

Genome Wide Association Study and Factors affecting Semen Volume and Concentration in Ethiopian Dairy Bulls

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Introduction

Dairy producers are demanding to the most fertile bull/semen. Selection of mature bulls to be sire of many progenies is practiced based on the phenotypic information of semen quality parameters. Semen quality traits are complex traits controlled by genetic and environmental factors. Therefore, the aim of the study was to evaluate the effect of breed, ejaculation number, origin of bulls, age, and artificial insemination centers and perform genome wide association underlying semen volume and concentration.

Methods

- Retrospective data collected from five AI centers
- 66 bulls genotyped using the Illumina BovineSNP50 BeadChip.
- Covariate adjusted: Breed (HF= Holstein Friesian, JE= Jersey, & FFB= Holstein Friesian Borena cross), AI center (AIC, five centers), origin (seven origins), number of insemination (NE) and age ((<2, 2 to 3, 3 to 4, 4 to 5, and >5 years) for volume & concentration.

- Mixed model used to estimate additive effects of SNP:

$$\hat{\alpha} = X^*b + Z^*g + e^*$$

- Significance tested ($H_0: g_i = 0$ vs. $H_1: g_i \neq 0$, where H is the hypothesis) of i^{th} SNP effects in g , the Wald test (W)

Results

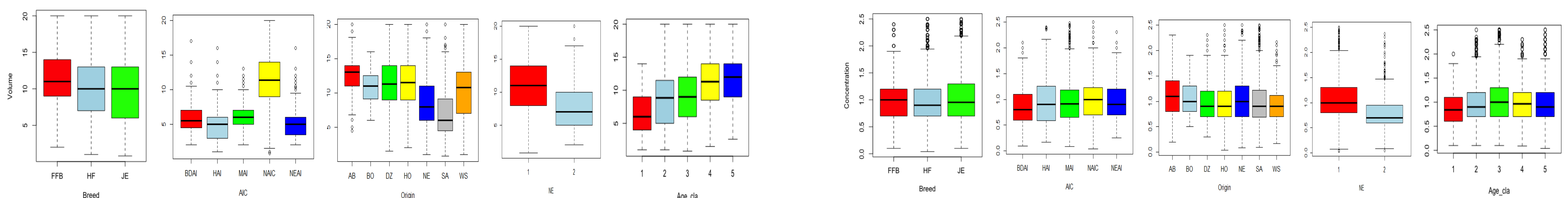
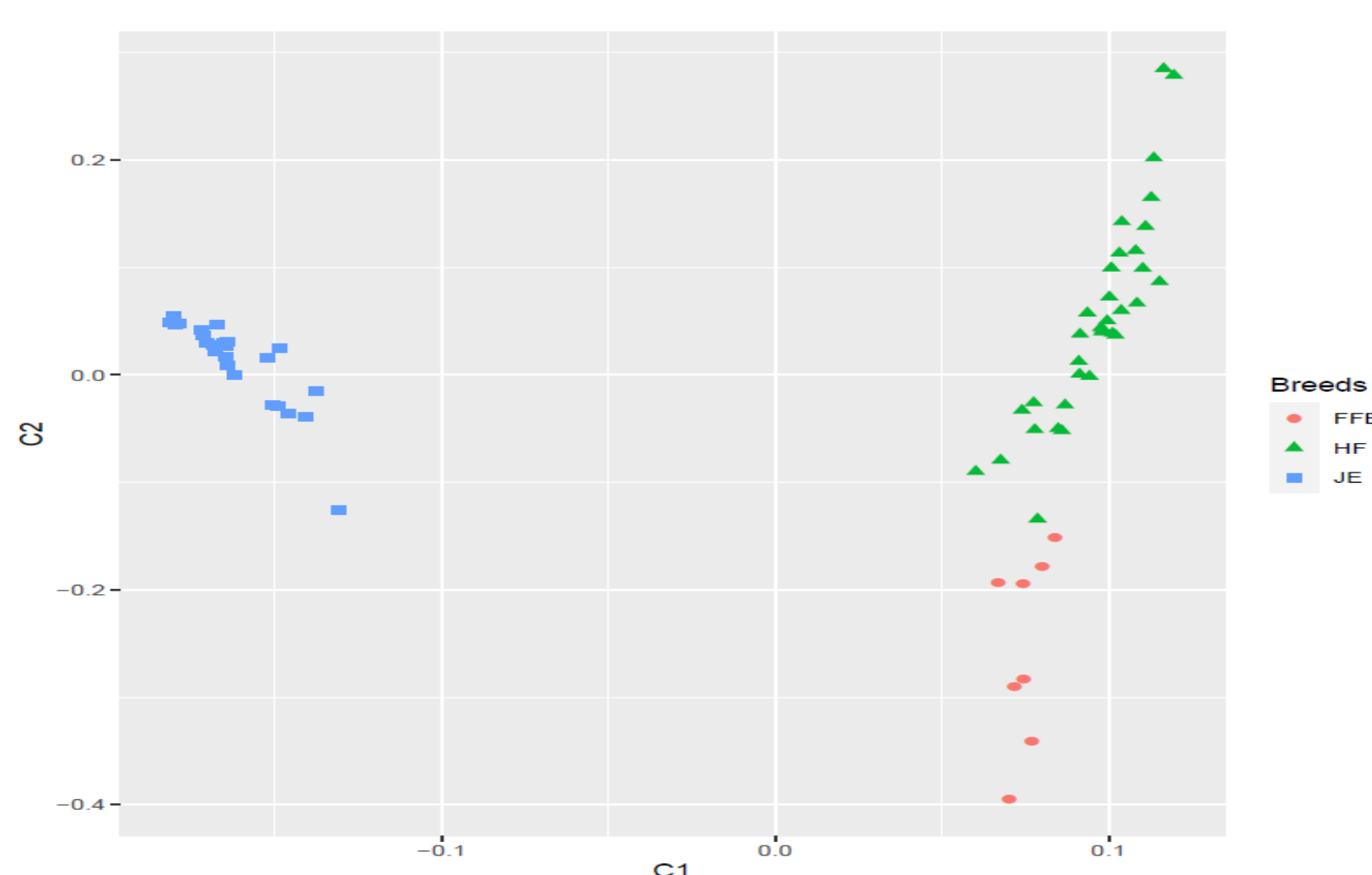


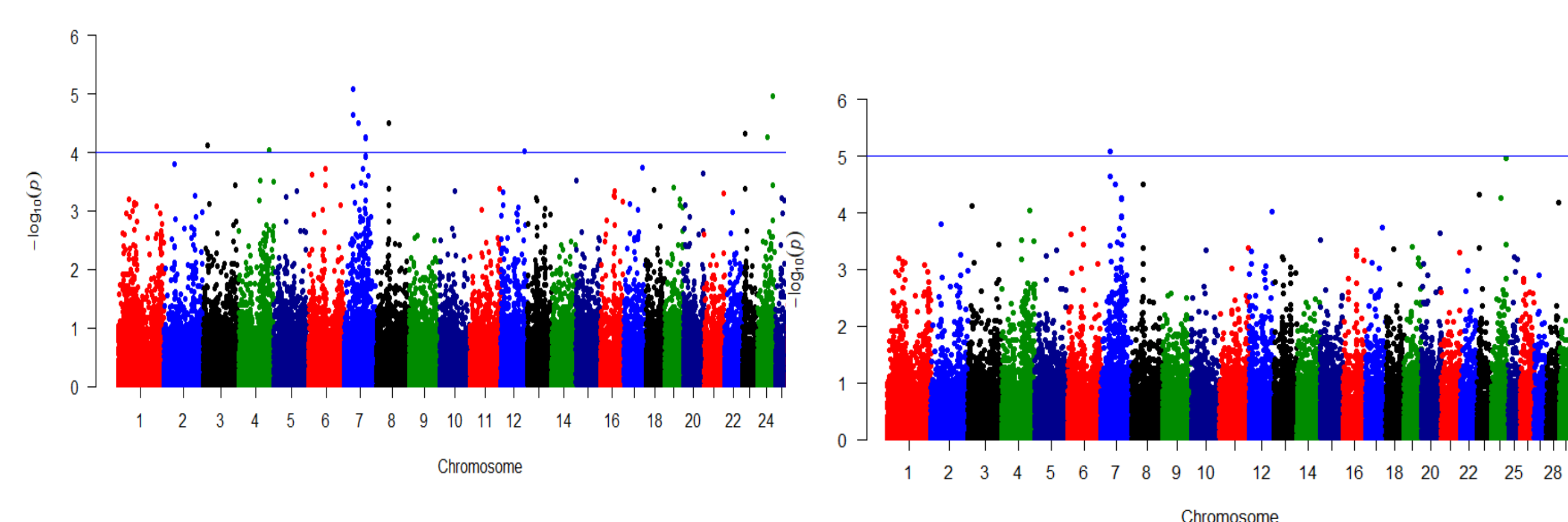
Figure 1. Effects of fixed factors on sperm volume and concentration

Sperm volume and concentration are affected significantly ($p < 0.001$) by breed, artificial insemination, origin, number of ejaculations and age of the bulls.

Principal component analysis



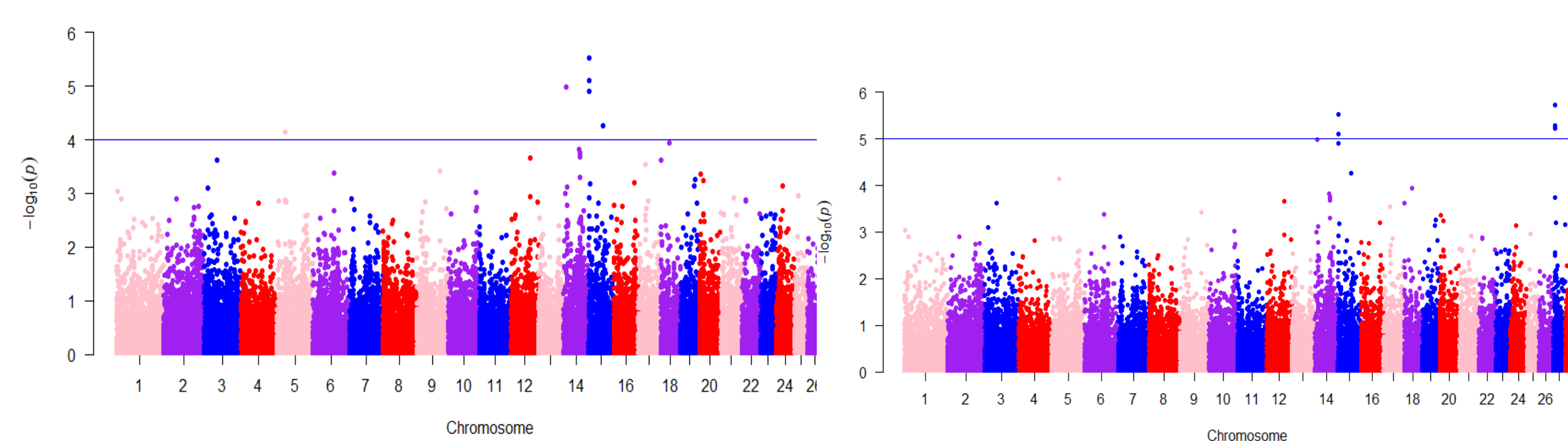
SNP association with sperm volume



Significant SNP,
-Log₁₀ P value > 5

rs134410301 7:32579149

SNP association with sperm Concentration



rs109814724 15:3264476
rs110956165 15:3276723
rs136532513 27:7091908
rs109497662 27:7125956
rs110788394 27:6955584

Conclusion: Identifying significantly associated SNPs with sperm quality traits helps to select candidate bulls for AI centers and decision could be made at early age.

ESAP Conference, October 28-30, 2021, Addis Ababa, Ethiopia