



# CONSERVATION OF GENETIC DIVERSITY WITHIN DOG BREEDS:

## *BREEDING PRACTICES AND THEIR IMPACTS*

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## *Genetic diversity and dog breeding, what are the issue?*

- A large number of dog breeds showing incredible variability in shape and morphologies
- By contrast, within a given breed, dogs are selected to fulfil a similarity to a standard (i.e. against genetic diversity).
- Decrease of genetic diversity may eventually impact health and welfare.
- About 551 inherited diseases identified in dogs (Nicholas 2011)

## *Some breeding practices, more or less specific of dog breeds*

- « **Popular sire** » **effect**, considered as one of the main cause of diffusion of inherited diseases in domestic animals

*The FCI (Federation Cynologique Internationale) recommend that no dog should have more offspring than equivalent to 5% of the number of puppies registered in the breed population during a five-year period.*

- **Close breeding**, i.e. mating between close relatives, is more or less common according to breeds

*The FCI consider that such mating should be avoided.*

**What are the consequences of those practices on genetic diversity and breed health ?**

## *Material & methods: simulation studies*

### **Simulated populations** (Leroy and Baumung 2011)

- 800 dams and 400 sires producing 800 litters of five puppies each, simulated over 25 discrete generations
- a single gene with two alleles, one of which being recessive and lethal (initial frequency of 2%)
- Closebreeding: 0%, 5%, 10% or 25% of mating between half-sibs
- Popular sire effect: a list of 40 sires producing 0%, 25%, 50% or 100% of litters

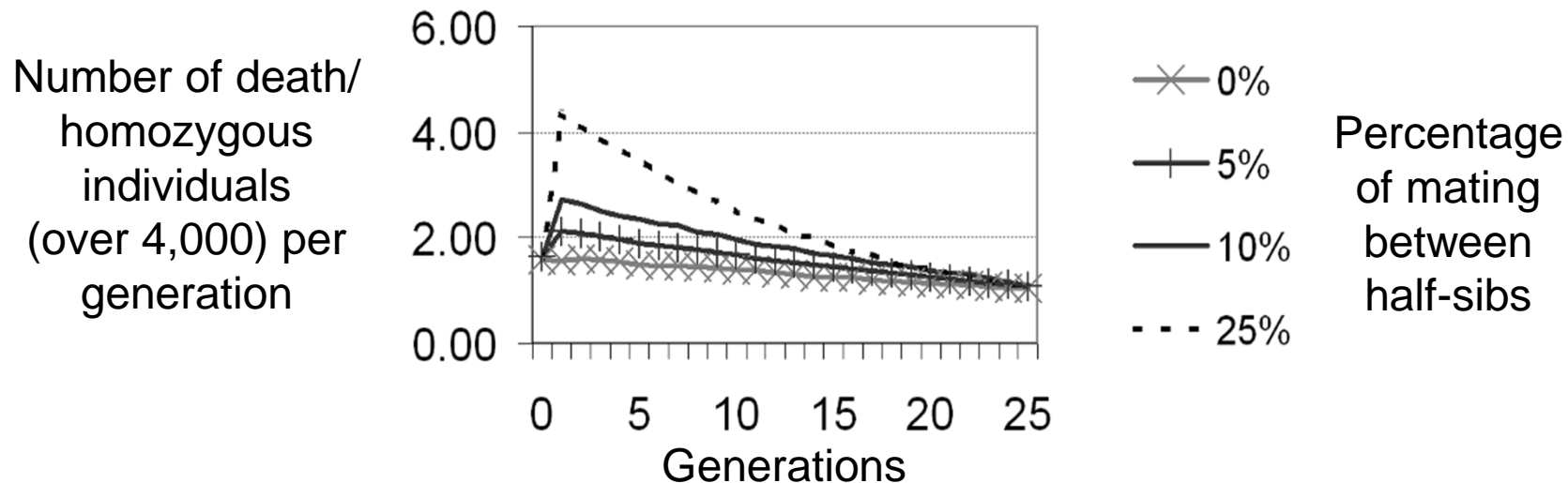
### **Modification of breed pedigree : the « what if » process**

(Leroy and Rognon 2012)

- Over 2001-2010 period, when a reproducer has exceeded the maximum number of offspring chosen (50, 100 or 200), it is not allowed to reproduce anymore.
- Random replacement of reproducers concerned

## II. Results

# *Impact of close breeding practices on health*



Evolution of average number of death/homozygous individuals per generation, according to proportion of mating between half sibs (Leroy and Baumung 2011)

- Increase of affected individuals proportional to the percentage of mating between half-sibs
- No impact on genetic diversity at the breed level
- Dissemination risk decrease related to inbreeding purge: the proportion of simulations where deleterious allele frequency reached 5% drops from 1.7% (in random mating), to 1.3% (5% of mating between close relatives).

## II. Results

# *Popular sire limitation and genetic diversity*

## *Simulations results*

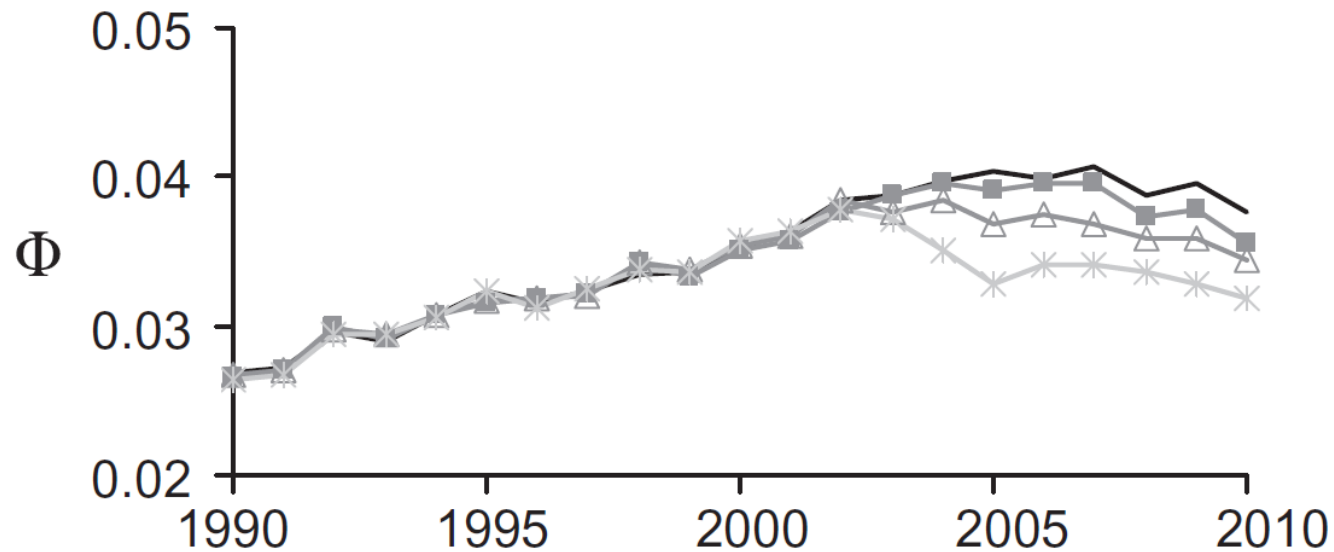
Impact of popular sire effect on the risk of dissemination of deleterious allele  
(Leroy and Baumung 2011)

<b>% of litters made by 40 « popular » sires</b>	<b>Effective number of sires</b>	<b>Dissemination risk: proportion of simulations where deleterious allele frequency reached 5%</b>
No popular sire	267	<b>1.7%</b>
25%	229	<b>2.3%</b>
50% ( <i>realistic conditions</i> )	122	<b>7.4%</b>
100%	38	<b>22.9%</b>

*Between random mating and realistic conditions, dissemination risk is multiplied by 4.4*

## II. Results

### *Popular sire limitation and genetic diversity* *“What if” procedure results*



— No limitation    —■— 200 offspring    —△— 100 offspring    —\*— 50 offspring

Evolution of average coancestry  $\Phi$  within the Coton de Tulear breed according to the limitation of offspring allowed per reproducers (Leroy and Rognon 2012)

*A limitation of offspring per reproducer may allow to limit the reduction of genetic diversity.*

# Applicability of FCI recommendations?

Impact of limitation of number of offspring per reproducer on average kinship

Breed	FCI threshold	Number of offspring per reproducer limited to		
		50	100	200
Braque Saint Germain	14	No impact	No impact	No impact
Berger des Pyrénées	182	-10%	No impact	No impact
Coton de Tulear	539	-15%	-8%	-6%
Epagneul Breton	1,366	-18%	-13%	-4%

Photo :  
SCC/Horvath



- In the small Braque Saint Germain breed, sires produce on average more offspring than the recommended threshold.
- In the other breeds, if the recommended threshold is chosen, no impact on genetic diversity.

*The threshold should be chosen according to the specific context of each breed.*



#### **Close breeding practice**

- It increases inbreeding depression and occurrence of genetic disorders at the individual level.
- It reduces the risk of disease disorder dissemination and increases inbreeding purge, at the population level.

*Further investigation on “inbreeding purge” effect is required.*

*Due to animal welfare concerns in balance, it should not be recommended for breeders.*

#### **« Popular sire » effect through offspring threshold**

- To have an impact on coancestry increase and on the dissemination risk, the threshold must be quite low (under 200).
- Threshold specific of context of each breed can be chosen according to “what if” procedure.

*Procedure can also be adapted to take into account breeding strategies against inherited diseases.*

*Some factors were not taken into account (non-random replacement of reproducers...).*

## *Conclusion*

- **« What if » procedure may constitute an interesting diagnosis tool for breed clubs interested to apply simple breeding programs.**
- **Some more efficient breeding schemes (minimizing coancestry for instance) may also be implemented.**

*It is however important to propose breeding plans that are not too binding for breeders*

- **Need to take account other traits to be selected, in particular related to dog health**

# Questions?

