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Human and conifer demographic expansions from linked microsatellites

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We extended the method for demographic inference based on the distribution of pairwise differences (i.e. mismatch distribution) between individuals of a sample (Schneider & Excoffier, 1999) to linked microsatellites by assuming the stepwise mutation model. The proposed method allows for the estimation of initial and final population sizes and time of expansion by a maximum pseudolikelihood approach. Confidence intervals have been estimated by parametric bootstrap.

The interest on linked microsatellites comes from their application in chloroplast and mammal Y-chromosome genetic evolutionary studies. The application of the method is illustrated with microsatellite data of the chloroplast genome from the Canary Island pine (*Pinus canariensis*) and of the human Y-chromosome. In both cases the distribution of the pairwise differences are unimodal, as expected under a demographic expansion (Figures 2 and 3).

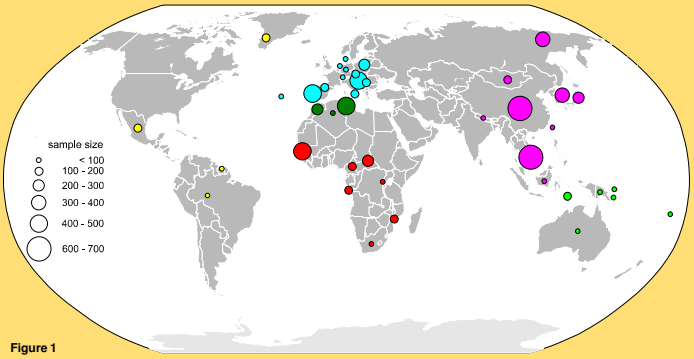
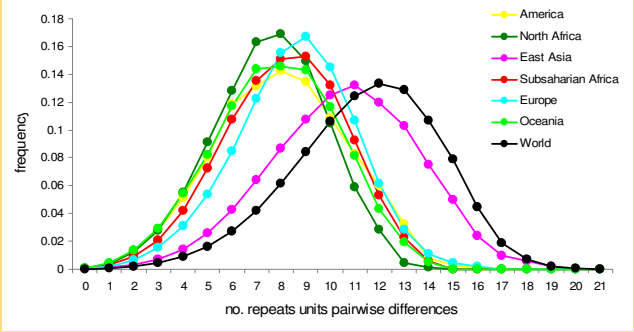


Figure 1

Figure 2



Human Y-chromosome population data for five microsatellite loci (DYS19, DYS390, DYS391, DYS392 and DYS393) have been obtained from published works. For the estimates of the time of expansion ($\hat{\tau}$) populations have been grouped according the geographical areas identified by Li *et al.*, 2008 (Figure 1). Estimates for expansion time (Table 1) are comparable with estimates from other studies using Bayesian statistics: 18000 (7000-41000) years in Pritchard *et al.*, 1999; 7400 (4300-14000) years in Wilson *et al.*, 2003. The differences among regions cannot be considered significant as their confidence intervals largely overlap.

Table 1

Group	# individuals	# populations	$\hat{\tau}$ (95%CI)	$\hat{t}$ years (95%CI)[b]
Sub-Saharan-Africa	1183	23	12.53 (1.29-26.18)	17612 (2672-36811)
N-Africa	694	13	13.69 (0.10-24.51)	19247 (441-34463)
Europe	2150	14	9.40 (5.00-12.81)	13213 (7030-18012)
East-Asia	2621	16	11.51 (8.18-15.75)	16182 (11502-22146)
Oceania	293	7	12.04 (6.76-17.45)	16924 (9505-23552)
America	422	8	8.70 (5.10-15.42)	12231 (7171-21682)
World[a]	9182	94	12.85 (9.25-14.41)	18061 (13006-20262)

[a] Includes samples not classified in previous groups
[b] mutation rate per generation over the five loci, $\mu = 0.89 \times 10^{-2}$ (www.ystr.org); generation time: 25 years

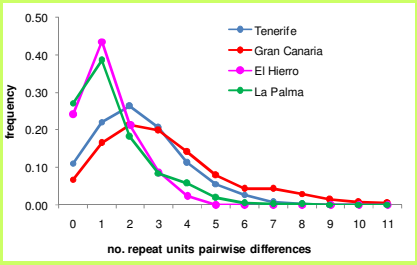


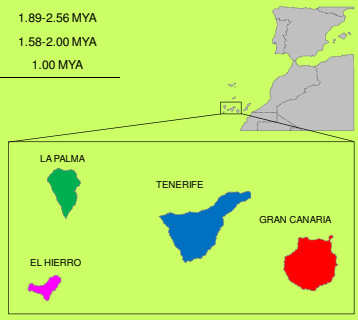
Figure 3

Table 2

Island	# individuals	$\hat{\tau}$ (90%CI)	$\hat{t}$ MYA (90%CI)[a]	geological age	weevil colonization[c]
Gran Canaria	145	1.98 (1.22-2.30)	1.65 (1.02-1.92)	5.5-3 MYA[b]	>2.56 MYA
Tenerife	280	3.11 (1.69-7.14)	2.60 (1.41-5.95)	3.5-0.2 MYA[b]	1.89-2.56 MYA
La Palma	48	0.49 (0.14-0.99)	0.41 (0.11-0.83)	2 MYA	1.58-2.00 MYA
El Hierro	24	1.61 (0.60-2.55)	1.34 (0.50-2.13)	1 MYA	1.00 MYA

[a] mutation rate per year and locus, $\mu = 10^{-5}$ (Provan *et al.*, 2000)
[b] Juan *et al.*, 2000
[c] Emerson *et al.*, 2000

Figure 4



Canary Island pine populations (Figure 4) have been analysed with six microsatellite loci (Pt15169, Pt30204, Pt71936, Pt87268, Pt26081 and Pt36480). Expansion time estimates (Table 2) are consistent with the geological history of the archipelago and have the same order of magnitude than the estimated colonization time of *Brachyderes rugatus* (specific parasite weevil of the Canary Island pine).

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