SI Appendix

In an island model with n sub-populations of N diploid individuals with c clonal rate, s selfing rate, m migration rate, and non-overlapping generations, three probabilities of identity by descent can be defined: Q_i , the probability that two alleles drawn at random from a single individual are identical by descent; Q_s, the probability that two randomly sampled alleles from two different individuals within a subpopulation are identical by descent; and Q_T, the probability that two randomly sampled alleles from two individuals in different subpopulations are identical by descent.

The recurrence equations between generations t and t+1 for the different identities by descent among adults in a monoecious population with mixed clonal and sexual reproduction in an island model are given in Balloux *et al.* (1) as:

$$\begin{cases} Q_{i(t+1)} = \gamma\left\{ cQ_{i(t)} + (1-c)\left[s\left(\frac{1+Q_{i(t)}}{2}\right) + (1-s)Q_{s(t)} \right] \right\} \\ Q_{s(t+1)} = \gamma\left\{ q_s\left[\frac{1}{N}\left(\frac{1+Q_{i(t)}}{2}\right) + \left(1-\frac{1}{N}Q_{s(t)}\right) \right] + (1-q_s)Q_{T(t)} \right\} \\ Q_{T(t+1)} = \gamma\left\{ q_d\left[\frac{1}{N}\left(\frac{1+Q_{i(t)}}{2}\right) + \left(1-\frac{1}{N}\right)Q_{s(t)} \right] + (1-q_d)Q_{T(t)} \right\} \end{cases} \quad (1)$$

with $\gamma=(1-u)^2$,

$$\begin{cases} q_s \cong (1-m)^2 + \frac{m^2}{n-1} \\ q_d = \frac{1-q_s}{n-1} \end{cases} \quad (2)$$

where q_s is the probability that two individuals taken at random within the same sub-population after migration were born in the same subpopulation and q_d the probability that two individuals sampled after migration in different sub-populations originated from the same subpopulation (2).

Wright's *F*-statistics (3), the parameters most widely used to describe population structure (e.g., 4), can be defined following Cockerham (5, 6) as:

$$\begin{cases} F_{IS} = \dfrac{Q_i - Q_s}{1 - Q_s} \\ F_{ST} = \dfrac{Q_s - Q_T}{1 - Q_T} \\ F_{IT} = \dfrac{Q_i - Q_T}{1 - Q_T} \end{cases} \tag{3}$$

Following Balloux et al. (Balloux et al., 2003) and assuming no selfing (i.e. $s=1/N$), the systems of equations (1), (2) and (3) lead to:

$$\begin{cases} F_{IS} = \dfrac{\gamma\{q_s - c[\gamma(q_s - q_d) - 1] - 1\}}{2N(1 - c\gamma)[\gamma(q_s - q_d) - 1] - \gamma\{q_s - c[\gamma(q_s - q_d) - 1] - 1\}} \\ \\ F_{ST} = \dfrac{\gamma(1 - c\gamma)(q_s - q_d)}{[2N(1 - c\gamma) - \gamma(1 - c)][1 - \gamma(q_s - q_d)] + \gamma\{q_d[\gamma(c+1) - 1] - q_s[\gamma(c+1) - 2]\}} \end{cases} \tag{4}$$

In Côte d'Ivoire there are two foci, an thus two putative subpopulations, Bonon and Sinfra (7), as is the case for Guinea (Dubreka and Boffa) (Forecariah being more isolated from the two others). In a two sub-populations framework with total clonality (n=2, c=1), as it is probably the case in the two areas investigated in the present study, we get:

$$\begin{cases} q_s = (1-m)^2 + m^2 = 1 - 2m(1-m) \\ q_d = 1 - (1-m)^2 - m^2 = 2m(1-m) = 1 - q_s \end{cases} \tag{5}$$

and combining equations (4) and (5):

$$\begin{cases} F_{IS} = \dfrac{\gamma\{q_s - \gamma(2q_s - 1)\}}{2N(1-\gamma)[\gamma(2q_s-1)-1] - \gamma\{q_s - \gamma(2q_s-1)\}} \\ \\ F_{ST} = \dfrac{\gamma(1-\gamma)(2q_s-1)}{[2N(1-\gamma)][1-\gamma(2q_s-1)] + \gamma\{(1-q_s)[2\gamma-1] + 2q_s[1-\gamma]\}} \end{cases} \tag{6}$$

After neglecting terms in u^2 and u (<<1 or q_s) and simplifications, these equations can be rearranged into:

$$\begin{cases} F_{IS} = -\dfrac{1-q_s}{(1-q_s)(1+8Nu)} \\ \\ F_{ST} = \dfrac{2u(2q_s-1)}{(1-q_s)(8Nu+1)} \end{cases} \tag{7}$$

From equation (7) it is easy to see that when $q_s \neq 1$ (i.e., m is in]0,1[) F_{IS} becomes independent from migration and can provide an estimate for N in the simple form:

$$N = -\frac{1+F_{IS}}{8uF_{IS}} \tag{8}$$

If we combine (7) and (8) we can also obtain an estimate for q_s:

$$q_s = \frac{1 + F_{ST}\dfrac{8Nu+1}{2u}}{2 + F_{ST}\dfrac{8Nu+1}{2u}} \tag{9}$$

Because we are in a two populations case, the genetic effect of migration is symmetric around 0.5 (m=0.49 is equivalent to m=0.51). We can thus focus on values below 0.5 for m. From there it is easy to see from (5) that:

$$m = \frac{1}{2}\left[1 - \sqrt{2q_s - 1}\right] \tag{10}$$

and thus combining (9) and (10) gives us access to m as:

$$m = \frac{1}{2}\left[1 - \sqrt{\frac{F_{ST}\dfrac{8Nu+1}{2u}}{2 + F_{ST}\dfrac{8Nu+1}{2u}}}\right] \tag{11}$$

that can be finally combined with (8) to obtain:

$$m = \frac{1}{2}\left[1 - \sqrt{\frac{F_{ST}}{F_{ST} - 4uF_{IS}}}\right] \tag{12}$$

SI References

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