Optimal management of gene and allelic diversity in subdivided populations

E. López-Cortegano[1], R. Pouso[1], A. Pérez-Figueroa[2], J. Fernández[3] and A. Caballero[1]
[1]Universidad de Vigo, Departamento de Bioquímica, Genética e Inmunología, Facultad de Biología, 36310 Vigo, Spain, [2]Centro de Investigaciones Biomédicas (CINBIO), Universidad de Vigo, 36310 Vigo, Spain, [3]Instituto de Investigación y Tecnología Agraria y Alimentaria (INIA), Departamento de Mejora Genética, Crta. de la Coruña, km. 7.5, 28040 Madrid, Spain; e.lopez@uvigo.es

Genetic diversity is generally assessed by means of neutral molecular markers, and it is usually quantified by the expected heterozygosity under Hardy-Weinberg equilibrium, while allelic diversity is measured by the number of alleles per locus. These two measures of diversity are complementary because, whereas the former is directly related to genetic variance for quantitative traits and, therefore, to the short-term response to selection and adaptation, the latter is more sensitive to population bottlenecks and relates more to the long-term capacity of populations to adapt to changing environments. In the context of structured populations undergoing conservation programs, it is critical to decide the optimum management strategy in order to preserve as much of both diversity measures as possible. Here we first present a new release of the software Metapop for the analysis and management of diversity in subdivided populations, and illustrate its use with cattle data. This new update includes computation of allelic diversity measures, as well as a simulation mode to forecast the consequences of taking different management strategies over time. We examine through computer simulations the consequences of choosing a strategy based either on heterozygosity or allelic diversity in the context of different demographic histories for a structured population. Our results indicate that maximisation of allelic diversity can maintain large levels of both heterozygosity and allelic richness, and thus it should be the recommended strategy in conservation programs for structured populations.

Session 01 Theatre 6

Assessment of the risk status of local breeds in Poland – preliminary results

G.M. Polak and J. Krupinski
National Research Institute of Animal Production, Horse Breeding, Sarego, 2 Str., 31-047 Cracow, Poland; grazyna.polak@izoo.krakow.pl

The risk assessment is the basis for an early warning system against the loss of local and indigenous breeds of domestic animals. It is also one of the main factors determining the implementation of genetic resources conservation programmes. Currently in Poland, the assessment of status risk of local breeds has been consistent with the guidelines of the Common agriculture Policy and Rural Development Programs, setting thresholds for particular species. The aim of this work was to develop a new method, considering the specifics of Polish conditions. The presented preliminary studies take into account 4 breeds: two horses, one sheep and one cattle. Analysis was carried out in the Institute of Animal Production used the method developed, taking into account the FAO guidelines from 2013 and research of other countries. The model is based on: number of females, effective population size and 5 additional features: geographical concentration, existence of branded products, *ex situ* protection, origin testing, cooperation of breeders. The results show that out of the 4 breeds surveyed, 3 were at risk and 1 required constant monitoring.

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Email: e.lopez@uvigo.es

[1] University of Vigo (Vigo, Spain)
[2] Biomedical Research Center (CINBO; Vigo, Spain)
[3] Spanish National Institute of Agrarian and Alimentary Research and Technology (INIA; Madrid, Spain)

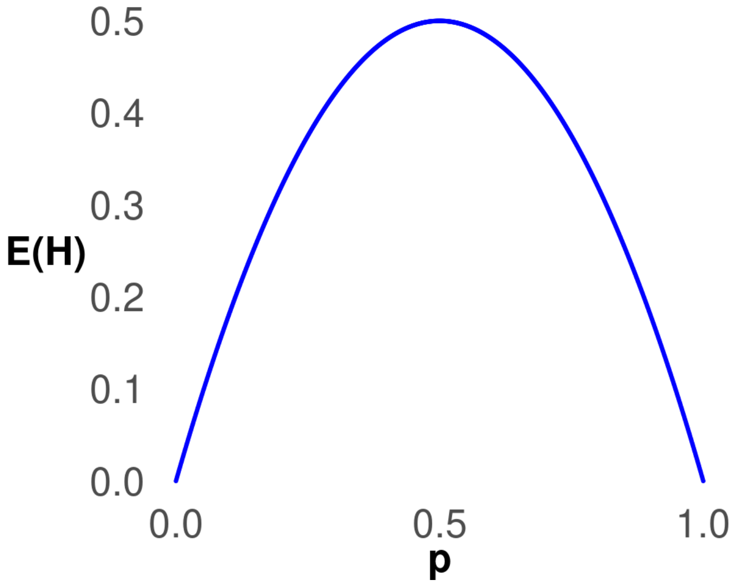
Managing genetic diversity

Heterozygosity

Depends on:

- allelic frequencies:

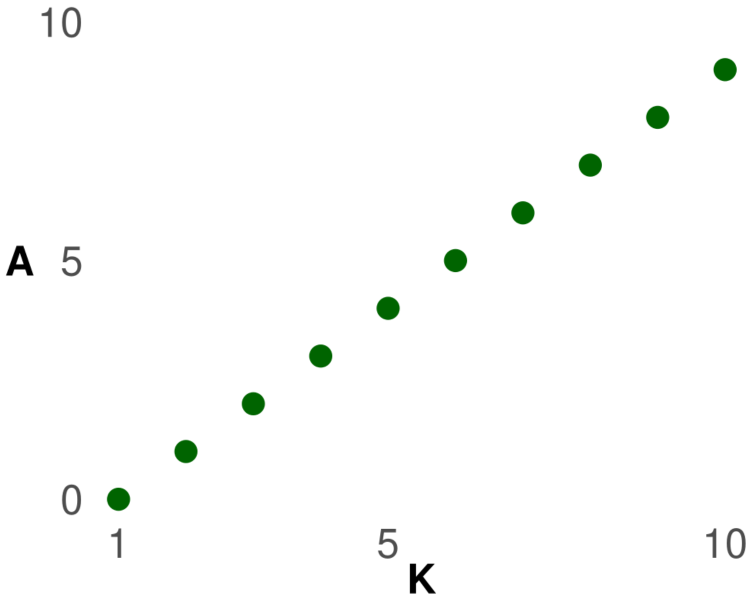
$$E(H) = 2\,p\,(1-p)$$



Allelic diversity

- the absence / presence of alleles

$$A = K - 1$$



Managing genetic diversity

Heterozygosity

Relates to:

- Inbreeding: ***F = 1 - H***

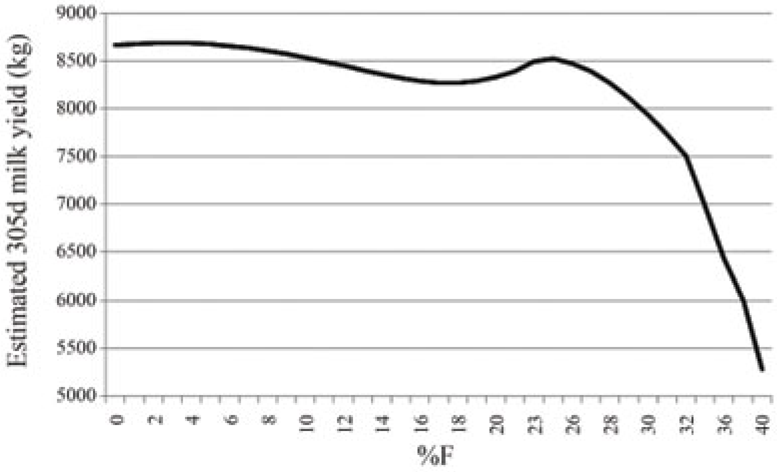


Figure 2 - Estimated 305 d milk yields (kg) by inbreeding level (%F) from the cubic-spline model adjusted for herd-year-season effects.

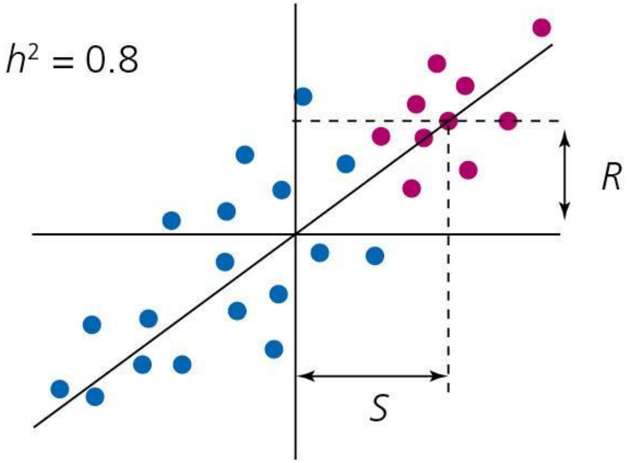
(from Geha MJ *et al.* 2011)

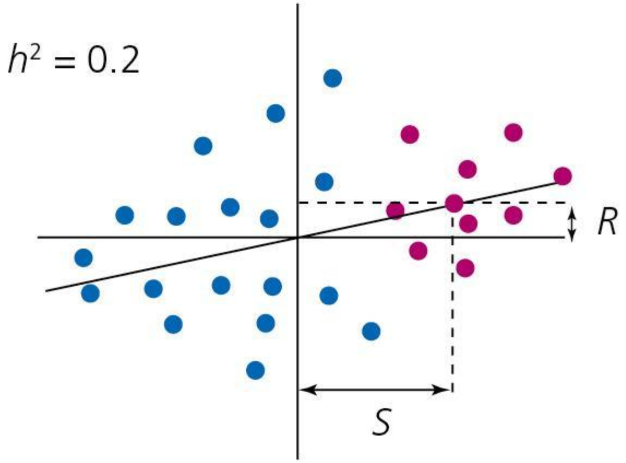
Managing genetic diversity

Heterozygosity

Relates to:

- Inbreeding: $F = 1 - H$
- Additive variance: $V_A = 2\,p\,(1-p)\,\alpha^2$
  (and the response to selection)



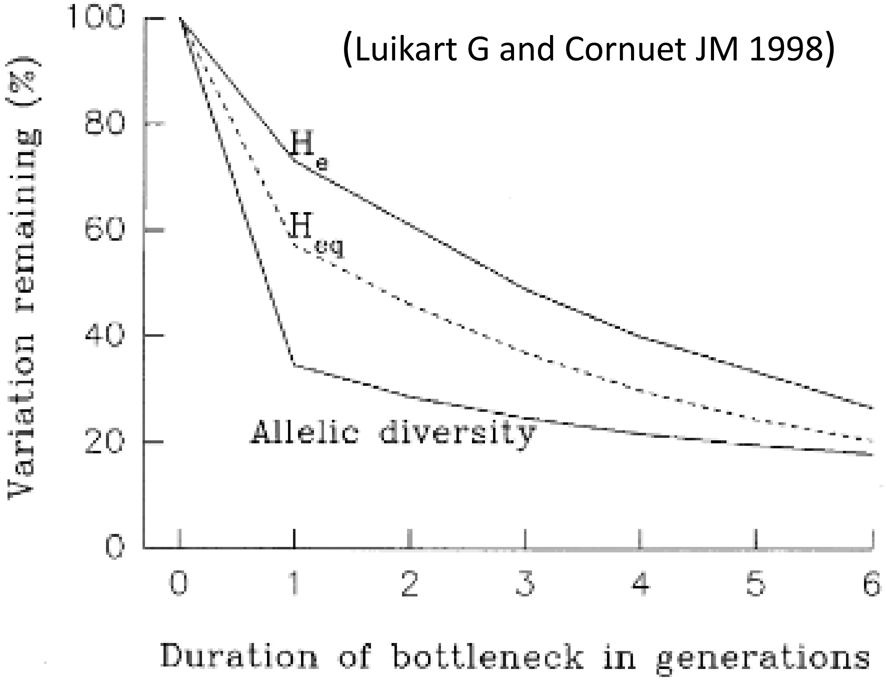


Managing genetic diversity

Allelic diversity

Is more sensitive to:

- Bottlenecks



(Luikart G and Cornuet JM 1998)

Managing genetic diversity

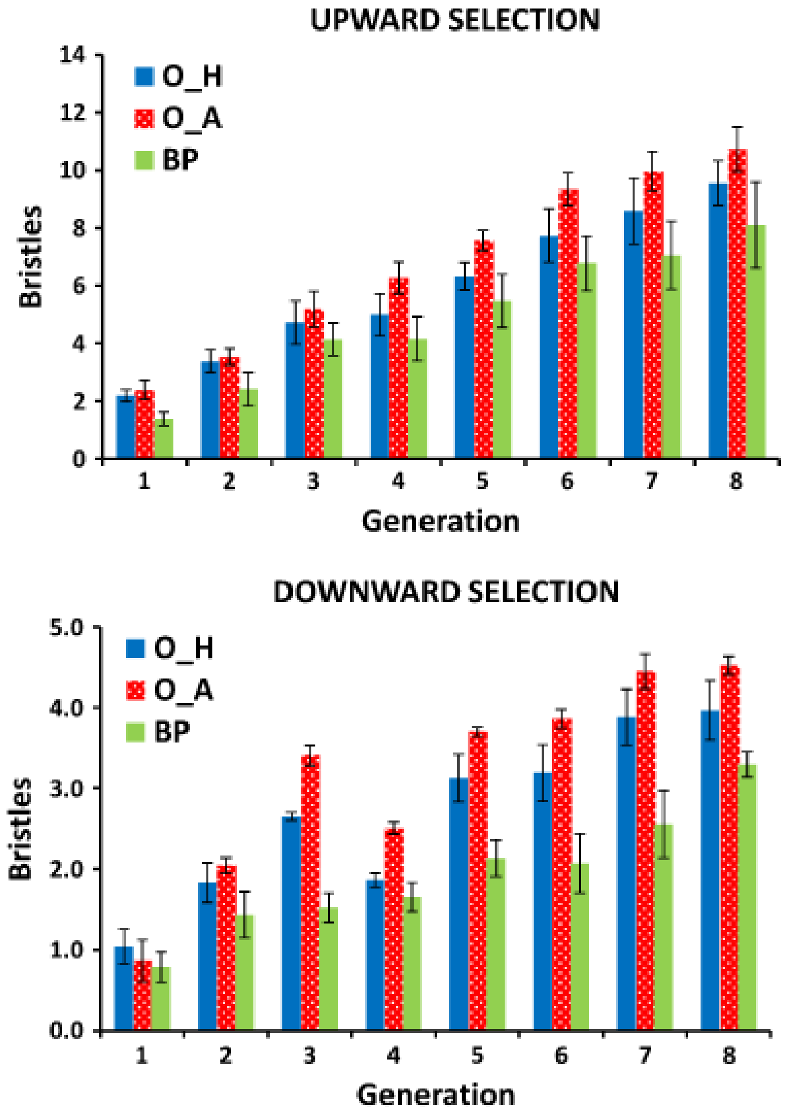
Allelic diversity

Is more sensitive to:

- Bottlenecks

Relates to:

- Long-term response to selection
  (*i.e.* adaptive potential)

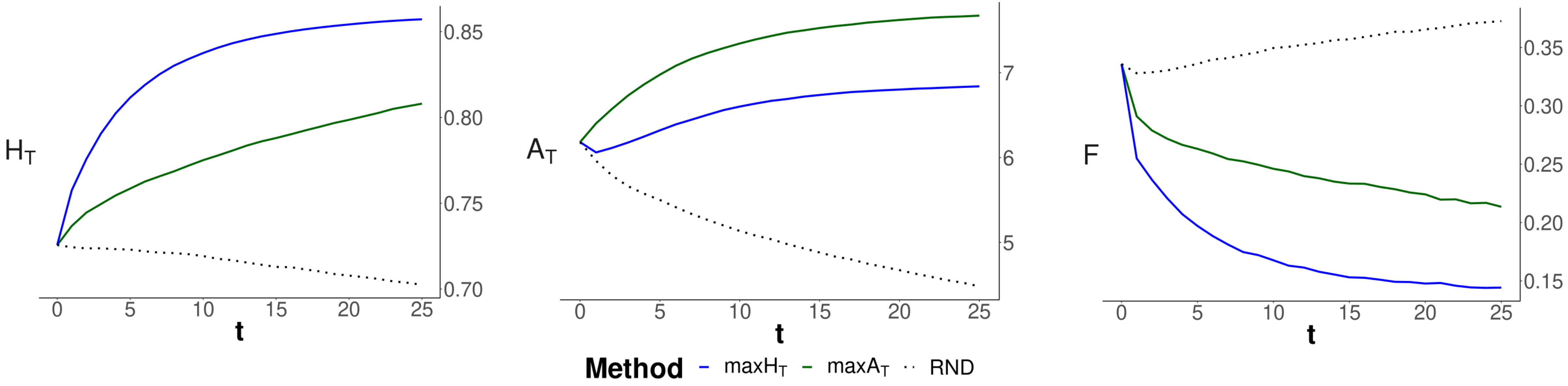


(from Vilas A *et al.* 2015)

Heterozygosity / Allelic diversity
Within populations

Maximization of heterozygosity should be the strategy of choice

(Fernández et al 2004)



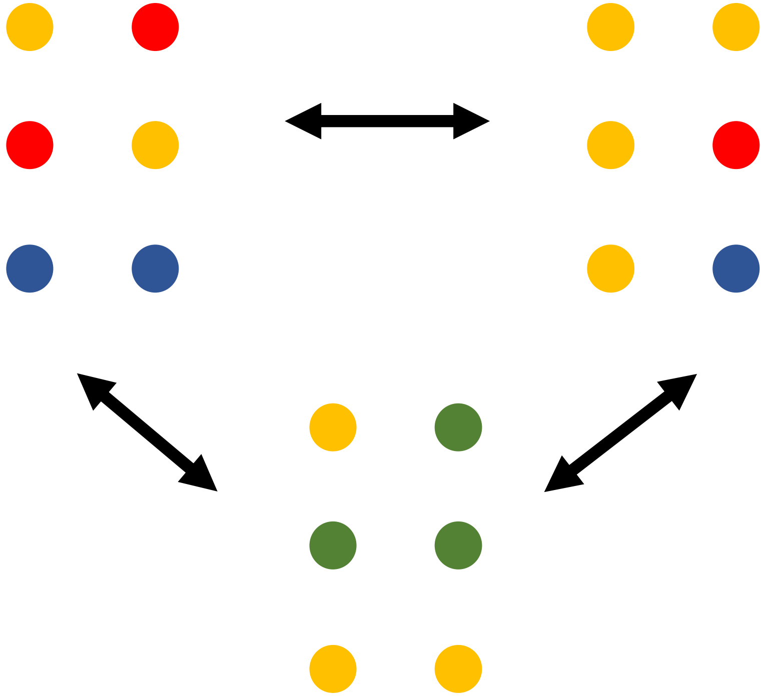
Allelic diversity

in subdivided populations

Total allelic diversity: $\boldsymbol{A}\ _{\boldsymbol{T}} = AS + DA$

$$A_S = \left(\frac{1}{n}\sum a_i\right) - 1$$

$$D_A = \frac{1}{n^2}\sum\sum d_{A,ij}$$



Allelic diversity
in subdivided populations

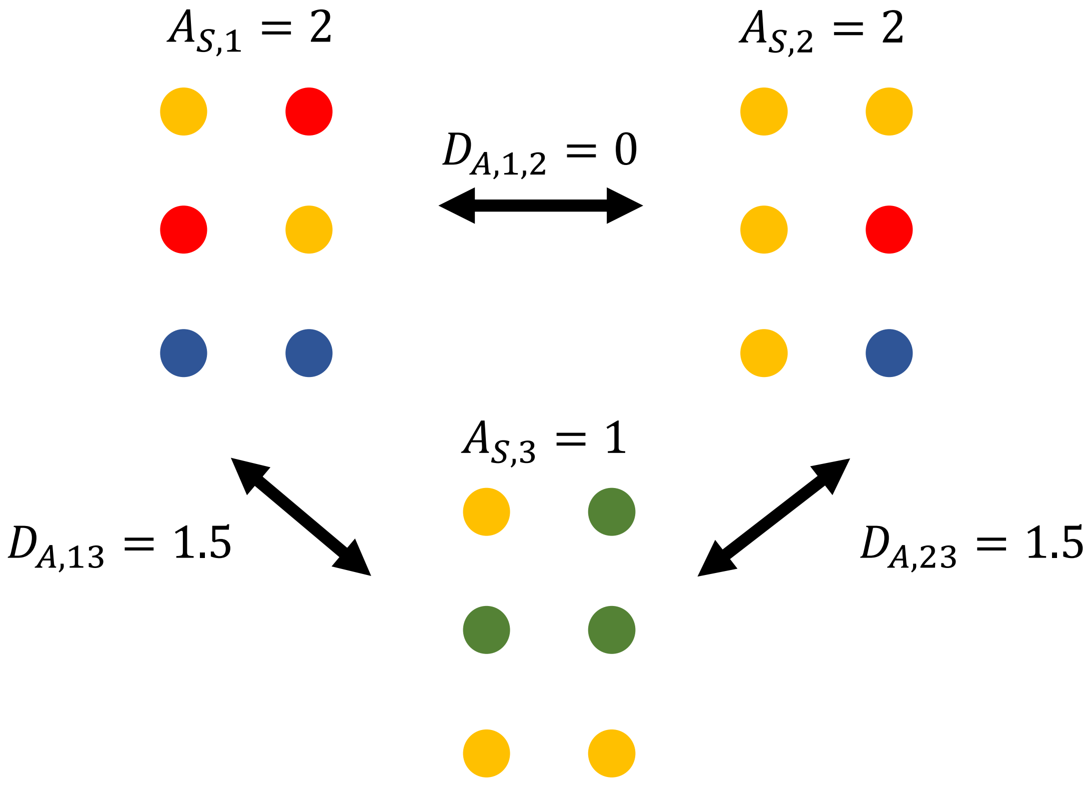
Total allelic diversity: $\boldsymbol{A_T} = AS + DA$

$$A_S = \left(\frac{1}{n}\sum a_i\right) - 1 = \mathbf{1.67}$$

$$D_A = \frac{1}{n^2}\sum\sum d_{A,ij} = \mathbf{0.67}$$

$$A_T = \mathbf{2.33}$$

$$K = \mathbf{4}$$



$A_{S,1} = 2$

$A_{S,2} = 2$

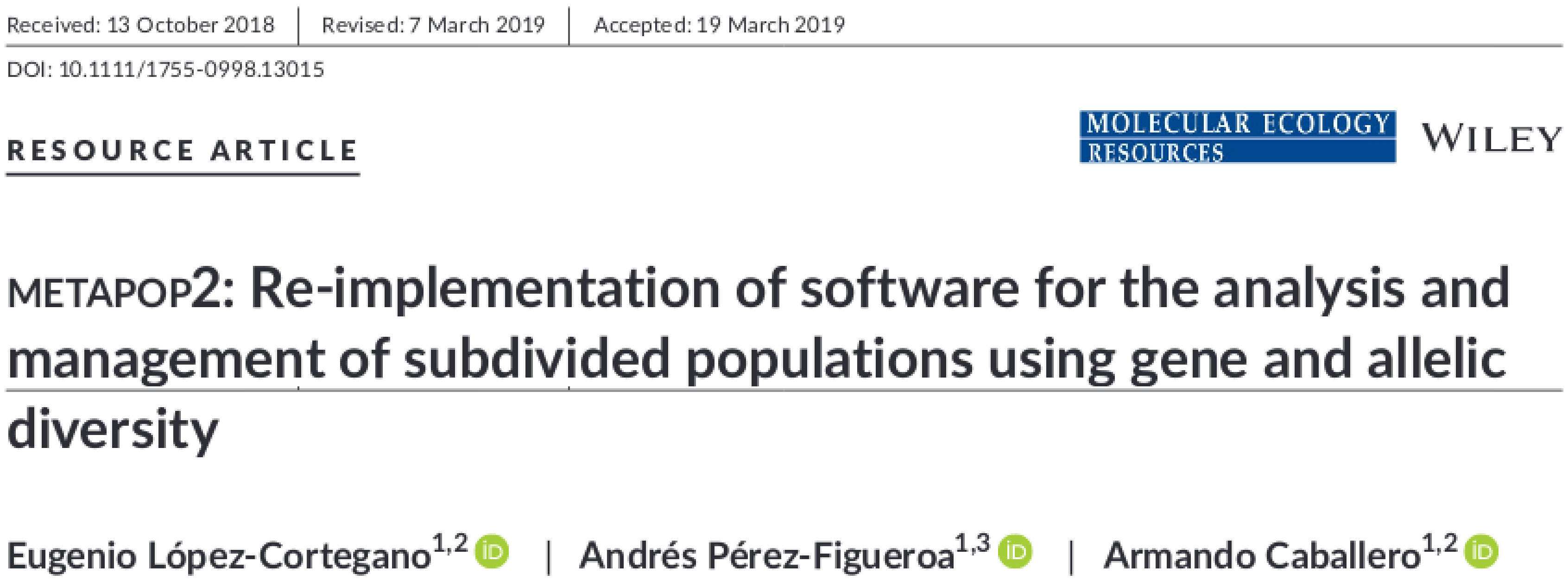
$D_{A,1,2} = 0$

$A_{S,3} = 1$

$D_{A,13} = 1.5$

$D_{A,23} = 1.5$

Metapop2 software



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METAPOP2: Re-implementation of software for the analysis and management of subdivided populations using gene and allelic diversity

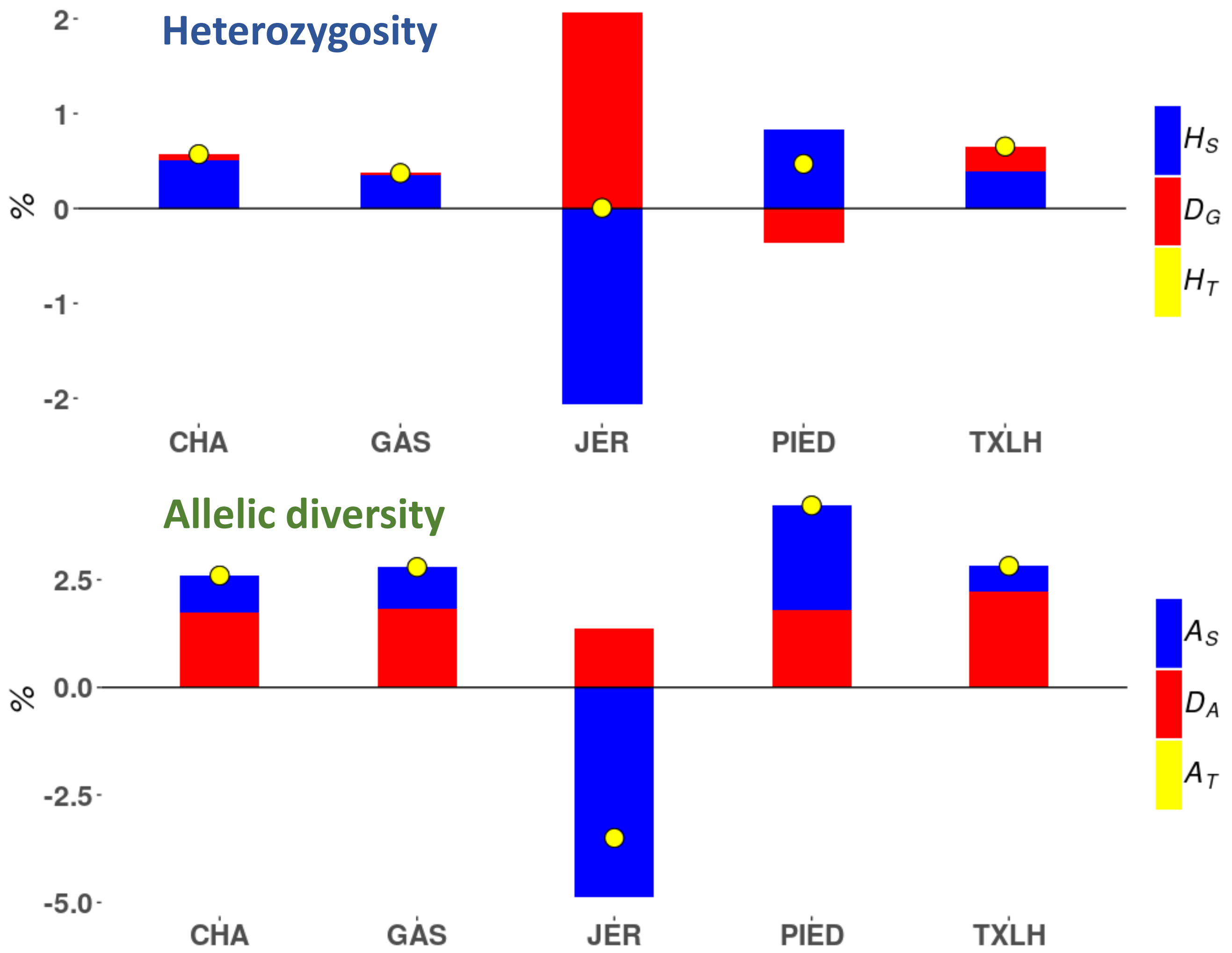
Eugenio López-Cortegano[1,2] | Andrés Pérez-Figueroa[1,3] | Armando Caballero[1,2]

- Available at GitLab: https://gitlab.com/elcortegano/metapop2

Example data from Cattle

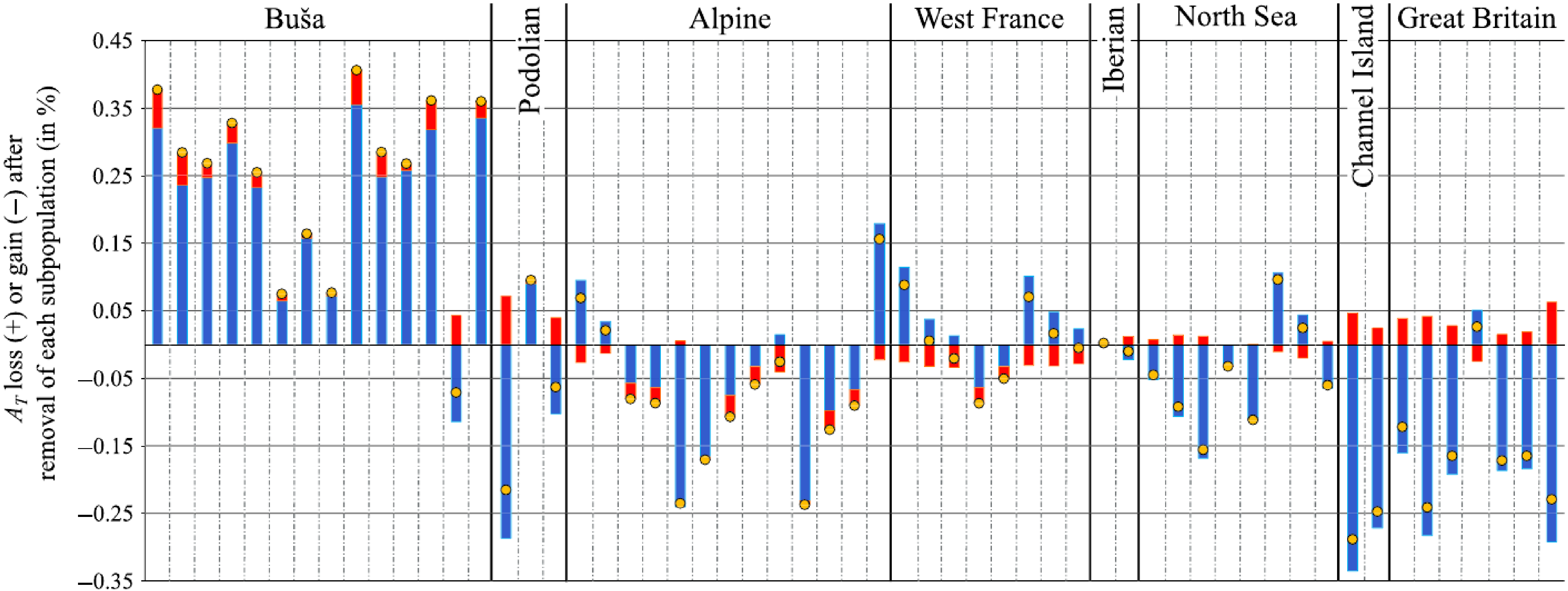
Subpopulations contribution to diversity:

- Most breeds contribute to total diversity
- JER breed breed harbors little H_S and A_S
- PIED contributes differently to D_G and D_A



(López-Cortegano et al 2019; Cattle data from Decker et al 2014)

Example data from Cattle



(Ramljak et al 2018)

1st Take-home message

Allelic diversity matters

Management simulations

Genomic markers:

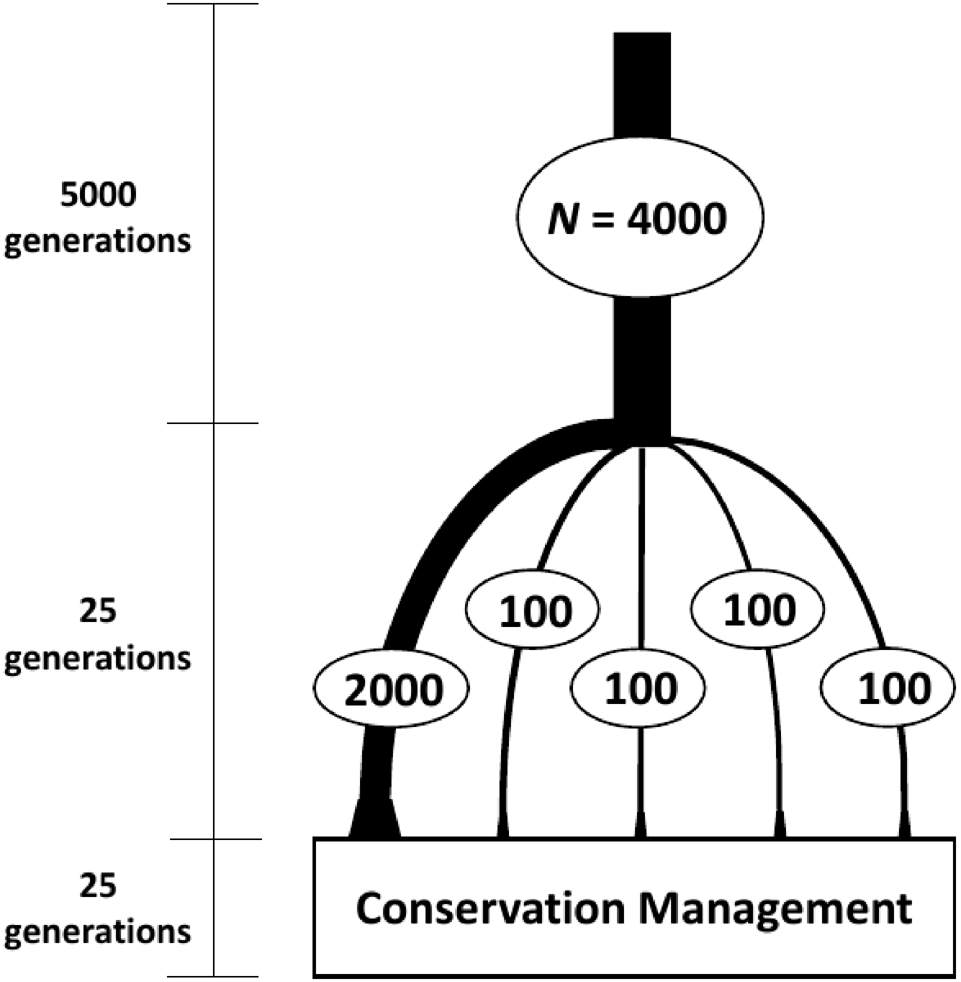
- High density of haplotypes (about 1,000 per Morgan)

Population composition:

- 5 subpopulations (*N* = 40)
- Balanced sex ratio

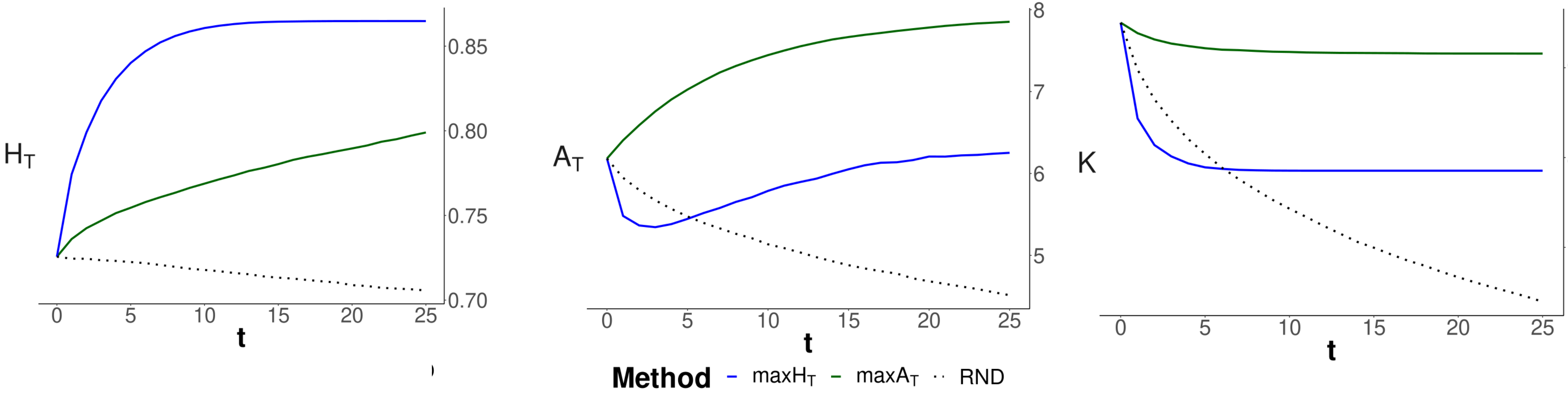
Computing individuals contributions:

- Using Simulated Annealing
- No limit to number of offspring
- Migration (5 migrants per generation)



Management simulations

The different optimization methods achieved their objectives

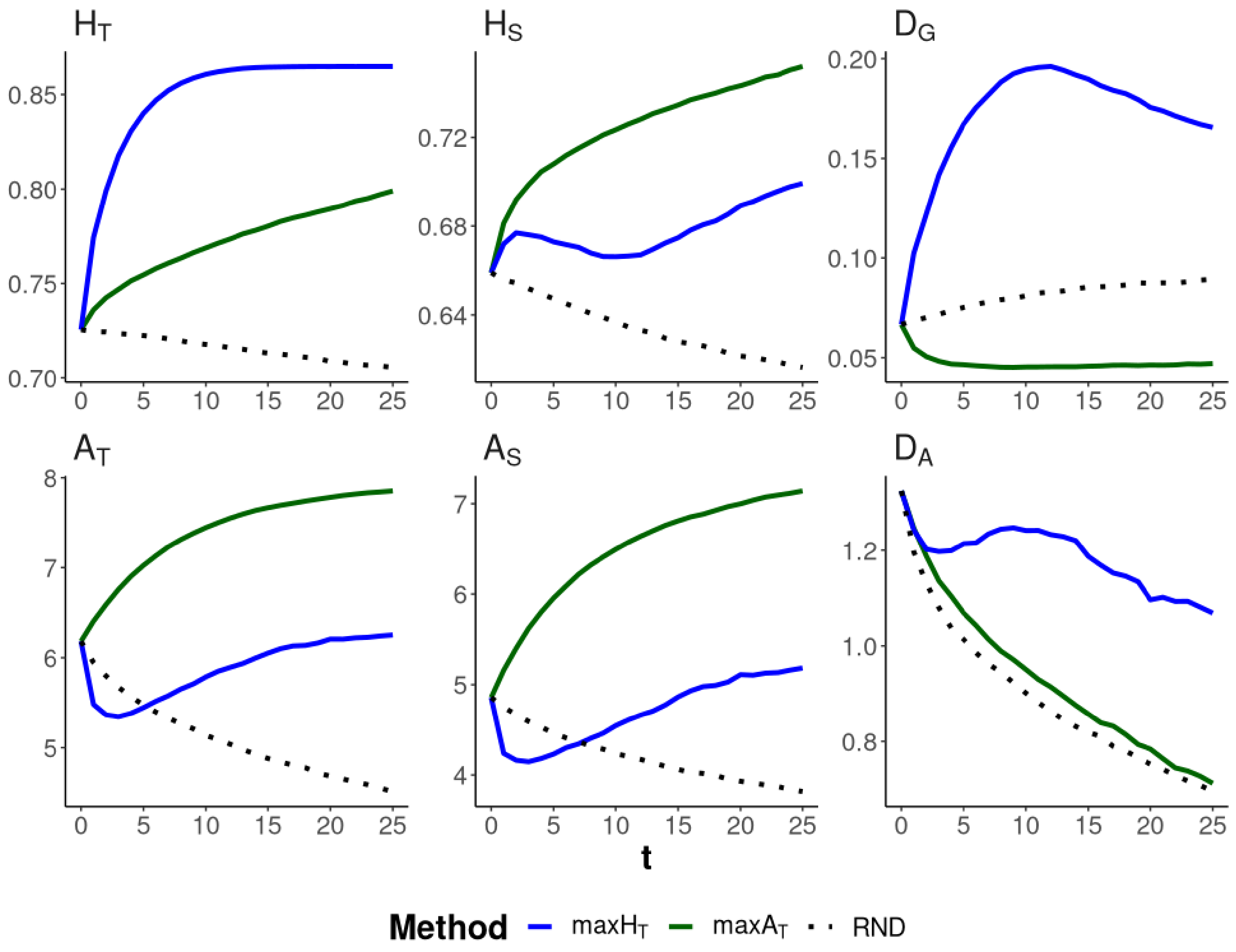


Management simulations

Optimizing allelic diversity

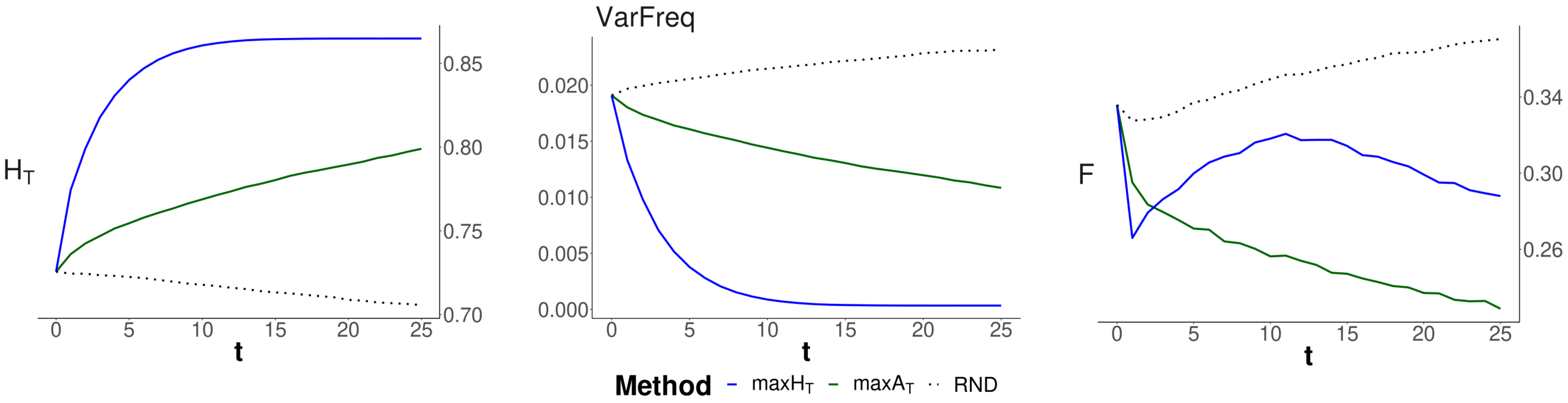
maximizes genetic diversity

within subpopulations



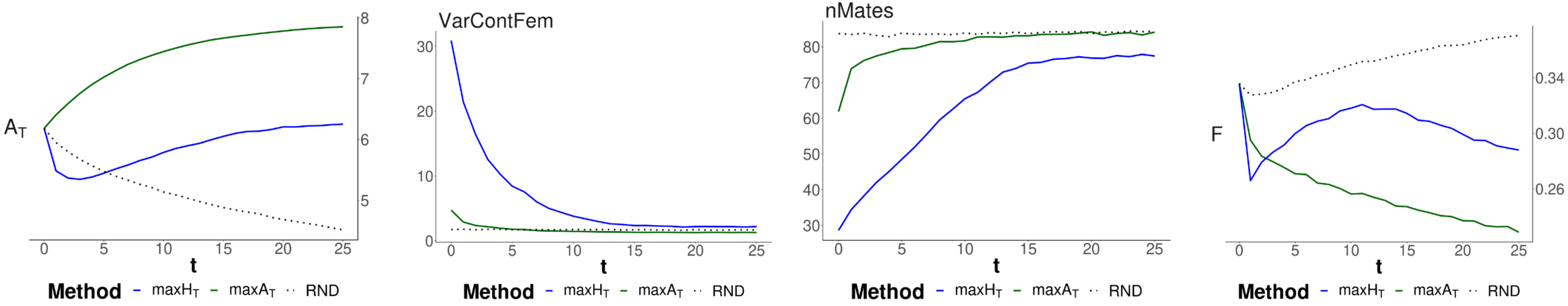
Management simulations

Maximizing total heterozygosity does not minimize inbreeding In subdivided populations



Management simulations

Maximizing allelic diversity can be reached by equalling individuals contributions, and minimizes inbreeding

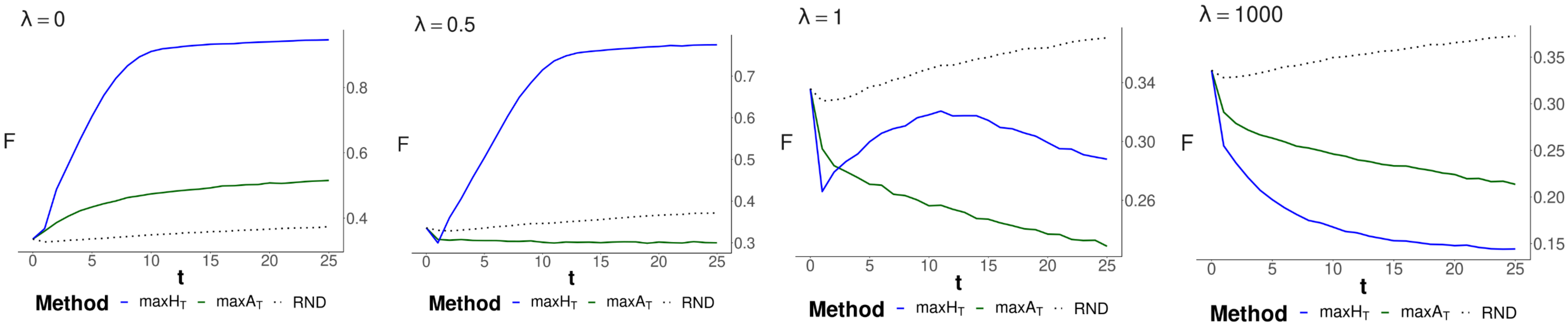


Management simulations

Maximizing heterozygosity is the best choice to minimize inbreeding

Only when managing single, undivided populations

$$\boldsymbol{A_T} = \lambda A_S + DA$$



2nd Take-home message

Allelic diversity
minimizes inbreeding
in subdivided populations

Optimal management of genetic diversity in subdivided populations

Eugenio López-Cortegano[1], Ramón Pouso[1], Adriana Labrador[1], Andrés Pérez-Figueroa[1], Jesús Fernández[2], Armando Caballero[3]*

[1]Facultad de Biología, Universidad de Vigo, Spain, [2]Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Spain, [3]University of Vigo, Spain