PRIORITISING BREEDS FOR CONSERVATION USING ALLELIC DIVERSITY

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Subpopulations in conservation programmes:

1. Gene diversity or expected heterozygosity
2. Allelic diversity:
    - a. Source or variation
    - b. Selection response
    - c. Fluctuations in population size

Population with the same gene diversity and different allelic diversity (and *viceversa*):

0.5	0.5				$H = 0.5$
0.69	0.08	0.08	0.08	0.07	$H = 0.5$
0.7	0.04	0.04	0.04	0.04	$H = 0.5$
0.04	0.04	0.02	0.02	0.02	

Gene differentiation:

$$H_T = H_S + D_G$$

$$H_T = 1 - \sum_{k=1}^{T} \left(\sum_{i=1}^{n} \frac{p_{i,k}}{n} \right)^2 \qquad H_S = 1 - \frac{1}{n} \sum_{i=1}^{n} \left(\sum_{k=1}^{T} p_{i,k}^2 \right)$$

$$F_{ST} = \frac{H_T - H_S}{H_T} = \frac{D_G}{H_T}$$

Allelic differentiation:

$$H_T = H_S + D_G \quad \rightarrow \quad A_T = A_S + D_A$$

Rarefaction (El Mousadik and Petit, 1996):

$$P_{ik} = \binom{N_i - N_{ik}}{g} \Big/ \binom{N_i}{g} \qquad a_i = \sum_{k=1}^{T} \left(1 - P_{ik}\right)$$

$$A_S = \left(\frac{1}{n} \sum_{i=1}^{n} a_i \right) - 1$$

Allelic differentiation:

$$d_{ij} = \frac{1}{2}\sum_{k=1}^{T}\left[\left(1 - P_{ik}\right)P_{jk} + P_{ik}\left(1 - P_{jk}\right)\right]$$

$$D_A = \frac{1}{n^2}\left[\sum_{i,j=1}^{n} d_{ij}\right]$$

$$A_T = A_S + D_A = \left[\frac{1}{n}\sum_{i=1}^{n}\left(a_i + \frac{1}{n}\sum_{j=1}^{n} d_{ij}\right)\right] - 1$$

Allelic differentiation:

$$A_{ST} = \frac{A_T - A_S}{A_T} = \frac{D_A}{A_T}$$

El Mousadik and Petit (1996):

$$\rho_{ST} = 1 - \frac{(R_S - 1)}{(R_T - 1)}$$

	Alleles								
	a	*b*	*c*	*d*	*e*	*f*	*g*	*h*	*i*
Sub I	1	1	1	1	0	0	0	0	0
Sub II	0	1	1	1	1	0	0	0	0
Sub III	0	0	1	1	1	1	0	0	0
Sub IV	0	0	0	1	1	1	1	0	0
Sub V	0	0	0	0	1	1	1	1	0
Sub VI	0	0	0	0	0	1	1	1	1

	Sub I	Sub II	Sub III	Sub IV	Sub V	Sub VI
Sub I	4	5	6	7	8	8
Sub II	5	4	5	6	7	8
Sub III	6	5	4	5	6	7
Sub IV	7	6	5	4	5	6
Sub V	8	7	6	5	4	5
Sub VI	8	8	7	6	5	4

	Sub I	Sub II	Sub III	Sub IV	Sub V	Sub VI
Sub I	0	2	4	6	8	8
Sub II	2	0	2	4	6	8
Sub III	4	2	0	2	4	6
Sub IV	6	4	2	0	2	4
Sub V	8	6	4	2	0	2
Sub VI	8	8	6	4	2	0

$$A_{ST} = 0.39$$

$$\rho_{ST} = 0.63$$

	Alleles								
	a	*b*	*c*	*d*	*e*	*f*	*g*	*h*	*i*
Sub I	1	1	1	1	0	0	0	0	0
Sub II	0	1	1	1	1	0	0	0	0
Sub III	0	0	1	1	1	1	0	0	0
Sub IV	0	0	0	1	1	1	1	0	0
Sub V	0	0	0	0	1	1	1	1	0
Sub VI	0	0	0	0	0	1	1	1	1

	Alleles								
	a	*b*	*c*	*d*	*e*	*f*	*g*	*h*	*i*
Sub I	1	1	1	1	1	1	1	1	1
Sub II	1	1	1	0	0	0	0	0	0
Sub III	1	1	1	0	0	0	0	0	0
Sub IV	1	1	1	0	0	0	0	0	0
Sub V	1	1	1	0	0	0	0	0	0
Sub VI	1	1	1	0	0	0	0	0	0

$A_{ST} = 0.39$

$\rho_{ST} = 0.63$

$A_{ST} = 0.22$

$\rho_{ST} = 0.63$

	Allele						
Subpopulation	**1**	**2**	**3**	**4**	**5**	**6**	**Statistic**
I	0.2	0.3	0.5				$F_{ST} = 0.22$
II		0.2	0.3	~~0.1~~	~~0.1~~	0.3	$A_{ST} = 0.39$
III	0.5	0.5					$\rho_{ST} = 0.55$
IV				0.3	0.3	0.4	

	Allelic Richness			Allelic Diversity		
Subpopulation	**Total**	**Within**	**Between**	**Total**	**Within**	**Between**
No rarefaction						
I	0.0	−1.7	+1.7	+0.6	−2.3	+2.8
II	0.0	+11.7	−11.7	+18.6	+15.8	+2.8
III	0.0	−8.3	+8.3	−8.5	−11.3	+2.8
IV	0.0	−1.7	+1.7	+6.6	−2.3	+8.9
$g = 10$						
I	−0.9	−1.1	+0.2	0.0	−1.2	+1.2
II	+1.3	+10.3	−8.9	+14.3	+11.5	+2.8
III	+2.4	−8.7	+11.1	−8.4	−9.8	+1.3
IV	+19.5	−0.5	+20.0	+10.3	−0.6	+10.9

Petit et al. (1998):

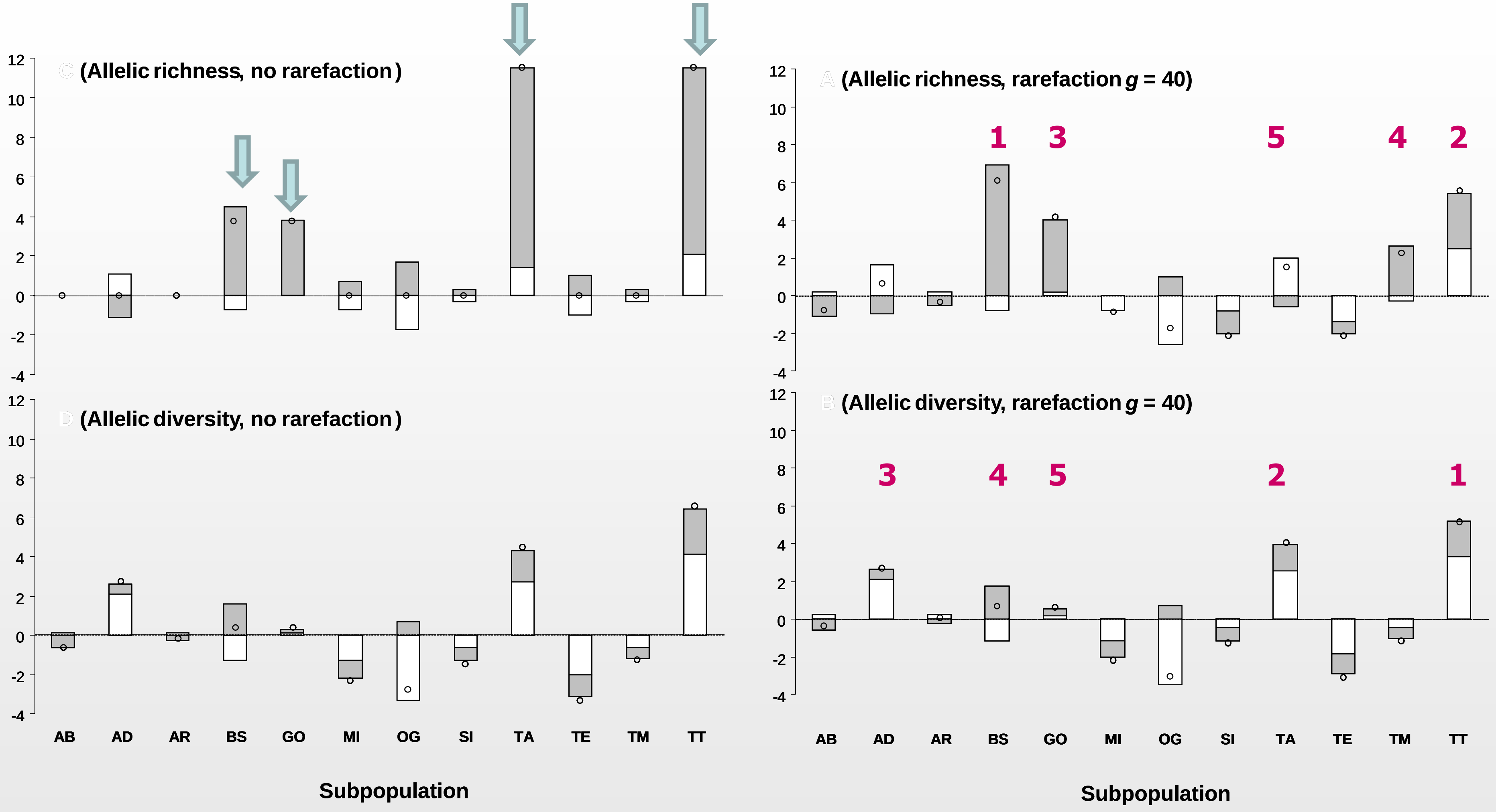
Argan tree:

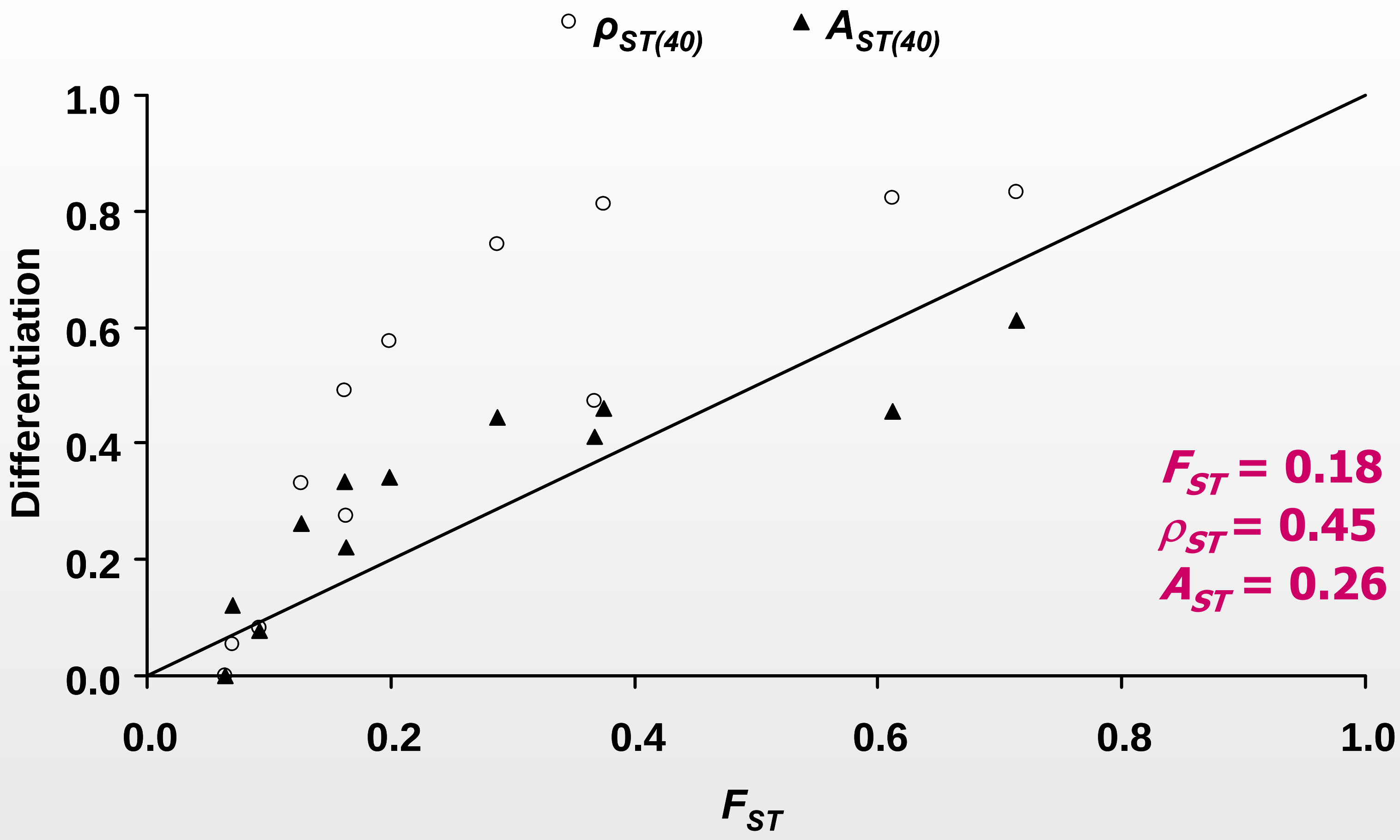
12 populations

12 markers

Contribution (%):

○ **Total** ☐ **Within-subpopulation** ▨ **Between-subpopulation**





$F_{ST} = 0.18$

$\rho_{ST} = 0.45$

$A_{ST} = 0.26$

1. It has been proposed a partition of allelic diversity into within and between-subpopulations components and, subsequently, an allelic differentiation coefficient, with interest from the point of view of priorisation of populations in conservation.

2. A_{ST} differs form ρ_{ST} because ρ_{ST} depends on the average allelic richness of the subpopulations and the allelic richness of the whole population, whereas A_{ST} depends on the particular arrangement of alleles in the subpopulations.

Thank you for your attention