

Genomic information on X-chromosome: assessing the imputation accuracy

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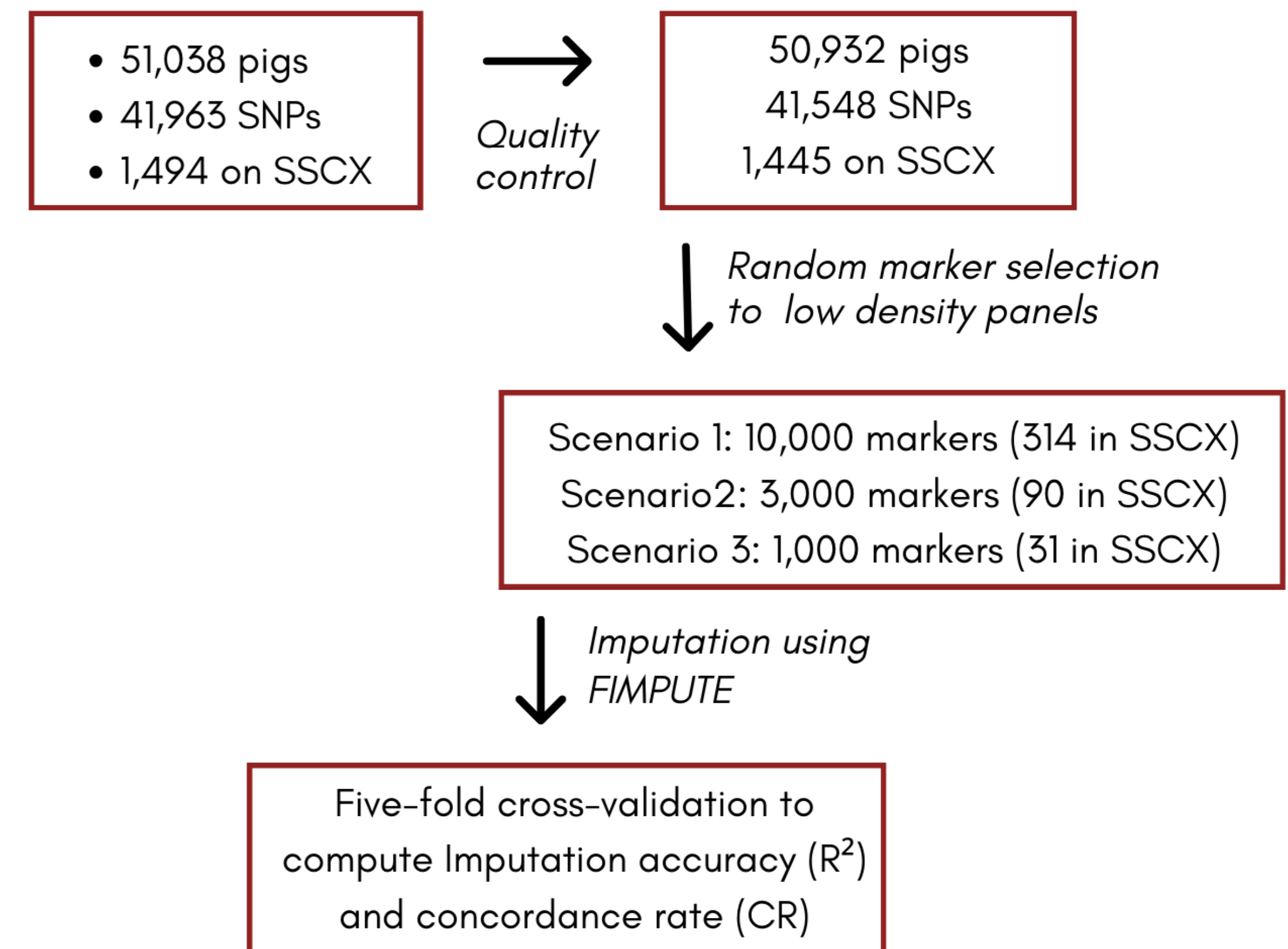
INTRODUCTION

- X chromosome (SSCX) is often overlooked in genomic predictions
- It may have important contributions to genetic variance
- Using SSCX information in genomic predictions may increase the breeding value accuracy
- Imputation is a crucial step in breeding values prediction
- Pseudoautosomal and non-pseudoautosomal regions may be challenging for imputation

OBJECTIVE

Investigate the imputation accuracy and concordance rate in chromosome X in different low-density SNP scenarios

MATERIAL AND METHODS



RESULTS AND DISCUSSION

Table 1. Imputation accuracy (R^2) and concordance rate (CR) from different scenarios for all chromosomes, autosomes, and X chromosome

Scenarios		All chromosomes	Autosomes	X-Chromosome
1	R^2	0.98126	0.9851	0.9872
	CR	0.99468	0.9958	0.9975
2	R^2	0.94582	0.95014	0.9276
	CR	0.98296	0.9840	0.9864
3	R^2	0.83584	0.84185	0.7760
	CR	0.94618	0.9471	0.9562

- Imputation accuracy and CR increased with the number of SNPs in the low density panel for the autosomes and SSCX
- The SSCX accuracies were lower than the accuracies in autosomes when using 1,000 and 3,000
- Lower R^2 and CR at the beginning and the end of CHR X in 1,000 and 3,000 scenarios, compared to the mid-region of CHR X
- Accuracy and CR trends across minor allele frequency (MAF) were similar for autosomes and CHR X

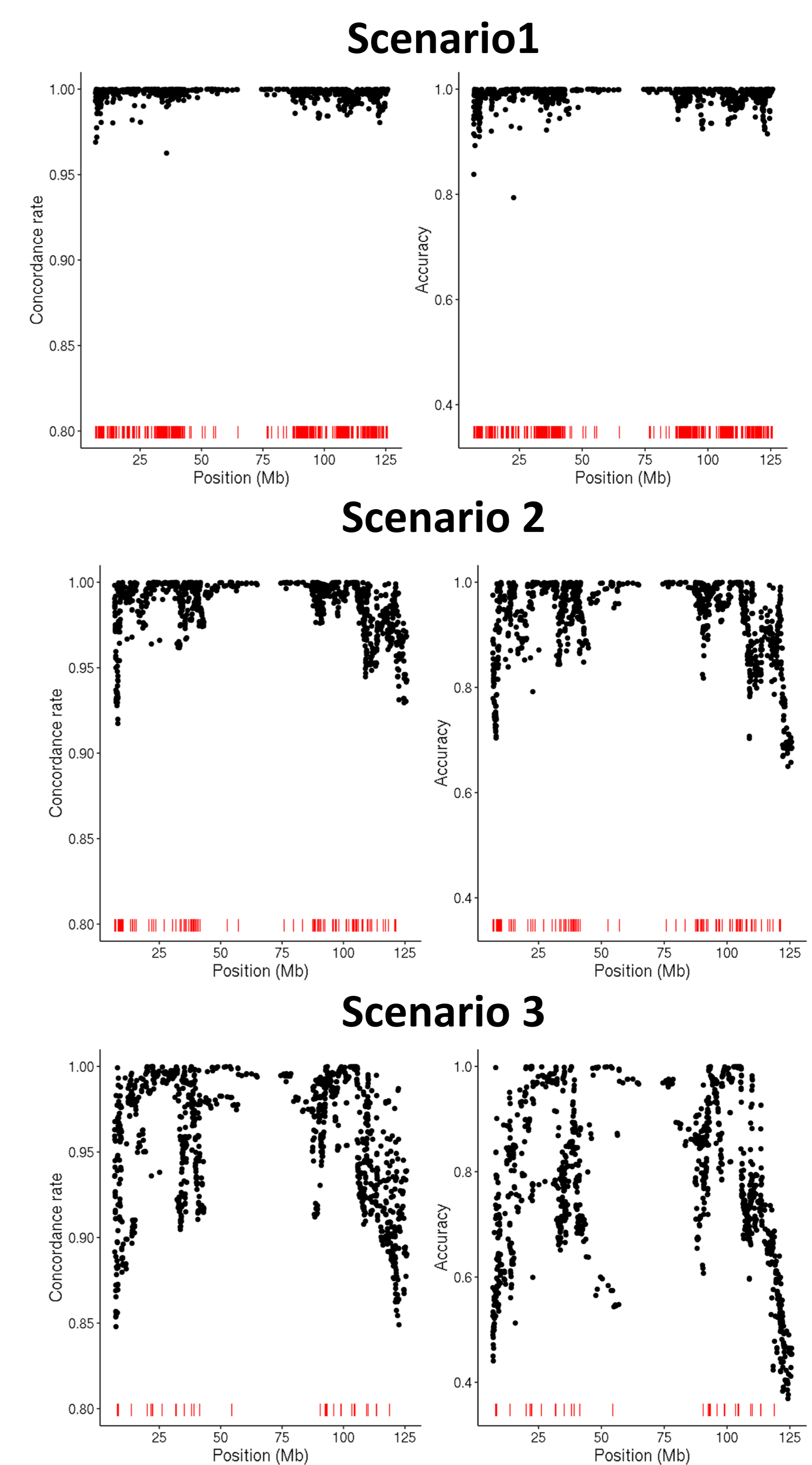


Figure 1. Concordance rate and imputation accuracy by X chromosome position with marker position highlighted in

CONCLUSION

Overall, imputing SNPs in CHR X is practical. Different LD panels should be tested to establish the minimum number of markers to ensure accurate imputation

ACKNOWLEDGEMENTS

This work was supported by Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES) and the Pig Improvement Company