



# Differentiation of allelic frequencies analysis identifies short genomic regions with signatures of artificial selection between canine breeds

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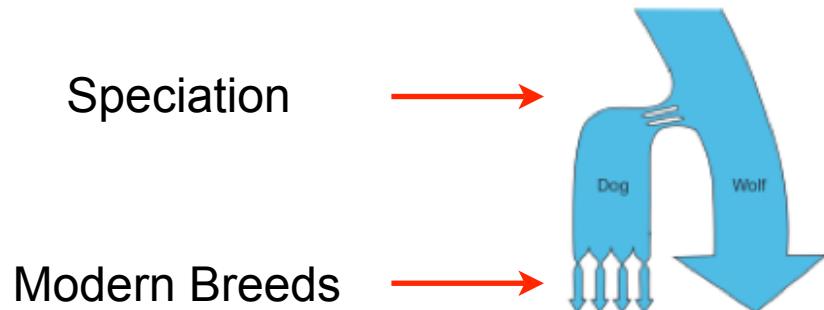
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# Canine model

- Domestication ~15 000 years



- Breeds creation ~200 years by artificial selection

350 inbred breeds / genetic isolates

Inter-breed diversity / intra-breed homogeneity

- Footprints on dog genome



# **Aim : Identify genetic signatures of artificial selection leading to breeds creation**

- 1- Breeds specific genetic selection signatures
- 2- Shared selection signatures
- 3- Do artificial selection signatures intersect natural evolution signature ?



## **Experimental data : acquired for the study**

- 174,570 SNP (Illumina whole-genome Array)
- 473 dogs (10 to 26 individuals per breed)
- 31 breeds (Shar Pei, Dachshund, Terrier Yorkshire, German Shepherd ... )

## **Principle : Inter-breeds changes in allele frequencies**

Compare breeds with Wright's population differentiation statistic Fst

$$F_{ST} = \frac{\Pi_{\text{Between}} - \Pi_{\text{Within}}}{\Pi_{\text{Between}}}$$

# Analysis pipeline (poster N°25)

**170K Fst x 465  
breed pair**

SNP_Id	chr	pos	Rtw_Wei	Rtw_TYo	Rtw_Ter	Rtw_ShP	Rtw_Sci	...
BICF2P1282632	1	3573121	0.01676	0.10578	0	0	0.10601	...

**Normalization**

$$\frac{F_{st} - \mu}{\sigma}$$

SNP_Id	chr	pos	Rtw_Wei	Rtw_TYo	Rtw_Ter	Rtw_ShP	Rtw_Sci	...
BICF2P1282632	1	3573121	-0.7076	-0.2153	-0.6625	-0.5322	-0.2679	...

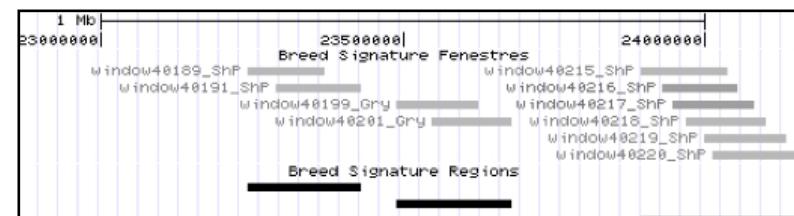
**Sum of normalized Fst for each breed (=di)**

SNP_Id	chr	pos	Rtw	Bet	BMD	BoT	BrS	...
BICF2P1282632	1	3573121	-11.7	16.59	-19.3	-10.3	-13.8	...

**Mean of di over 150Kb windows with a 25 kb sliding step**

window	chr	Gry	Gsh	IrW	ShP	StP	TYo	...
40189	13	29.12	8.12	9.24	35.44*	9.54	-2.166	...
40190	13	32.25	5.30	11.48	41.44*	12.31	-1.871	...

**Selection of windows with mean di > 95<sup>th</sup> percentile of the breed di**



**Fusion of overlapping windows in candidate region of artificial selection**

# Results

- 1) Each breed has **40** (*mean*) specific regions [sizes **175** Kb -*mean-*]  
→ Less **1%** of the genome of a breed is detected
- 2) Each breed share **50** candidate region with at least one other breed.  
(ex. Body size, coat-type)
- 3) **1865** candidate regions of selection - **13%** of the canine genome
- 4) Gene content of the 1865 candidate regions of selection :
  - 1293 regions contain **3053** protein coding genes (~2 genes/region)
  - 441 regions contain no genes
  - **61** genes-variants are specific for each breed

# Results validation

## The Shar-pei sin-wrinkle coat-type

**HAS2** :Chr13:23.3 Mb  
(Akey et al. PNAS 2010)

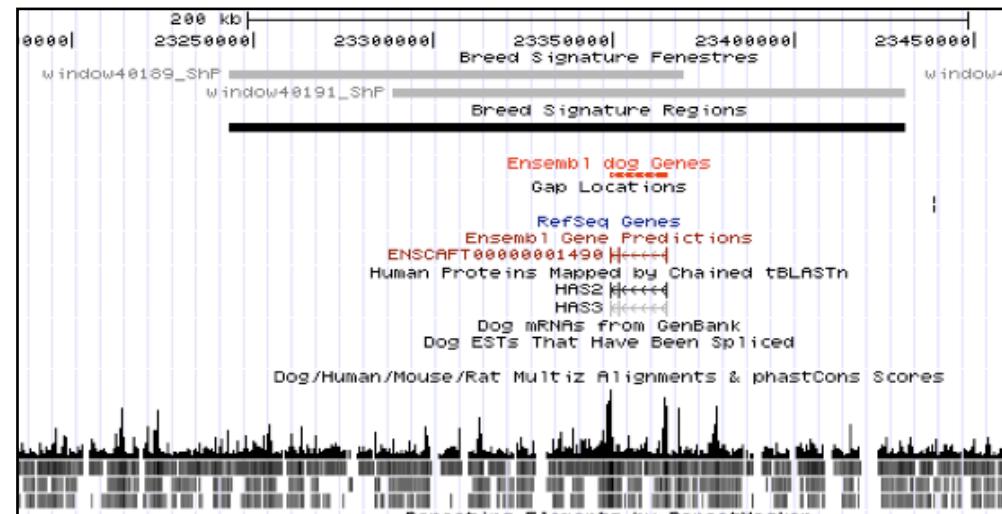


## Fst-di approach :

Region size = **126 kb** chr13:23.3Mb

One breed identified : ShP

Only one gene in the region : **HAS2**



- **Chondrodysplasia**: Chr18:23.4 Mb

- **Body size** : Chr15:44.2 Mb

- **Coat-type** : Chr13:23.1 Mb

**(poster N°25)**

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## Conclusions

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- 1) Pipeline for whole genome allelic differentiation
- 2) Less **1%** of the genome of a given breed is detected
- 3) **1865** candidate regions **13%** of the canine genome is detected

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## Directions

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- 1) Test for false positive
- 2) Integrate with other metrics for selection (XP-EHH; Rel-Het)

collaboration with Kerstin Lindblad-Toh - Matthew Webster (Uppsala University)

- 3) Compare with natural selection signals  
(dN/dS of 10,000 orthologous genes)

collaboration with Hugues Roest Crollius (DYOGEN team at the ENS Paris)



- 4) Identify the phenotypes under selection

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