# Use of inbred matings for population management in conservation programmes

## de Cara, M.A.R., Villanueva, B., Toro, M.A., Fernández, J.

*Departamento de Mejora Genética Animal (INIA)*
*Departamento de Producción Animal (UPM)*

INIA
Instituto Nacional de Investigación
y Tecnología Agraria y Alimentaria

# Main objectives of a conservation programme

- **to minimise the loss of genetic diversity**

  *allowing populations to adapt to possible changes*
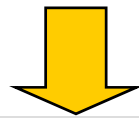
- **to reduce the increase in inbreeding**

  *avoid inbreeding depression*

# Consensus optimum strategy: maximize effective population size

- **optimize contributions to minimise global coancestry**

  ***contributions*: number of offspring that each potential parent contributes to the following generation**

  ***coancestry*: genealogical or molecular**

**Deleterious mutations are maintained**

**↓less viability in the long term**

**However inbreeding when combined with natural selection may eliminate deleterious alleles in a process known as *purging***

# Does it purging occurs in livestock species?

## A viable herd of genetically uniform cattle

Deleterious alleles seem to have been purged in a feral strain of inbred cows.

P. M. Visscher*, D. Smith†, S. J. G. Hall‡, J. A. Williams†

## Chillingham cattle

-effective population size of about 8 since 1700
-homozygous genotypes for 24 of 25 markers (13 individuals)

**but**

-there has been no drop in fertility or viability

# Does it purging occurs in livestock species?

**INFERRING PURGING FROM PEDIGREE DATA**

*Evolution 61-5: 1043–1051* (2007)

Davorka Gulisija[1,2] and James F. Crow[1,3]

-pedigreess of 59778 **U.S. Jersey cows**

-The effect of purging is negligible due
-limited number of generations
-breeders have tended to avoid consanguineous matings

# Does it purging occurs in livestock species?

**Purging of inbreeding depression within the Irish Holstein-Friesian population**

Sinéad Mc Parland[*1,2], Francis Kearney[3] and Donagh P Berry[1]

**Irish Holstein-Friesian** population
      -88,366 records of milk production
      -39,741 records on fertility

-some purging for milk production
-no evidence of purging for fertility

# Proposal

Combine optimal contributions with inbred matings

⬇

Recessive deleterious mutations are exposed

⬇

and natural selection eliminates them
process: purging

# Objective

**To establish if the management that combines**
**Optimal contributions**
**Inbred matings**

**Improves viability in the long term and maintains diversity**

*Using a large number of markers (SNP) to calculate the coancestry*

# Simulations

- **Base population** (10000 generations with N= 1000)

  *Mutation-selection-drift equilibrium*

- **Genome: 20 chromosomes of 1M each**

  - **1000 selected loci/chromosome affecting viability**

    |         | aa | aA         | AA        |
    |---------|----|------------|-----------|
    | *fitness* | *1* | *1 − $h_i s_i$* | *1 − $s_i$* |

    *multiplicative fitness* $w = \Pi_i w_i$

  - **2000 neutral loci/chromosome**

    *used to measure diversity*

  - **1000 SNP/chromosome**
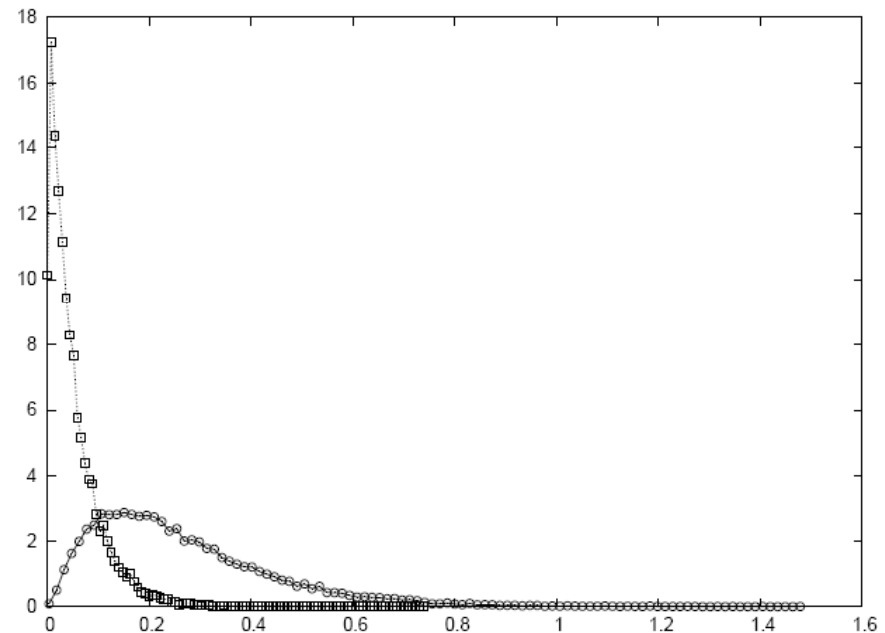
    *used in the genetic management*

# Simulations

- **Mutational models**
  - Mukai (↑ M ↓e)

    *Many mutations of small effect*

  - Caballero and García-Dorado (CGD) (↑m↓E )

    *Few mutations of large effect*



**Distribution of mutational effects**

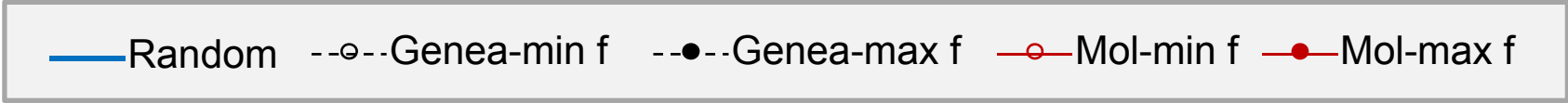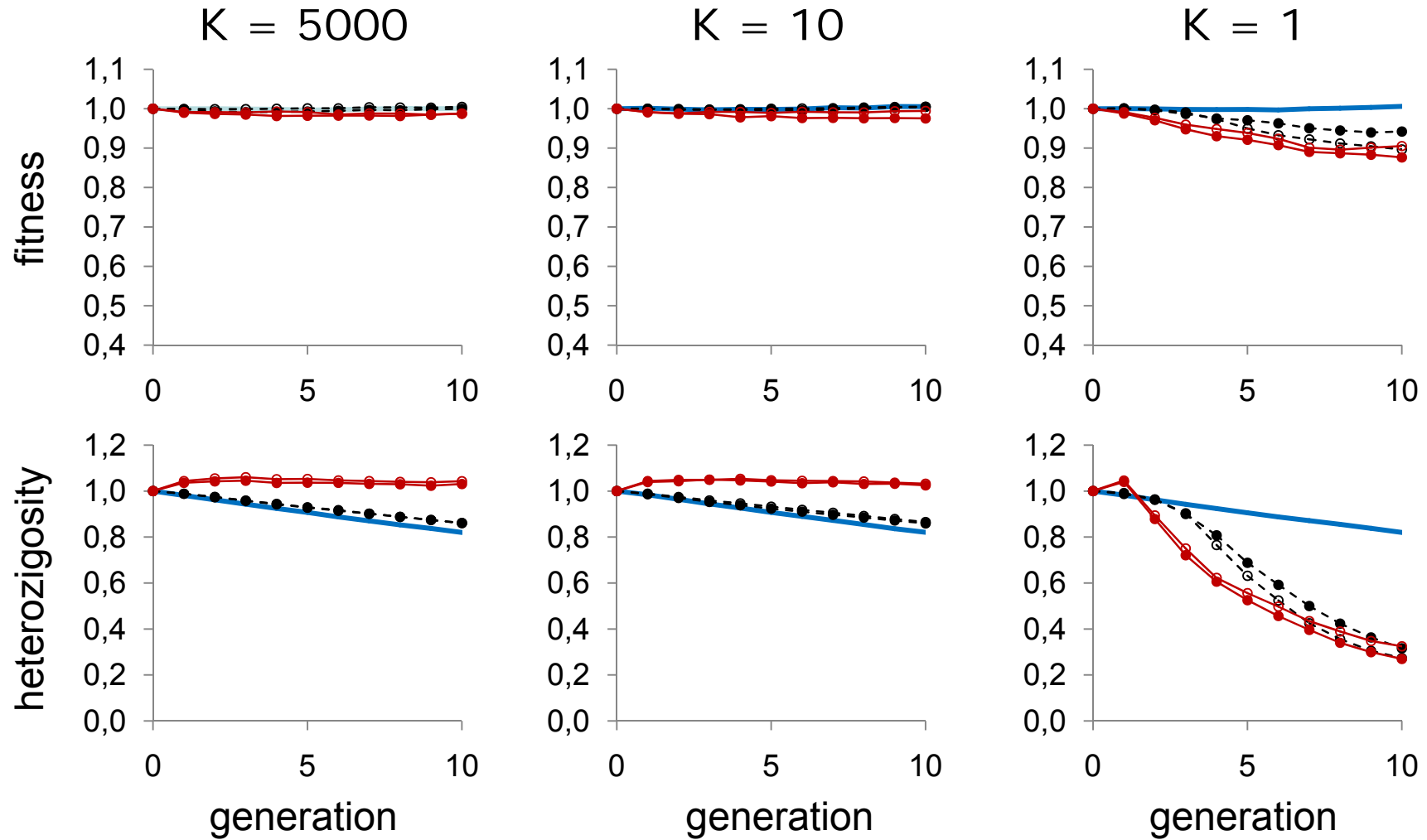| | $\lambda$ | $\bar{s}$ | $\beta$ | $\bar{h}$ |
|---|---|---|---|---|
| Mukai | 0.5 | 0.05 | 1 | 0.35 |
| CGD | 0.03 | 0.264 | 2.3 | 0.20 |

# Simulations

• Size of the managed population: 100

• 10 generations of management: Each generation:

**1.Decide optimal contributions using molecular coancestry ($f_M$) or genealogical coancestry ($f_G$)**

**2.Arrange matings of minimum or maximum coancestry with $f_M$ or $f_G$ or at random**

**3.Each mating pair attempts $K$ times to produce viable offspring (natural selection)**
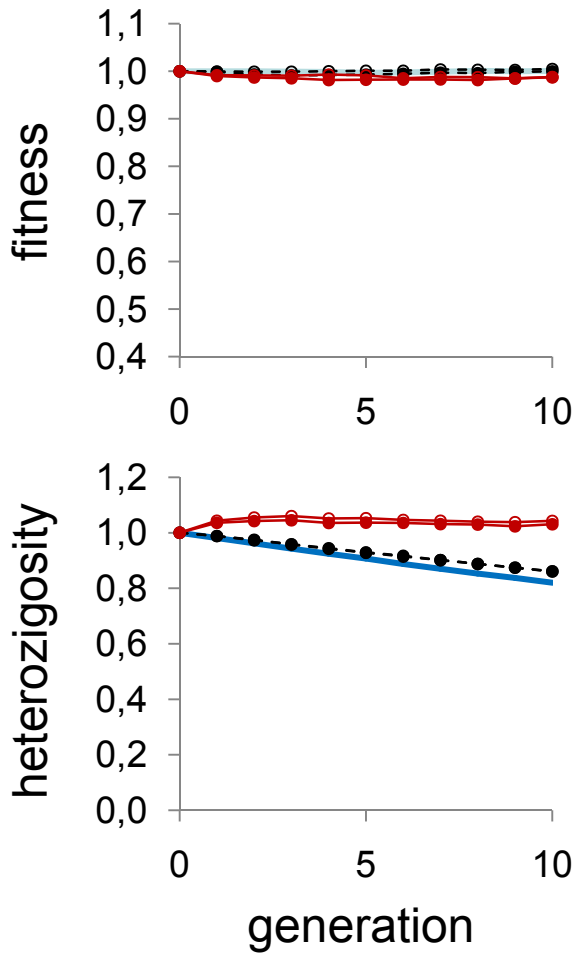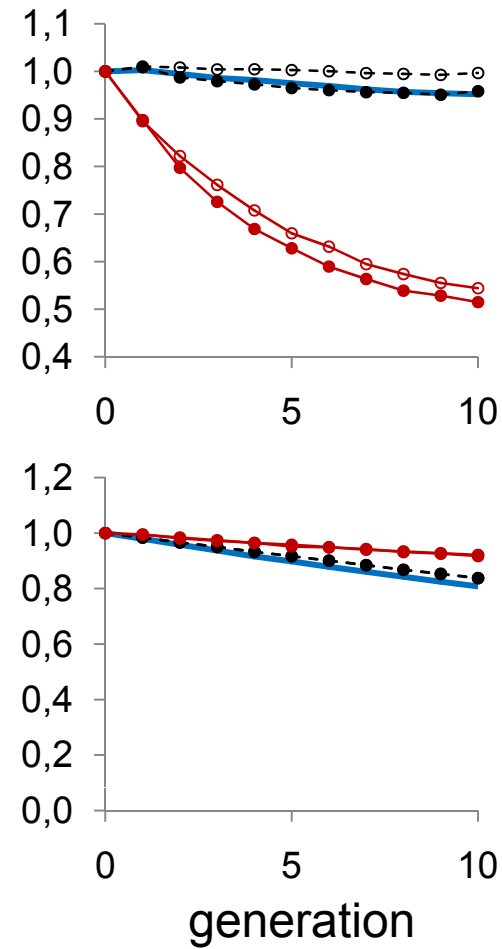
# Mutational model  ↓m↑E

## K = 5000

fitness

## K = 10

## K = 1

heterozigosity

generation

generation

generation

Random    ---○--- Genea-min f    ---●--- Genea-max f    —○— Mol-min f    —●— Mol-max f

# Compararison of mutational models K = 5000

↓m ↑E

↑M ↓e



Random ——— | Genea-min f --o-- | Genea-max f --•-- | Mol-min f —o— | Mol-max f —•—

# Conclusions

- **Mating schemes have low impact once contributions have been optimised**

- **Strong impact of mutational model and reproductive rate**

**Large $K$**

$\downarrow$**m**$\uparrow$**E**   **f mol** → *maintains more diversity than $f_G$ and same fitness*

$\uparrow$**M**$\downarrow$**e**   **f mol** → *more diversity than $f_G$ but less fitness*

**Small $K$**

**f mol** → *could maintains less diversity than $f_G$*

# Thanks