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Paternal haplogroups in European and African domestic goats

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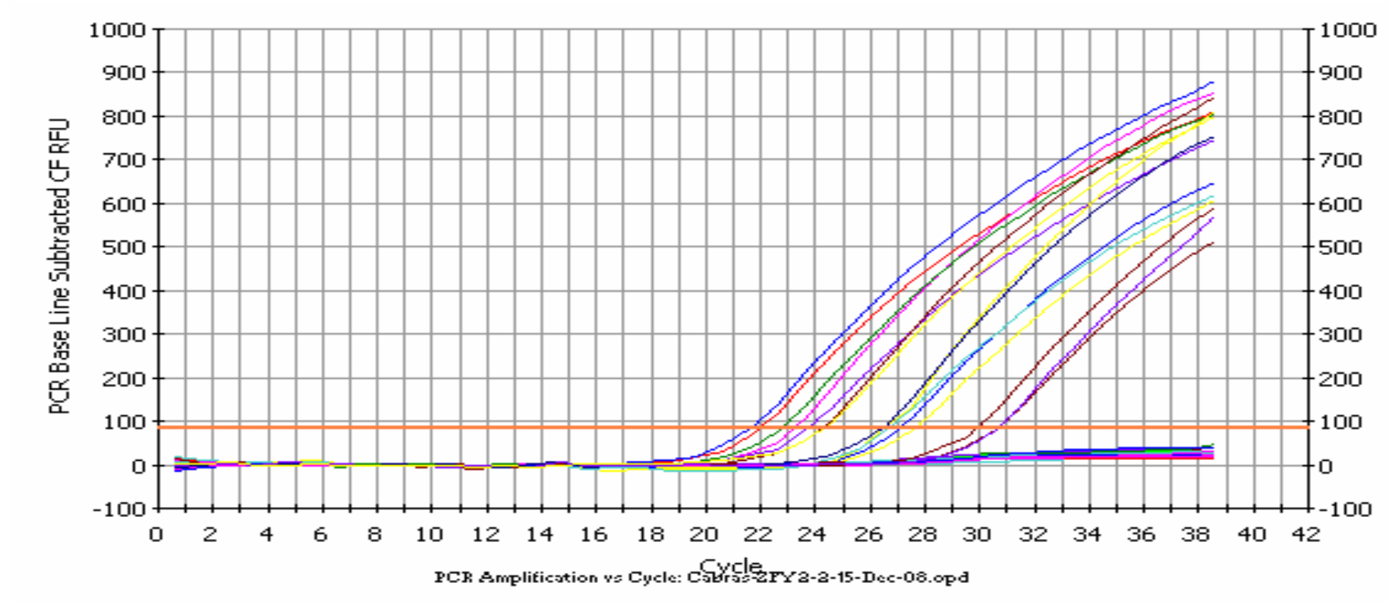
Population genetic studies on goats are mainly based on mitochondrial DNA sequencing, thus only describing the female legacies. So far, using Y-chromosome specific SNPs, two common (C1 and C2) and one rare (C3, just found in one sample) Y-chromosome haplogroups have been described in domestic goats. Apparently, there is no geographic structure in the distribution of the two common haplogroups (Pidancier et al., 2006). In this preliminary work we have developed a dual fluorescent multiprobe assay for the genotyping of 3 SNPs located in two genes (AmelY and ZFY), which are able to differentiate among the 3 domestic haplogroups.

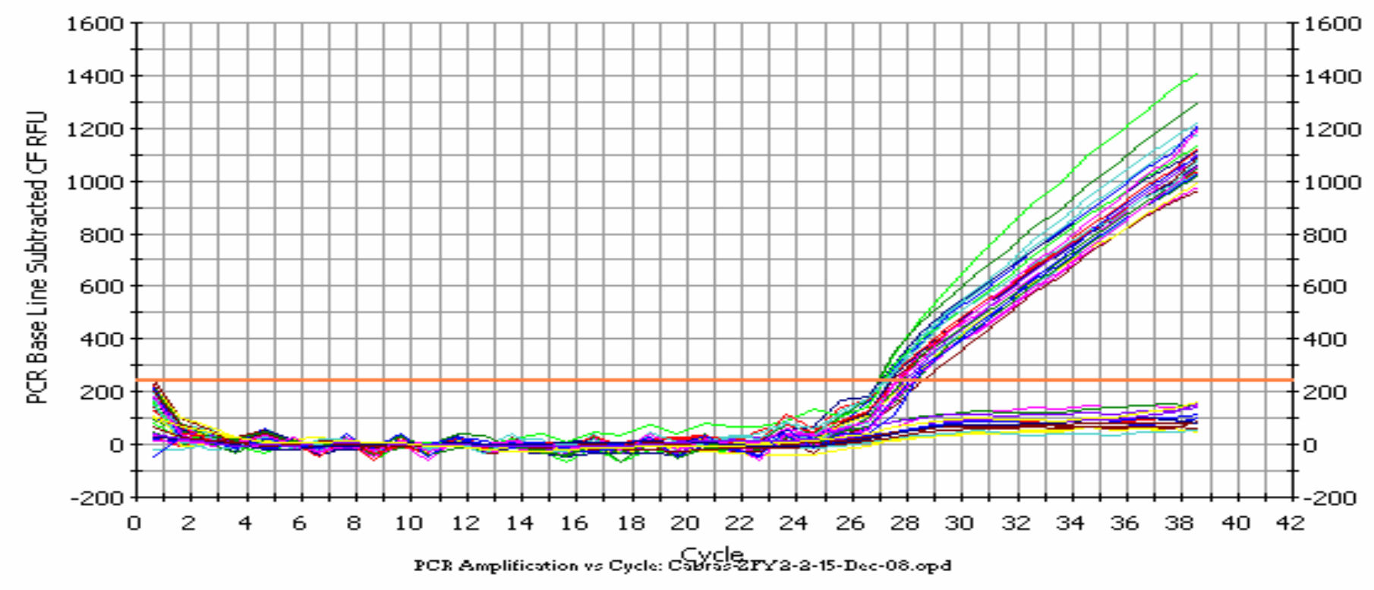
A total of 257 bucks belonging to 18 different populations (12 in Europe and 6 in Africa) were genotyped and assigned to Y-haplogroups. No C3 samples were identified. Although the two major haplogroups (C1 and C2) were found in both continents, their distribution seems to show some geographic structure. C2 haplogroup is the only one found in Central Europe, with very low frequency in the Iberian Peninsula (4.7%) as well as in Sub-Saharan Africa (3.4%). C1 is the most frequent haplogroup in Sub-Saharan Africa (0.966) and Iberia (0.953), and is absent in central Europe. Mediterranean Africa goat could have an intermediate situation (C1: 0.27, C2: 0.73). The use of Y-specific microsatellites and a sampling over the world, will allow us to ascertain the paternal phylogeography of the species.

Dual fluorescent multiprobe RT-PCR assay designed to diagnose the Y-specific SNPs identified by Pidamar et al. (2006, Mol. Phyp. Evol.)

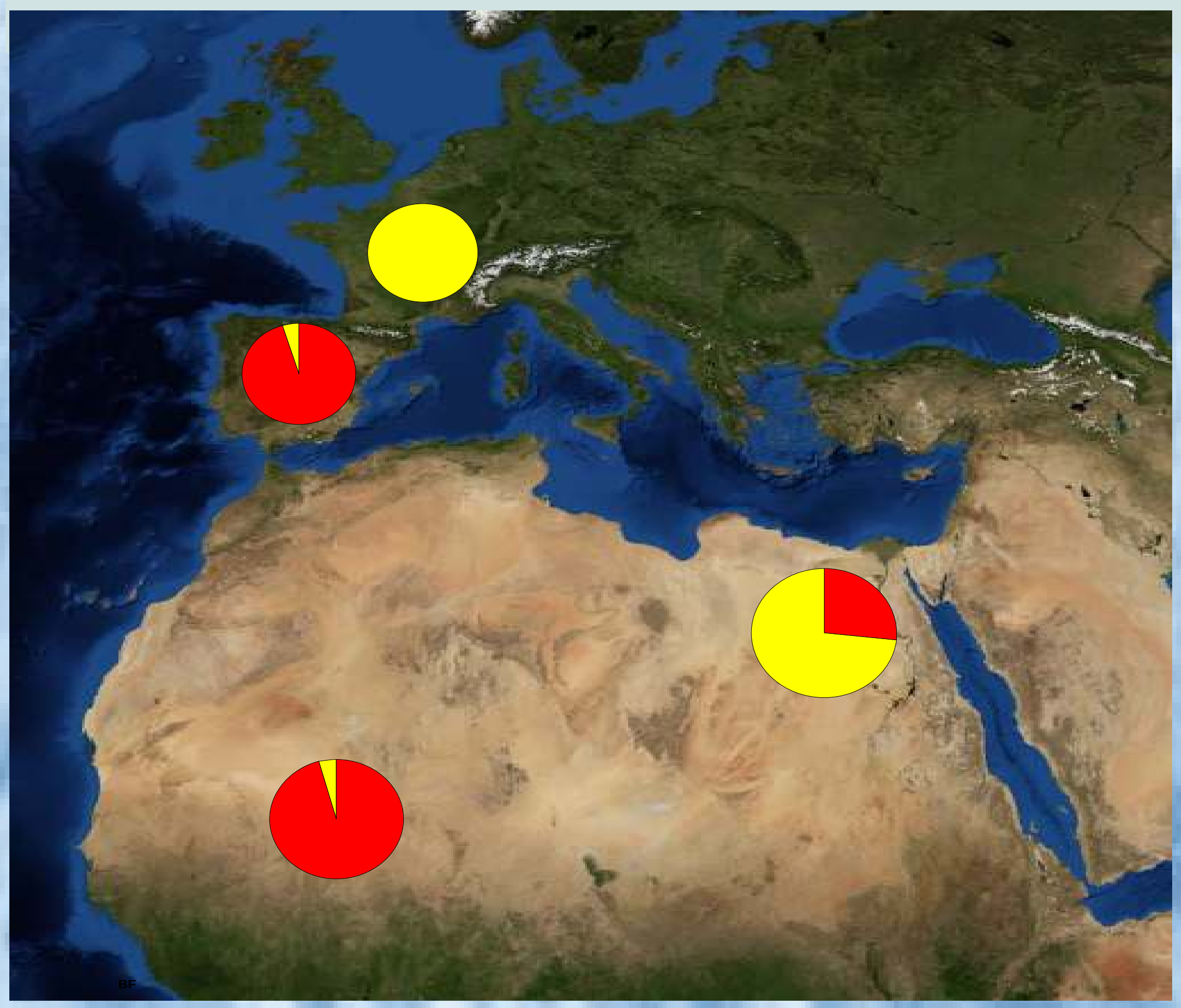
Alelle ZFY-2G
CTAAGCAAGTGTGGCTTTCAA



Alelle ZFY-2A
CTAAGCAAGTATGGCTTTCAA



Geographic map showing the frecuency of the haplogroups C1 (in red) and C2 (in yellow)



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