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# Human and conifer demographic expansions from linked microsatellites



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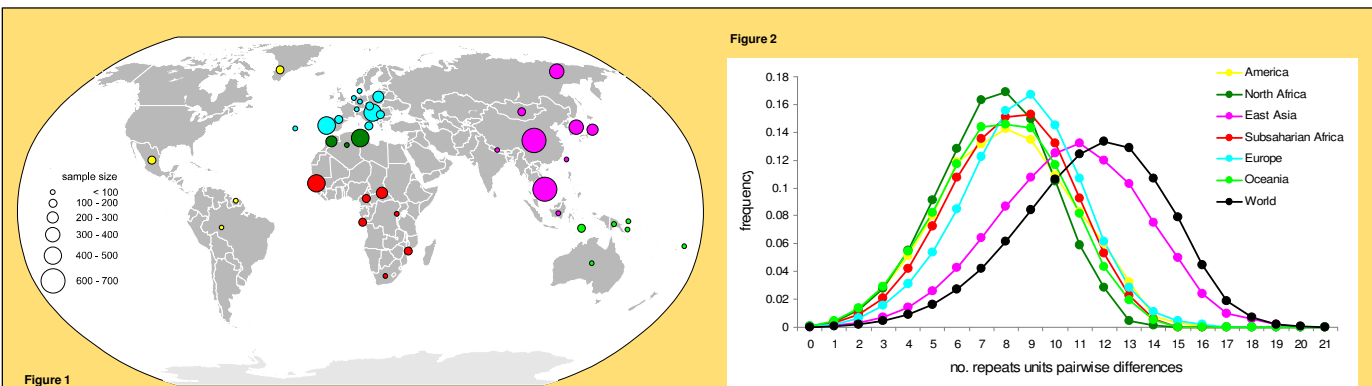


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We extended the method for demographic inference based on the distribution of pairwise differences (i.e. mismatch distribution) between individuals of a sample (Schneider & Excoffier, 1999) to linked microsatellites by assuming the stepwise mutation 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).

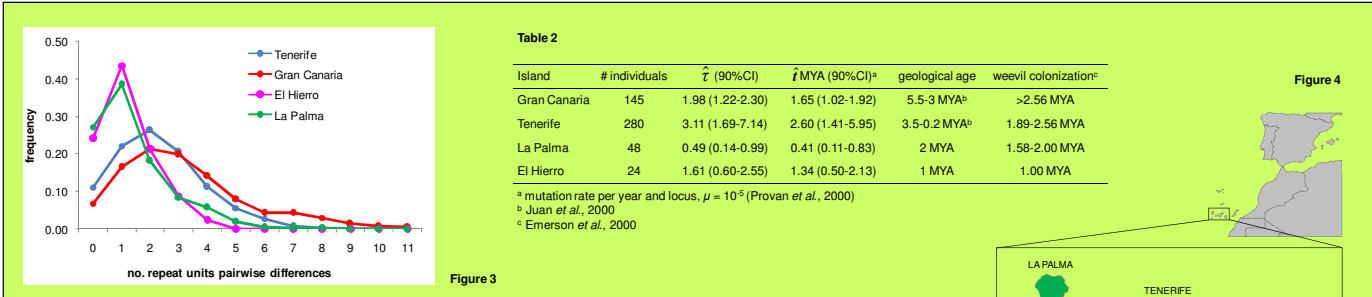


**Human Y-chromosome population data** for five microsatellite loci (DYS19, DYS390, DYS391, DYS392 and DYS393) have been obtained from published works. For the estimates of the time of expansion ( $\hat{t}$ ) populations have been grouped according to the geographical areas identified by Li *et al.*, 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	$\hat{t}$ (95%CI)	$\hat{t}$ years (95%CI) <sup>a</sup>
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 <sup>b</sup>	9182	94	12.85 (9.25-14.41)	18061 (13006-20262)

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



**Table 2**

Island	# individuals	$\hat{t}$ (90%CI)	$\hat{t}$ MYA (90%CI) <sup>a</sup>	geological age	weevil colonization <sup>b</sup>
Gran Canaria	145	1.98 (1.22-2.30)	1.65 (1.02-1.92)	5.5-3 MYA <sup>b</sup>	>2.56 MYA
Tenerife	280	3.11 (1.69-7.14)	2.60 (1.41-5.95)	3.5-0.2 MYA <sup>b</sup>	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

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

**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).

REFERENCES

Schneider & Excoffier 1999. *Genetics* 152: 1079-1089; Li et al. 2008. *Science* 319: 1100-1104; Pritchard et al. 1999. *Mol. Biol. Evol.* 16(12): 1791-1798; Wilson et al. 2003. *J. R. Statist. Soc. A.* 166: 155-201; Provan et al. 1999. *Genetics* 153: 943-947; Juan et al. 2000. *TREE* 15: 104-109; Emerson et al. 2000. *Evolution* 54: 911-923.

Alves et al. 2005. *Forensic Sci. Int.* 156(2): 136-133  
 Anwar et al. 2007. *Forensic Sci. Int.* 170(2): 290-295  
 Ayala et al. 2006. *Forensic Sci. Int.* 164(2): 249-253  
 Barak et al. 2003. *Forensic Sci. Int.* 138(1): 127-133  
 Bennett et al. 2007. *Forensic Sci. Int.* 164(2): 414-412  
 Berger et al. 2005. *Forensic Sci. Int.* 150(2): 208-222  
 Bennett et al. 2005. *Int. J. Legal Med.* 119(1): 36-50  
 Bennett et al. 2007. *Forensic Sci. Int.* 164(2): 414-412  
 Blanch-Casadevall et al. 2003. *Forensic Sci. Int.* 138(2): 247-250  
 Bennett et al. 2003. *Hum. Sci.* 33(2): 208-222  
 Carrasco et al. 2003. *Forensic Sci. Int.* 134(1): 29-35  
 Caputo et al. 2007. *Forensic Sci. Int.* 167(1): 70-76  
 Chertk et al. 2005. *Forensic Sci. Int.* 152(1): 95-99  
 Cizek et al. 2004. *Am. J. Hum. Genet.* 161(2): 67-67  
 Cizek et al. 2004. *Am. J. Hum. Genet.* 161(2): 67-67  
 Daston-Breit et al. 2004. *Mol. Biol. Evol.* 21(9): 1673-1682

Cizek et al. 2004. *Am. J. Hum. Genet.* 161(2): 67-67  
 Daston-Breit et al. 2004. *Mol. Biol. Evol.* 21(9): 1673-1682  
 Figli et al. 2006. *Forensic Sci. Int.* 164(1): 80-81  
 Foster et al. 1998. *Mol. Biol. Evol.* 15(10): 1100-1114  
 Garcia et al. 2004. *Forensic Sci. Int.* 145(1): 65-68  
 Hu 2006. *Forensic Sci. Int.* 164(2): 385-385  
 Kasper et al. 2001. *Am. J. Hum. Genet.* 68(4): 890-916  
 Khoshdel et al. 2005. *Forensic Sci. Int.* 148(2): 121-126  
 Kung'u et al. 2007. *Forensic Sci. Int.* 171(1): 78-78  
 Lantieri et al. 2007. *Forensic Sci. Int.* 168(2): 154-161  
 Liang et al. 2007. *Forensic Sci. Int.* 167(1): 71-76  
 Liang et al. 2007. *Forensic Sci. Int.* 171(1): 213-213  
 Park et al. 2005. *Forensic Sci. Int.* 152(2): 133-147  
 Pavesi et al. 2005. *Ann. N.Y. Acad. Sci.* 666: 309-318  
 Quintana-Murci et al. 2004. *Forensic Sci. Int.* 140(1): 113-115

Roussel et al. 2007. *BMC Evolutionary Biology* 7(1): 124  
 Subramanian et al. 2007. *Forensic Sci. Int.* 168(1): 47  
 Soudani et al. 2006. *Forensic Sci. Int.* 158(2): 207-203  
 Tenevski et al. 2001. *Am. J. Hum. Genet.* 68(2): 271-283  
 Vassilov et al. 2009. *Forensic Sci. Int.* 178(2): 252-258  
 Ximel et al. 2008. *Forensic Sci. Int.* 178(2): 244-248  
 Zhang et al. 2008. *Forensic Sci. Int.* 176(2): 244-248  
 Zhu et al. 2005. *Forensic Sci. Int.* 153: 285-285

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