

Assessment of runs of homozygosity and estimates of inbreeding in three purebred turkey (*Meleagris gallopavo*) lines



Sarah M. Adams¹, Martijn F.L. Derks², Bayode O. Makanjuola¹, Ben J. Wood^{1,3,4}, and Christine F. Baes^{1,5}

¹Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, Ontario, N1G 2W1, Canada; ²Animal Breeding and Genomics, Wageningen University and Research, 6700 AH, Wageningen, The Netherlands; ³Hybrid Turkeys, A Hendrix Genetics Company, Kitchener, Ontario, N2K 3S2, Canada; ⁴School of Veterinary Science, The University of Queensland, Brisbane, QLD, 4072 Australia; ⁵Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, 3001, Switzerland

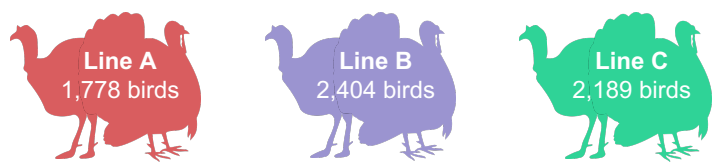
Background

- Runs of homozygosity (ROH) are continuous stretches of homozygous genotypes and can be used to characterize genomic data
- ROH are correlated with other measures of inbreeding and can provide a more accurate estimation of individual autozygosity

Objectives

1. Describe ROH in the turkey genome
2. Estimate and compare pedigree based inbreeding (F_{PED}) with genomic estimates based on ROH (F_{ROH}) and the genomic relationship matrix (F_{GRM})

Materials and Methods



ROH detected using R package “detectRUNS”

- Minimum 50 SNP and 1 Mb in length
- No missing or heterozygous genotypes
- Maximum gap between consecutive SNP: 1 Mb

Results

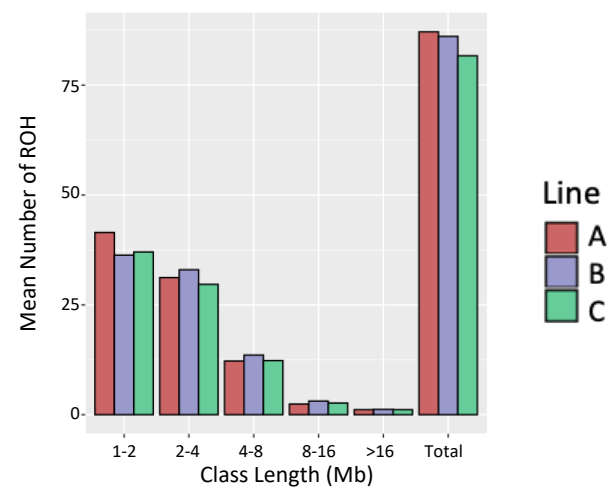


Figure 1. Mean number of ROH per animal for each class length.

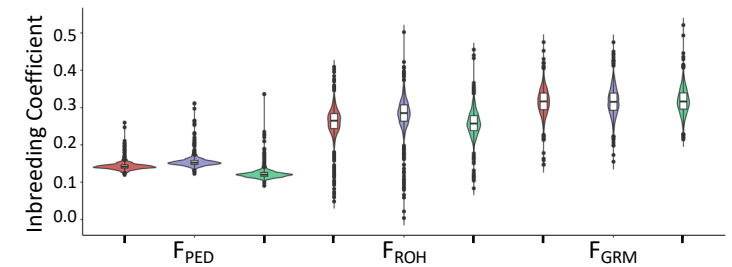


Figure 2. Distribution for inbreeding coefficients ($F_{PED}=0.14$, $F_{ROH}=0.27$, and $F_{GRM}=0.32$).

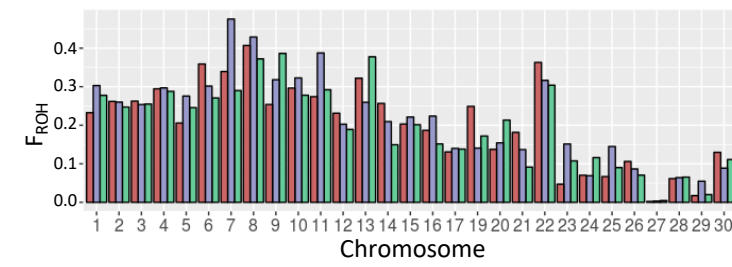


Figure 3. Mean percent coverage of ROH per chromosome.

	Line A			Line B			Line C		
	F_{ROH}	F_{GRM}	F_{PED}	F_{ROH}	F_{GRM}	F_{PED}	F_{ROH}	F_{GRM}	F_{PED}
F_{PED}	0.19	0.17	1.0	0.24	0.21	1.0	0.31	0.30	1.0
F_{GRM}	0.68	1.0		0.69	1.0		0.73	1.0	
F_{ROH}	1.0			1.0			1.0		

Figure 4. Correlation coefficients of inbreeding coefficients for three turkey lines.

Conclusions

- ROH did not cluster on specific chromosomes
- F_{ROH} and F_{GRM} were greater than F_{PED} with low to moderate correlations between respective inbreeding coefficients
- Incorporation of ROH based inbreeding measures in breeding programs will allow for closer monitoring of inbreeding levels and maintenance of genetic diversity in turkey populations

Acknowledgements: This study was conducted as part of the project entitled ‘Application of genomic selection in turkeys for health, welfare, efficiency, and production traits’ funded by the government of Canada through the Genome Canada Genomic Application Partnership Program and administered by Ontario Genomics (recipients: C.F. Baes (Academic), B.J. Wood (Industry)). This study was also financially supported by Hybrid Turkeys (Kitchener, Canada).

