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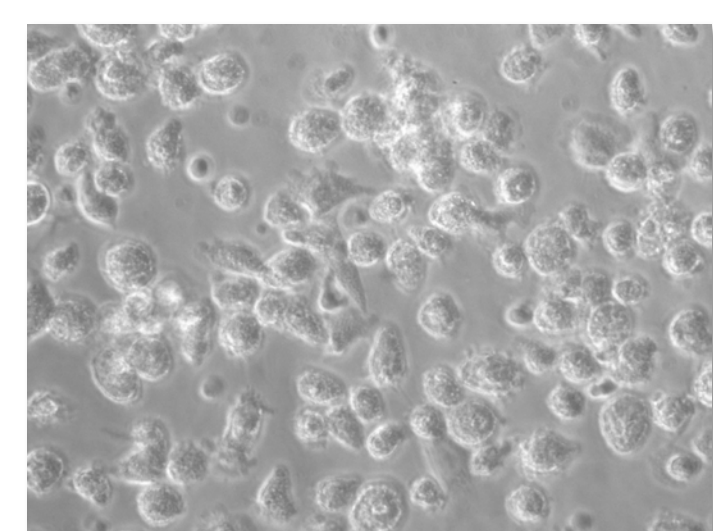
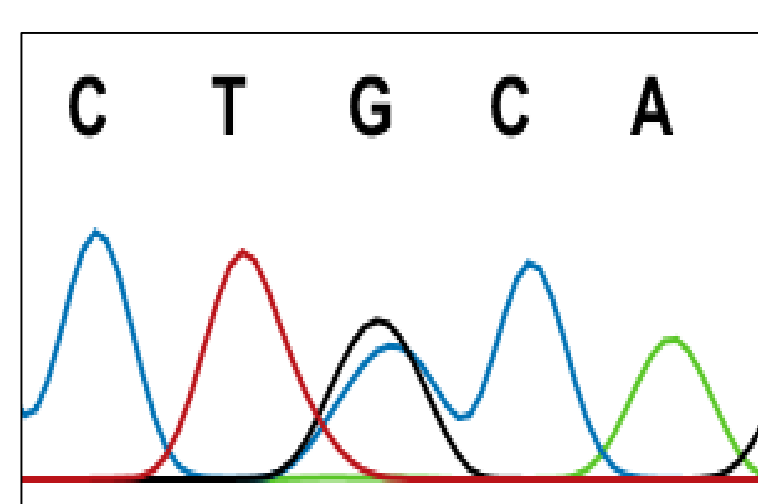
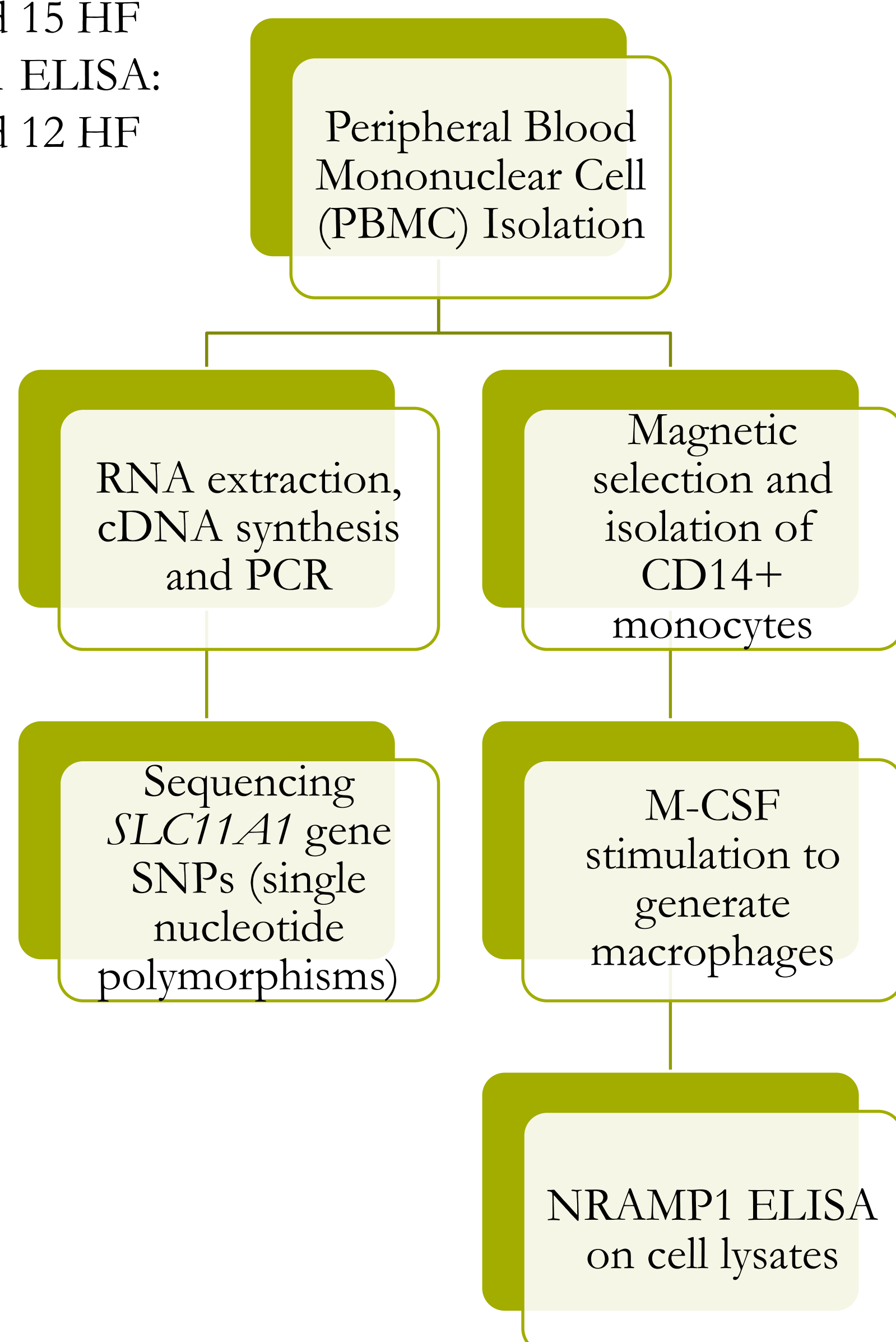
Background

- Bovine Tuberculosis (bTB) is caused by *Mycobacterium bovis*.
- Cattle breeds show varying incidence of bTB susceptibility [1].
- Brown Swiss (BS) cattle show more resistant responses to intracellular bacteria compared to Holstein Friesians (HF)^[2], and therefore maybe more resistant to bTB.
- The solute carrier family 11 member 1 (*SLC11A1*) gene encodes for natural resistance-associated macrophage protein 1 (NRAMP1) which confers resistance against intracellular bacteria such as *M. bovis*^[4,5,6].
- **Study aims:** to compare *SLC11A1* polymorphisms between HF and BS cattle and assess how these impact NRAMP1 protein expression.



Methods

- Study population:**
- SLC11A1 sequencing: 15 BS and 15 HF
 - NRAMP1 ELISA: 11 BS and 12 HF



Results

Genetic Analysis

Three non-synonymous SNPs were identified in the *SLC11A1* gene.

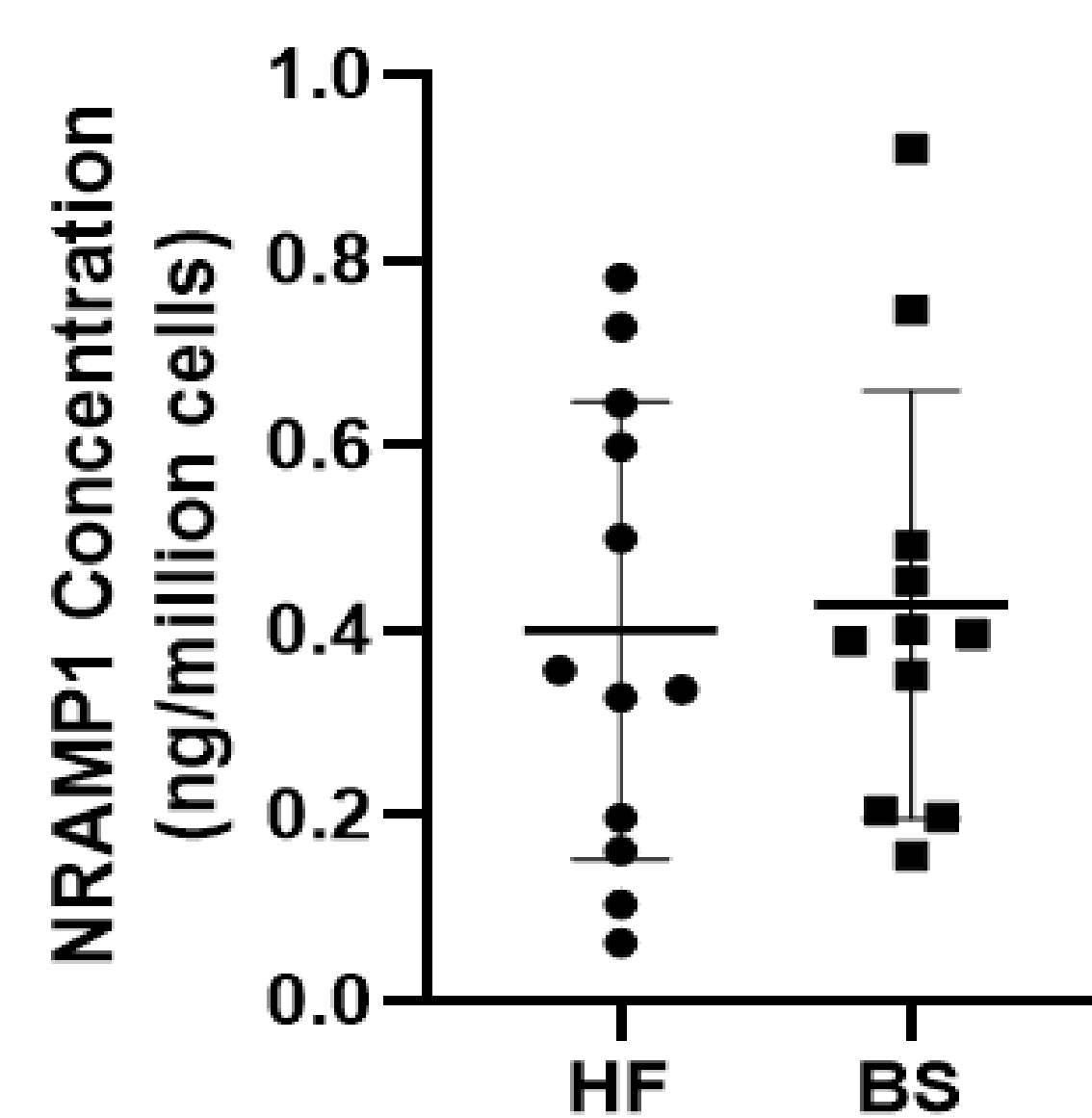
- SNP1 c.650C>T
- SNP2 c.961G>A
- SNP3 c.1066C>G

SNP1 and SNP2 were present at very low frequencies (<10%) in both HF and BS cattle.

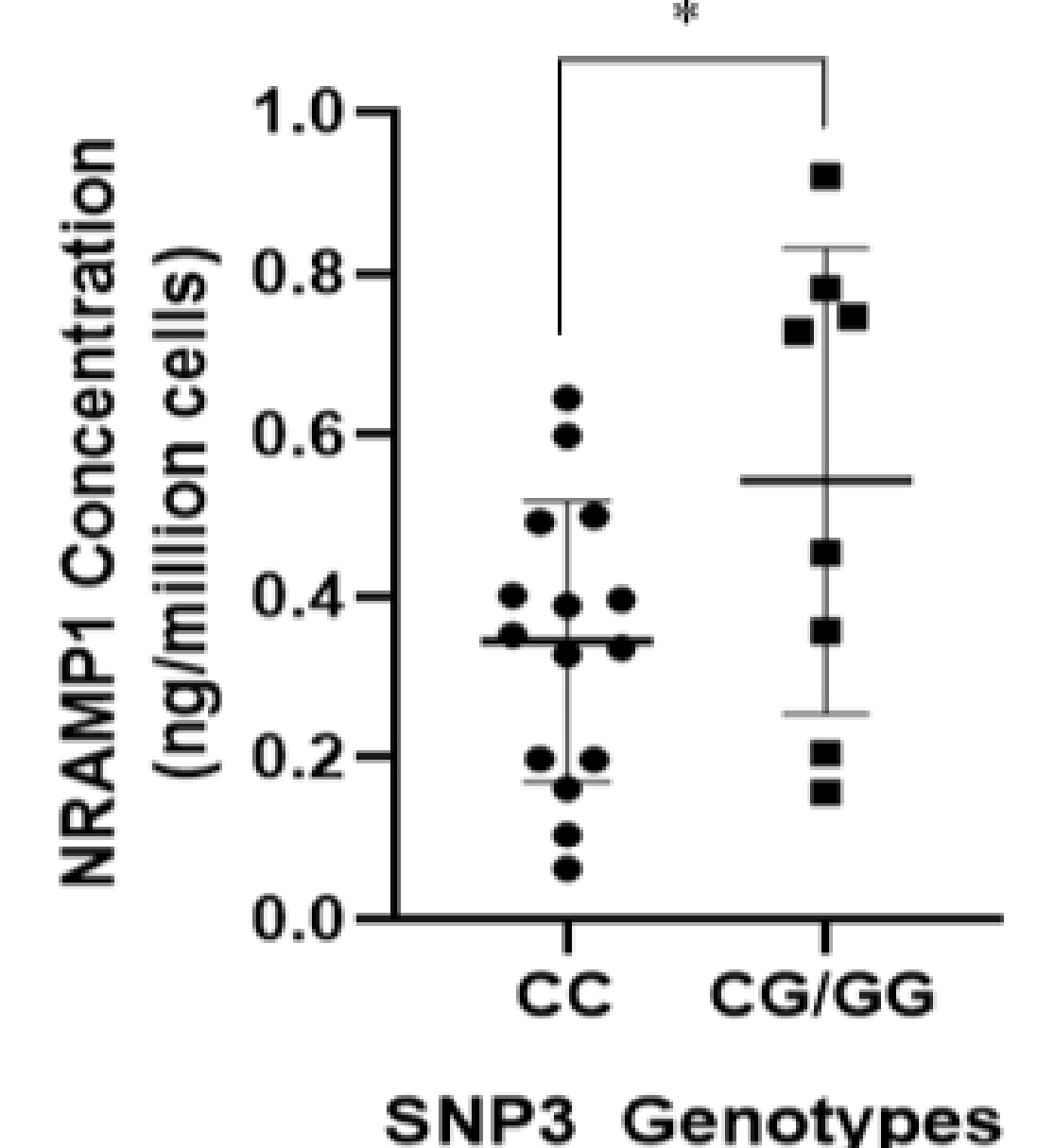
For SNP3 the alternative G allele was present at a higher frequency in BS (30%) compared to HF (13%), but this was not significant.



NRAMP1 ELISA



Macrophages from HF and BS do not produce significantly different amounts of NRAMP1 protein.



Macrophages from cattle which are CG/GG at SNP3 produce significantly more NRAMP1 protein (p=0.0496) compared to those which are the CC genotype.

Conclusions

- Breed did not appear to influence *SLC11A1* genotype or macrophage NRAMP1 protein production.
- The presence of the alternative G allele at SNP3 (c.1066C>G) was significantly associated with higher amounts of NRAMP1 protein expression in macrophages.
- NRAMP1 has previously been shown to play a vital role in innate immune responses against intracellular pathogens^[7].
- Therefore, the presence of the G allele at SNP3 (c.1066C>G) could influence resistance to bTB.
- Further studies with larger animal populations are necessary to confirm our findings
- If confirmed, these findings could be considered for incorporation into cattle breeding programmes seeking to breed cattle resistance to bTB

References

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