

Criollo

Ecuadorian
Nacional

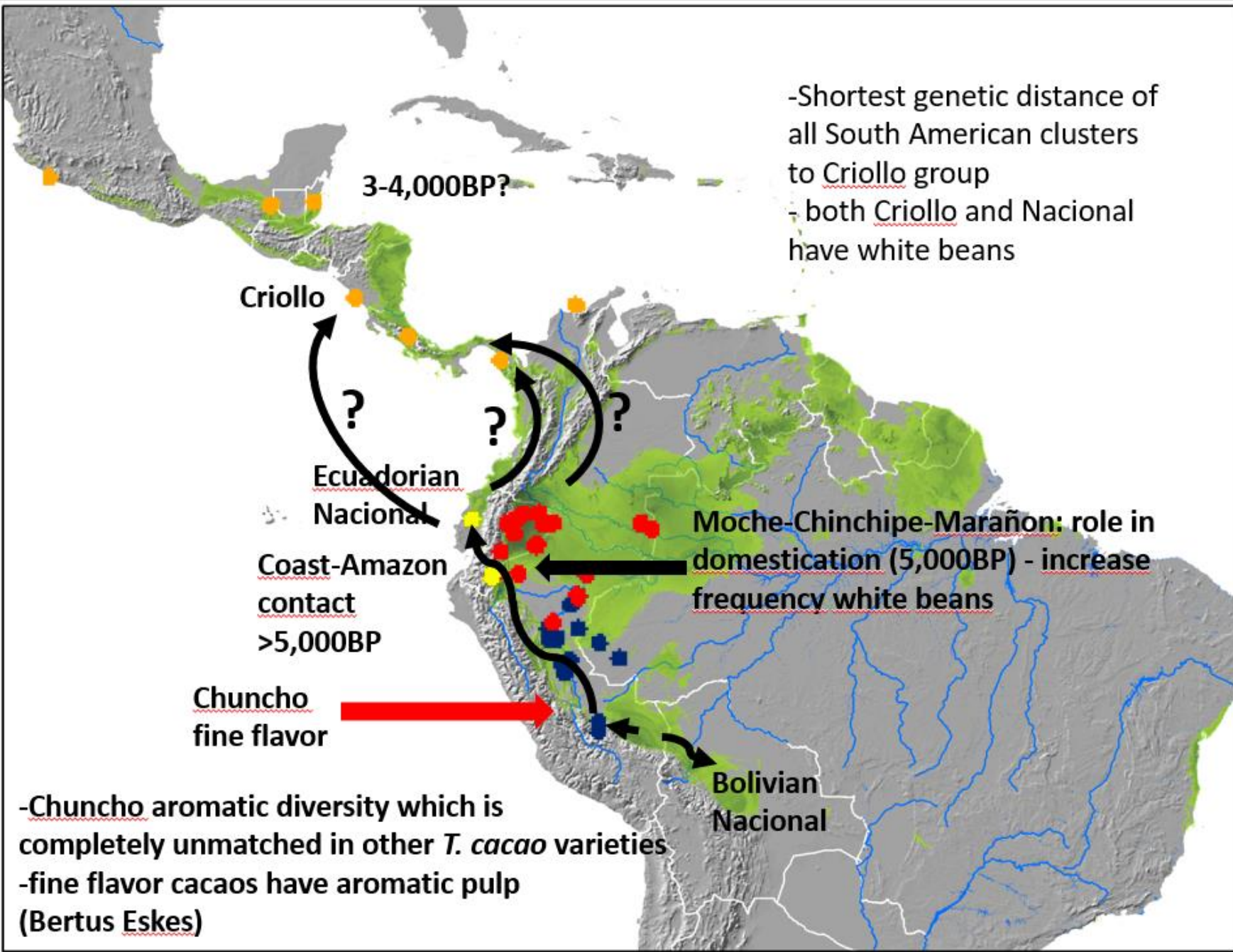
Coast-Amazon
contact
>5,000BP

Chuncho
fine flavor

Moche-Chinchi-Marañon: role in
domestication (5,000BP) - increase
frequency white beans

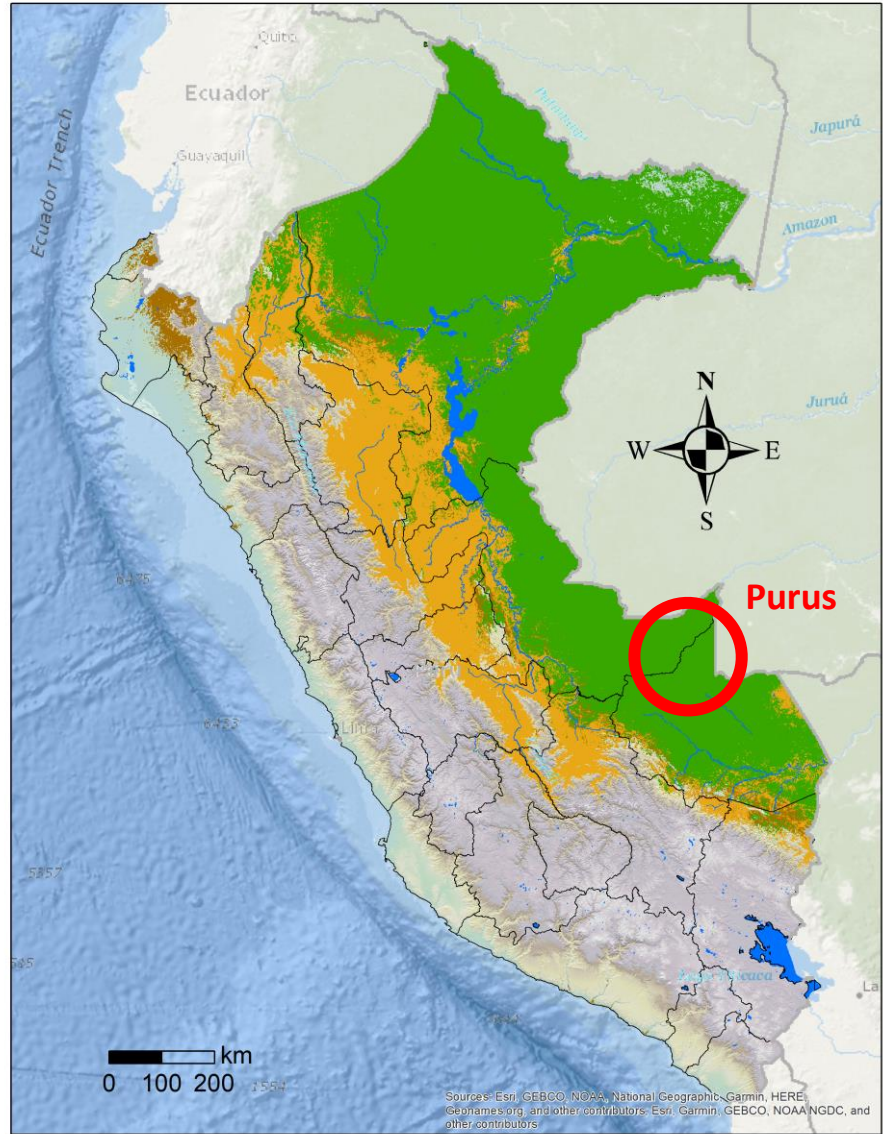
Bolivian
Nacional

-Chuncho aromatic diversity which is
completely unmatched in other *T. cacao* varieties
-fine flavor cacaos have aromatic pulp
(Bertus Eskes)



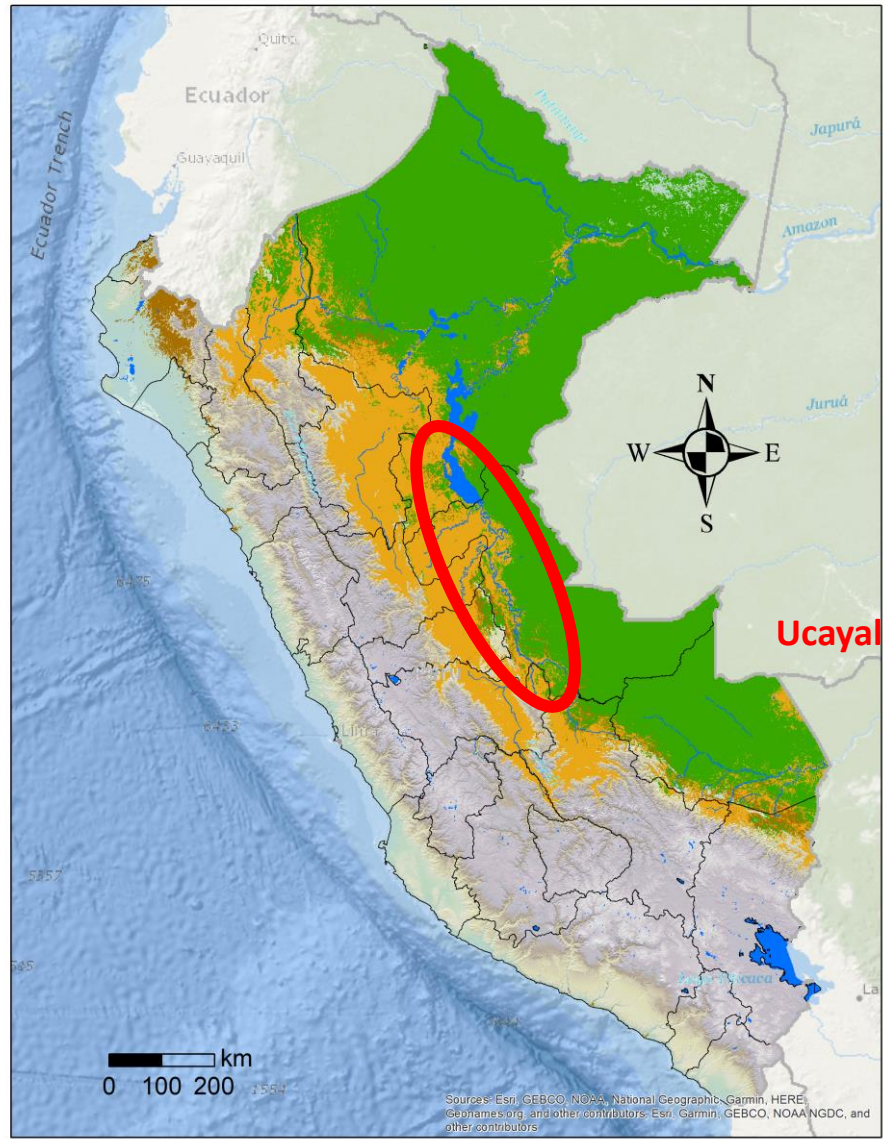
**Entonces que variedades de cacao tenemos en el
Peru?**







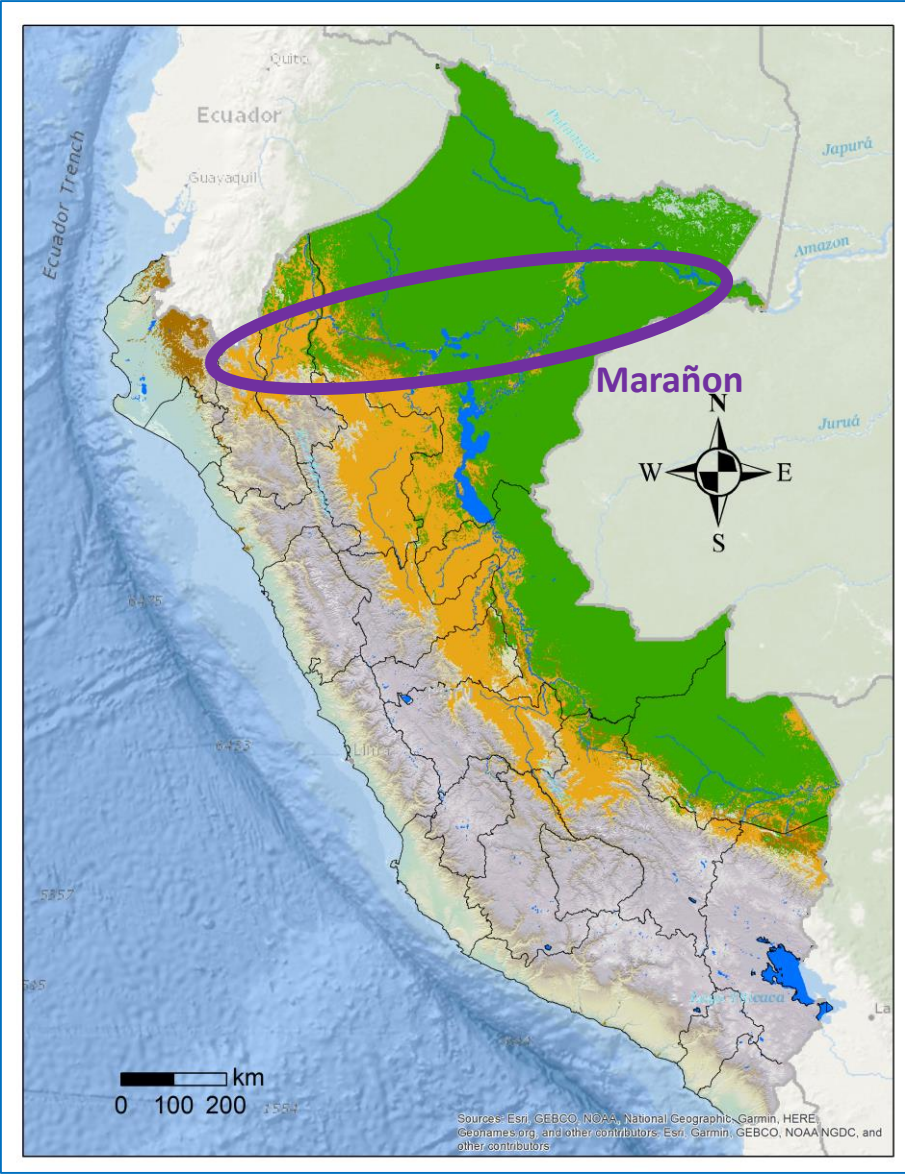


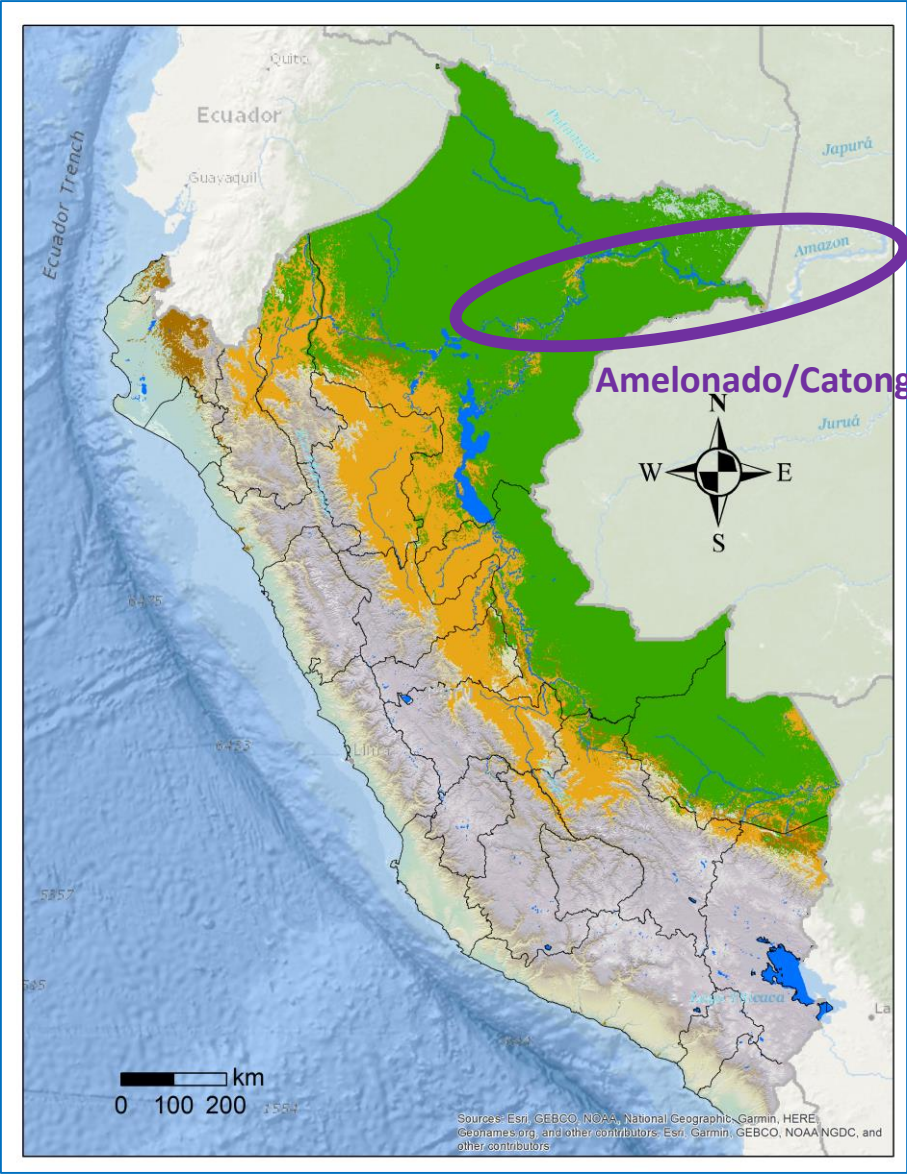


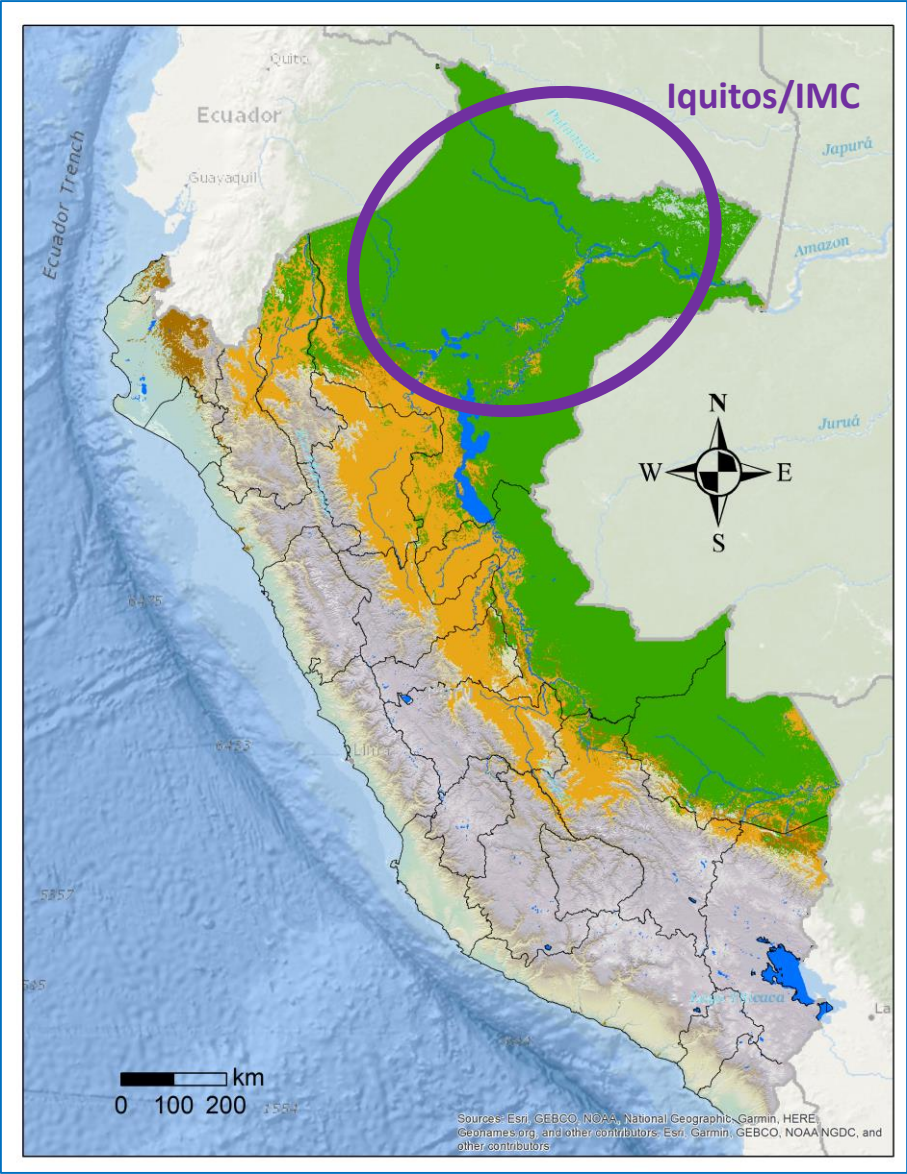
Ucayali (Contamana)

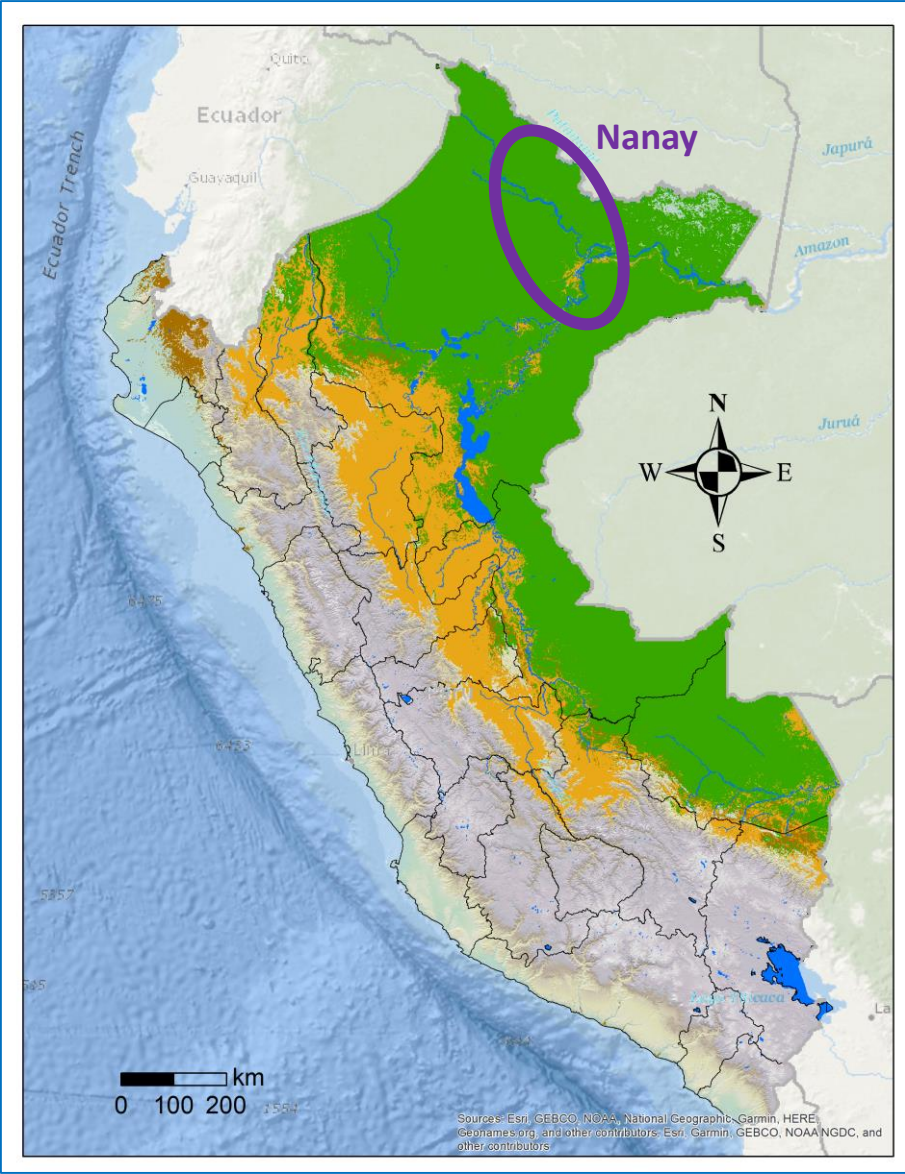
**Nacional de Ecuador
Blanco de Piura
Fortunato? etc**

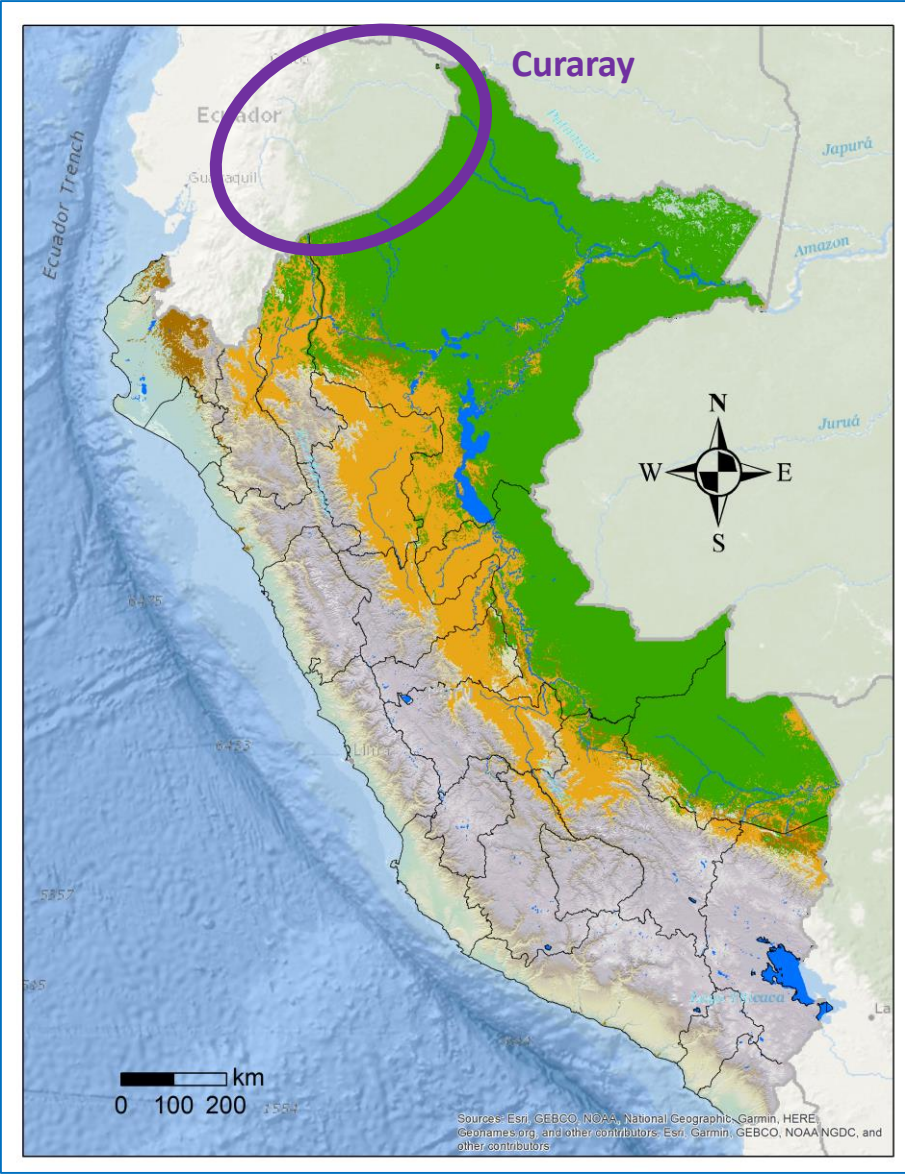






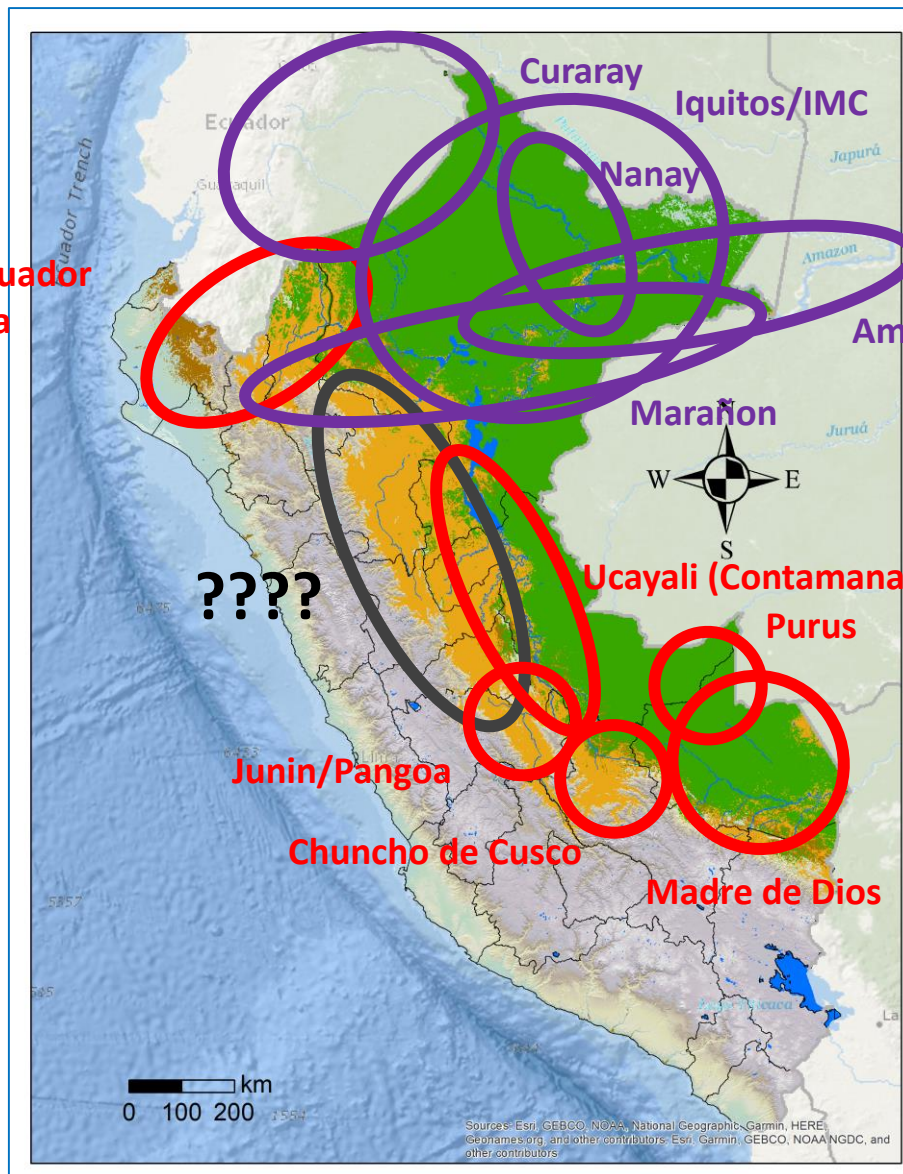








Nacional de Ecuador
Blanco de Piura
Fortunato? etc



Amelonado/Catongo

???

Ucayali (Contamana)

Purus

Junin/Pangoa

Chuncho de Cusco

Madre de Dios

0 100 200 km

Sources: Esri, GEBCO, NOAA, National Geographic, Garmin, HERE, OpenStreetMap contributors, Swatch, Mapbox, and other contributors. Esri, Garmin, GEBCO, NOAA NGDC, and other contributors.



FORMULARIO

ZONAS ECOGEOGRAFICAS

Dónde se ubica tu finca?

Perú Ecuador Nicaragua Honduras El Salvador Guatemala

Por favor, seleccione la ubicación de su finca/plantación haciendo zoom en el mapa y haciendo clic en el área de interés. Si lo prefiere, puede ingresar directamente las coordenadas (en grados decimales) en los espacios a continuación.

Latitud

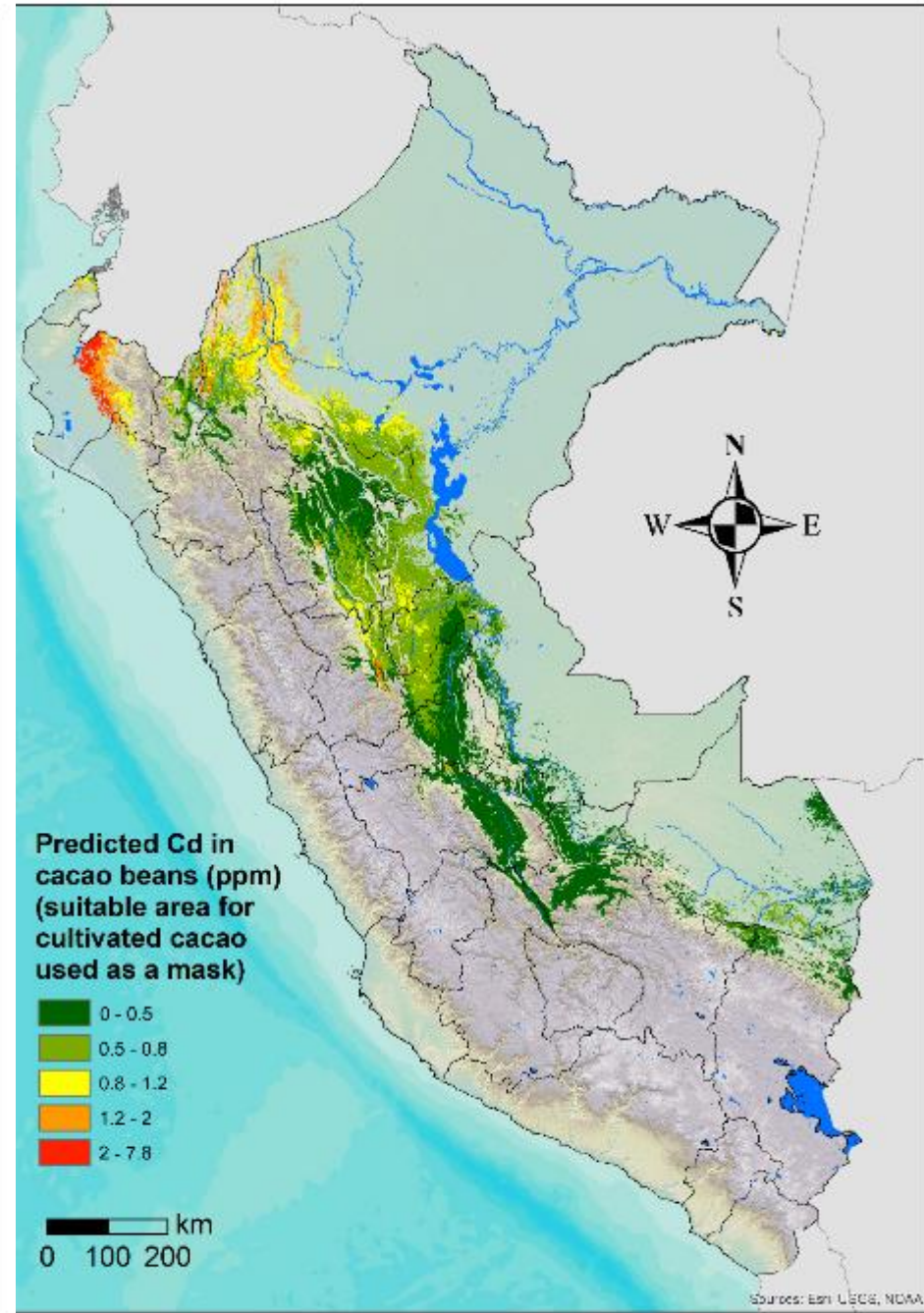
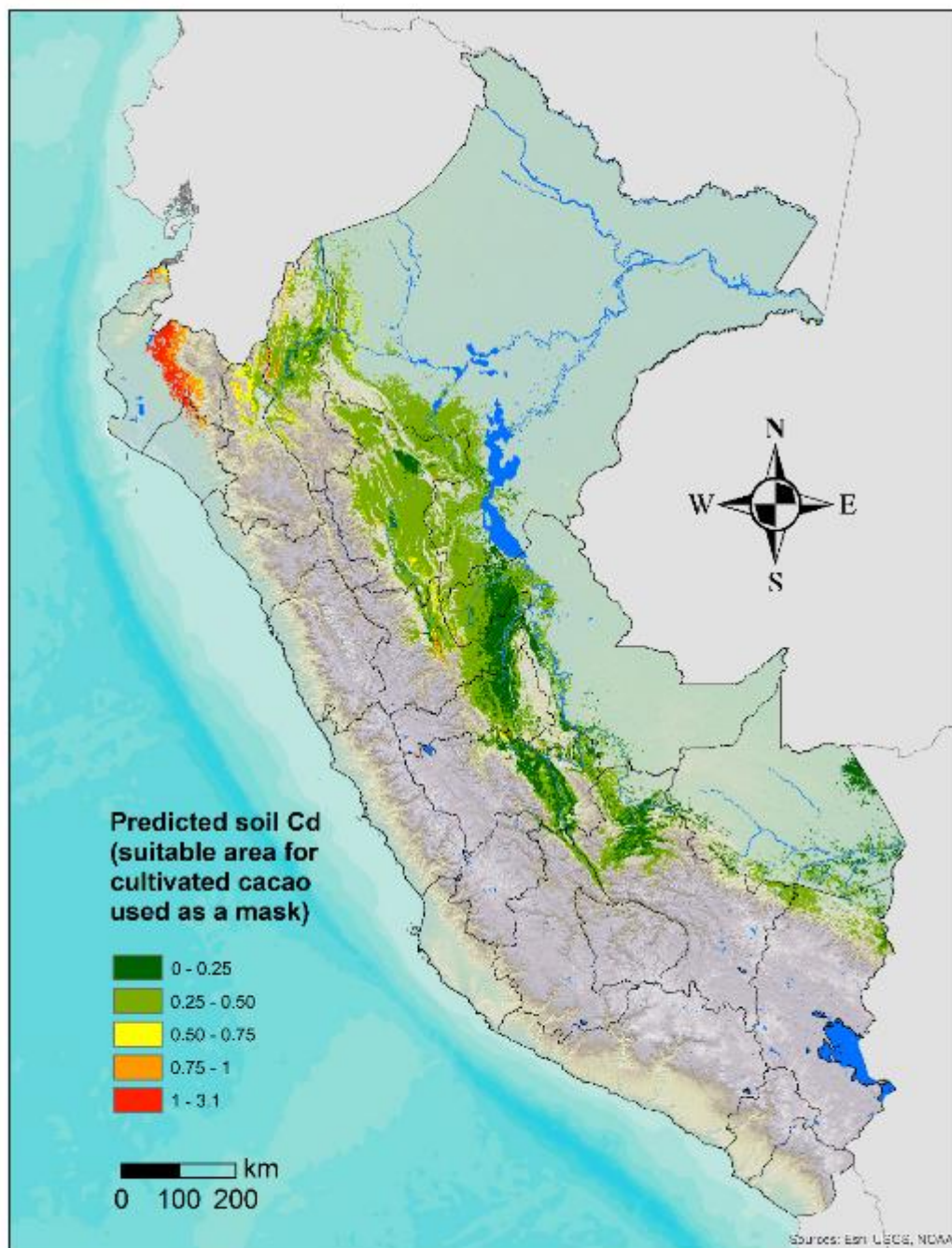
Longitud

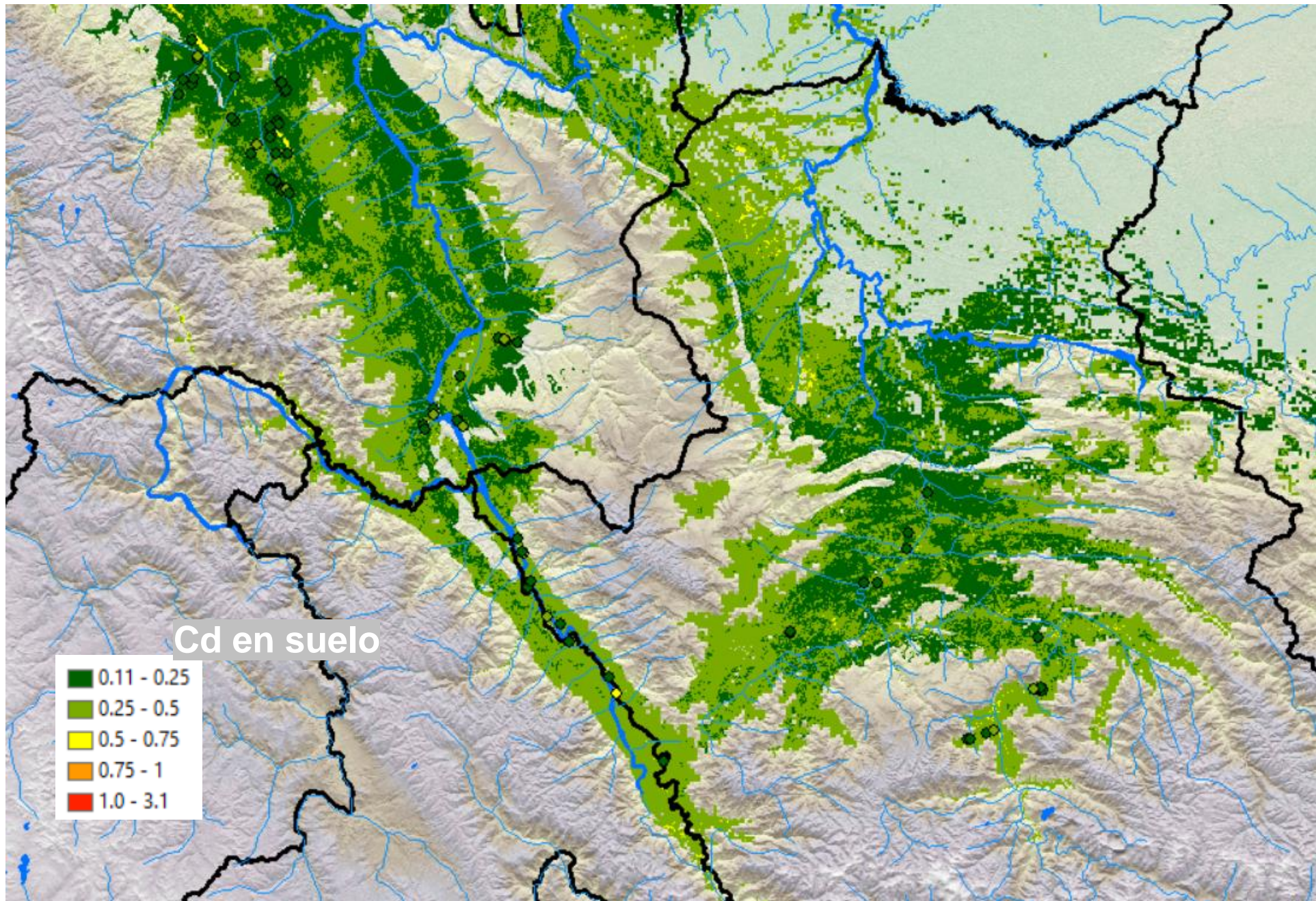
Siguiente

Quiere obtener información sobre el contenido de cadmio en el suelo y los granos de cacao en tu finca?

Quiere obtener información sobre el impacto previsto del cambio climático en tu finca?

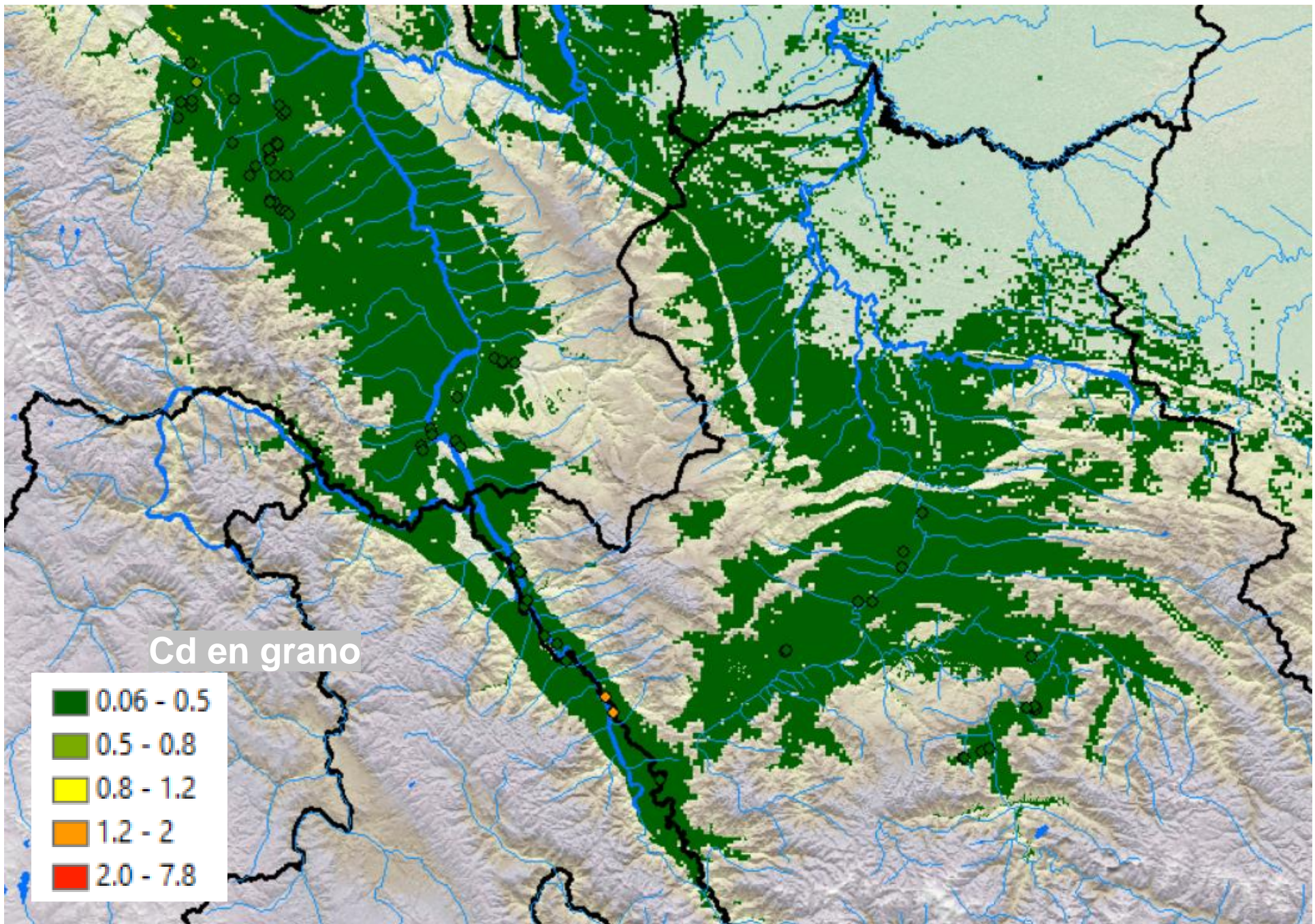
Cadmio en cacao





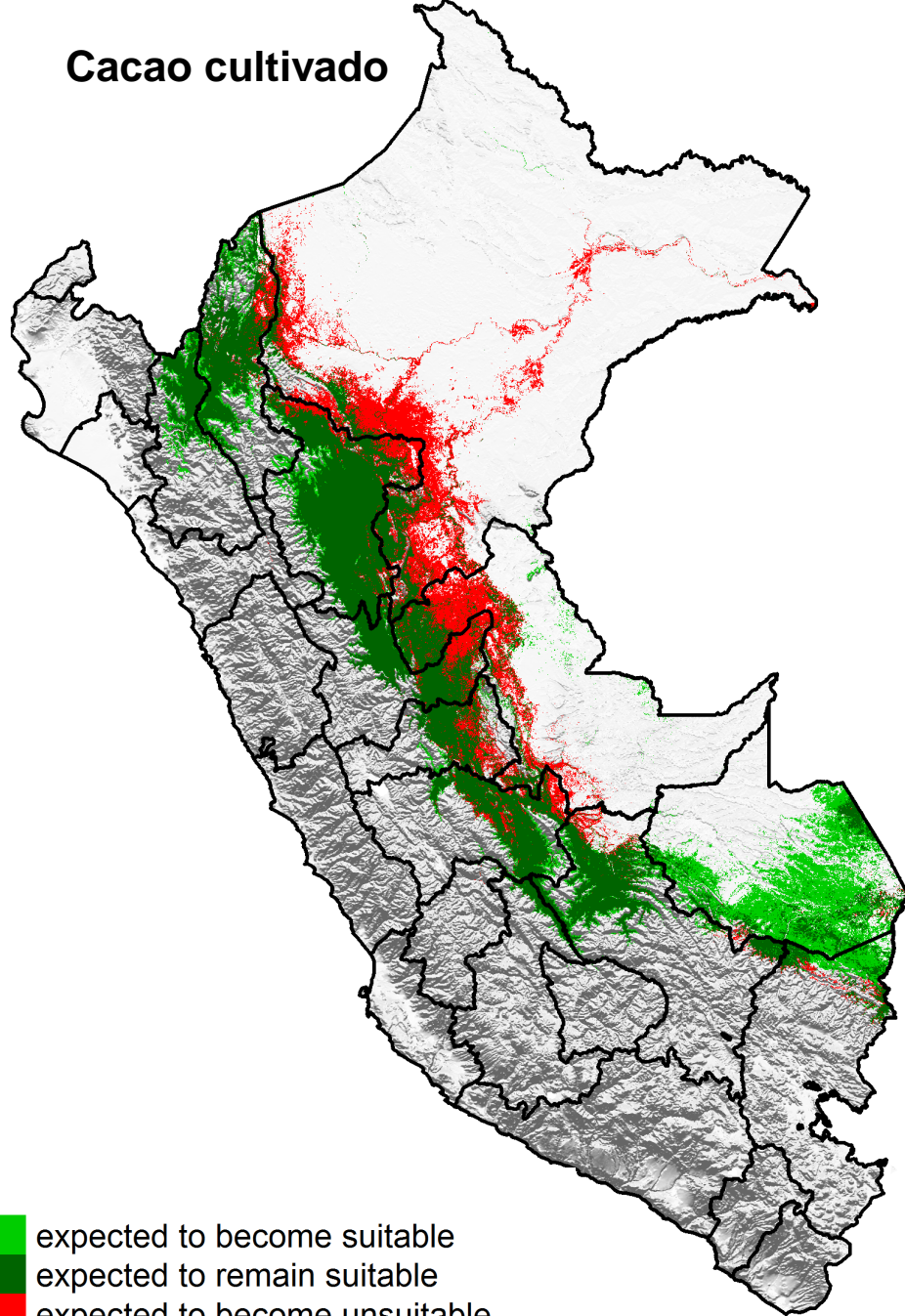
Cd en suelo

■	0.11 - 0.25
■	0.25 - 0.5
■	0.5 - 0.75
■	0.75 - 1
■	1.0 - 3.1

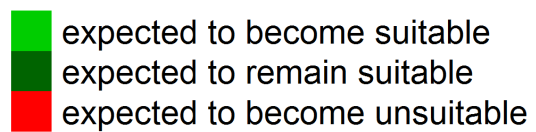
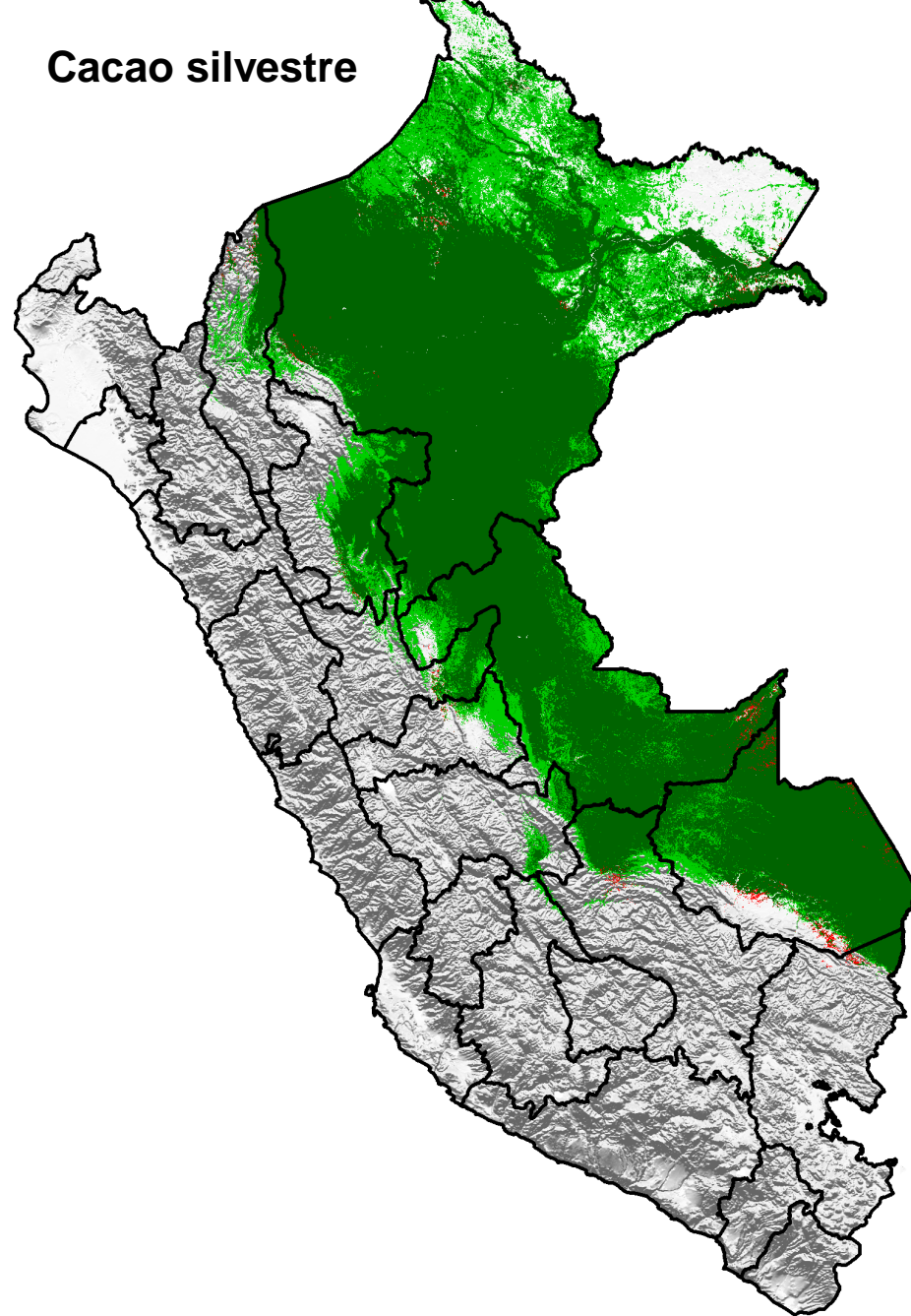


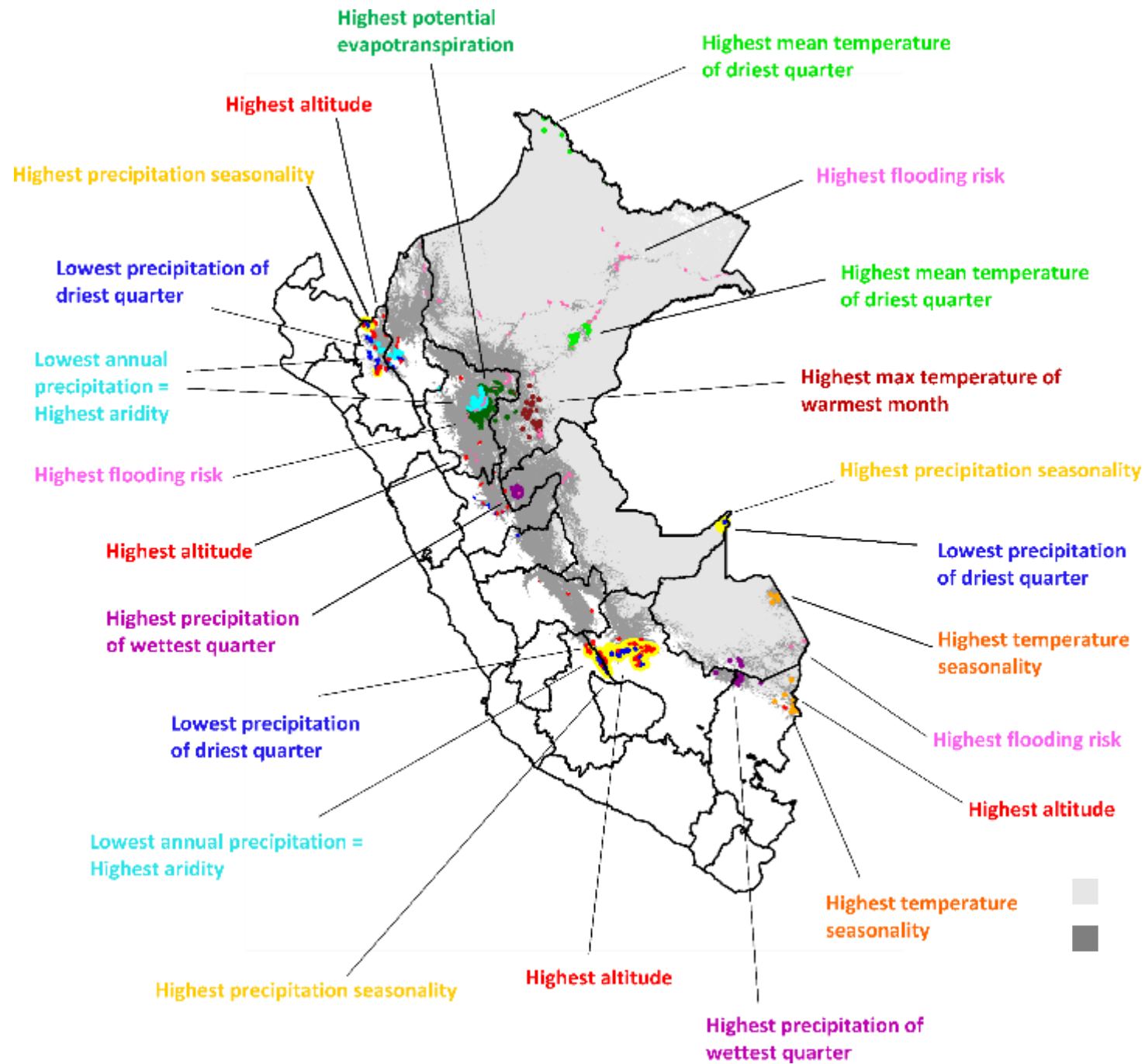
cambio climático

Cacao cultivado



Cacao silvestre









FORMULARIO

ZONAS ECOGEOGRÁFICAS

Dónde se ubica tu finca?

[Perú](#) [Ecuador](#) [Nicaragua](#) [Honduras](#) [El Salvador](#) [Guatemala](#)

Por favor, seleccione la ubicación de su finca/plantación haciendo zoom en el mapa y haciendo clic en el área de interés. Si lo prefiere, puede ingresar directamente las coordenadas (en grados decimales) en los espacios a continuación.

Latitud

Longitud

[Siguiente](#)

Quiere obtener información sobre el contenido de cadmio en el suelo y los granos de cacao en tu finca?

Quiere obtener información sobre el impacto previsto del cambio climático en tu finca?

e.thomas@cgiar.org