Inbreeding and genomic runs of homozygosity in Vietnamese local chickens

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Introduction

Most researches on genetic variety evaluation in Vietnamese local chicken breeds have been based up to now on microsatellite markers (Cuc et al., 2011; Pham et al., 2013). Thanks to the genotyping of ~580,000 SNPs on 95 chickens, this study aimed to assess the genetic diversity in four Vietnamese local breeds (Mia, Mong, Ho and Dong Tao). Inbreeding was examined through the detection of runs of homozygosity (ROH; Curik et al., 2014). The ROHs are long stretches of homozygous genome that are likely to reflect autozygosity.

Method

95 individuals

4 breeds: Dong Tao, Ho, Mia and Mong

Selection of SNPs:

• Exclusion of SNPs that failed an exact test of Hardy-Weinberg equilibrium in each breed separately

• Linkage disequilibrium pruning

Table 1: Number of SNPs used in each breed.

Breeds	SNPs	Sample
Ho	97 440	27
Dong Tao	152 687	32
Mong	167 804	18
Mia	267 636	18

Detection criterion of ROH:

• Window of 5000 kb (50 SNPs)

• Minimum length of a ROH = 300kb

• 1 heterozygous call per window

• 5 missing calls per window

Inbreeding coefficient:

$$F_{ROH} = \sum L_{ROH} / L_{AUTOSOME}$$

where $\sum L_{ROH}$ is the total length of all ROH in the genome of an individual and $L_{AUTOSOME}$ is the length of the autosomal genome covered by SNPs

Results

Inbreeding coefficient (see figure 1):

• High variation across the breeds ($\chi^2(3)=25.6$, P<0.0001).

• Mia chickens: lower F_{ROH} covering only, in means, 2.6 % of the autosomes.

Subdivision of ROHs into different lengths (see Table 2) :

• ROH < 1Mb: present in all individuals.

• ROH > 2.5Mb: low frequency in Mia chickens.

• ROH > 5Mb: common in Ho chickens.

Table 2: Percentage of individuals having at least one ROH according to four length of category.

	< 1Mb	1-2.5 Mb	2.5-5 Mb	> 5Mb
Dong Tao	100	96.87	84.37	31.25
Ho	100	96.30	85.18	62.96
Mia	100	94.44	44.44	33.33
Mong	100	94.44	83.33	44.44

$\Rightarrow$**Ho chickens: consanguinity ↗**

$\Rightarrow$**Mia chickens: consanguinity ↘**

Total length of long ROHs (> 5Mb):

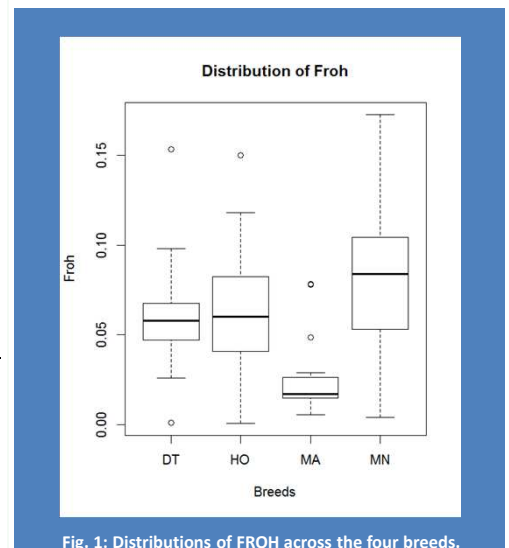No significant difference between the four breeds.

Fig. 1: Distributions of FROH across the four breeds.

Individuals variation (see figure 2):

• Clustered by breed.

• Ho and Mong chickens: Large inter-individuals variations .

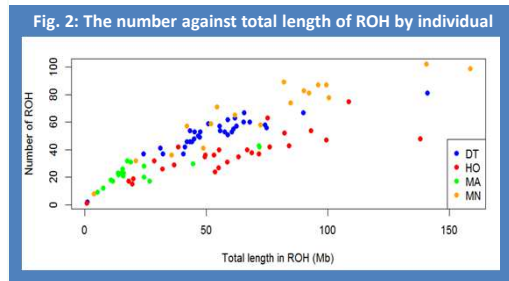• In each breed: Individuals with high consanguinity (= to the right with respect to their cluster).

Fig. 2: The number against total length of ROH by individual

Conclusion

Given that Ho chickens have a small effective population size, more inbreeding and consequently longer ROHs are expected. Conversely, Mia chickens, with a larger effective population size should show less consanguinity and shorter ROHs. As expected, Mia chickens led to less ROHs than the three other breeds and Ho chickens reported more long ROHs.

In conclusion, the analysis of ROHs reported less consanguinity in Mia than in Ho chickens. In each breed, some individuals are found more consanguineous than expected. This study also confirms that ROHs are a useful tool in inbreeding research.

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