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Genomics of boar semen quality traits in U.S. Large White and Duroc breeds

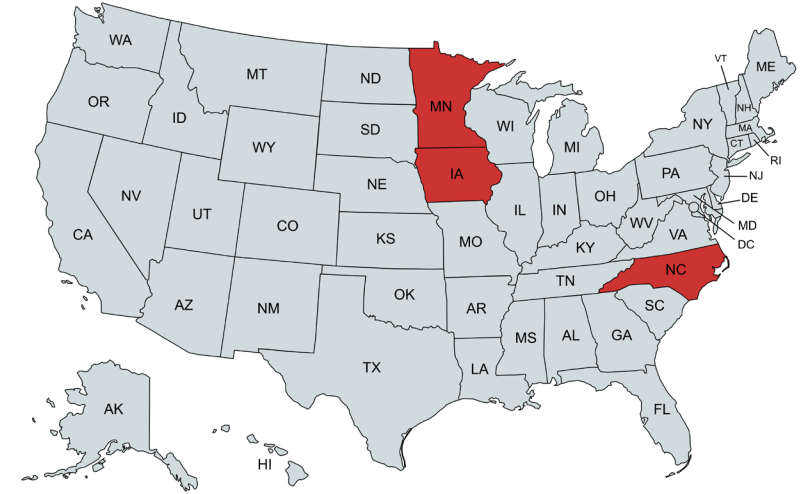
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Introduction

- Pig meat sector is US **major source of income** in livestock sector (worth 178 billion \$ in 2021)
- **Production system shifting** from farrow-to-finish to greater specialization (feeder pig producers and feeder pig finishers)
- **Decreasing trend** in farm number (-70% since 1990) while **increasing** farm size (61% of farms rear 5000+ heads)
- In 2021, 70 millions heads in 60,000 farms, with **total meat production** of 12.5 million tons (23 kg consumption/capita)



Introduction

- Profitability is driven by **excellent productive and reproductive efficiency**, which are commonly included in breeding objectives
- Small attention placed in **semen quality traits selection**, yet economically advantageous coupled with AI technologies (Gonzalez-Pena et al., 2016)

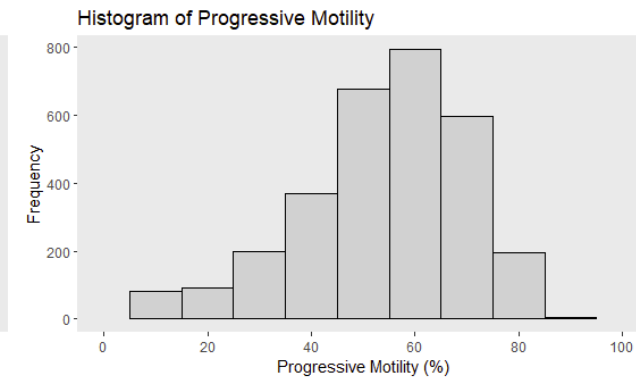
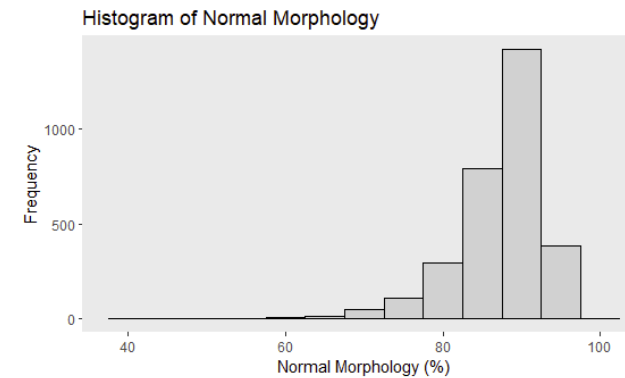
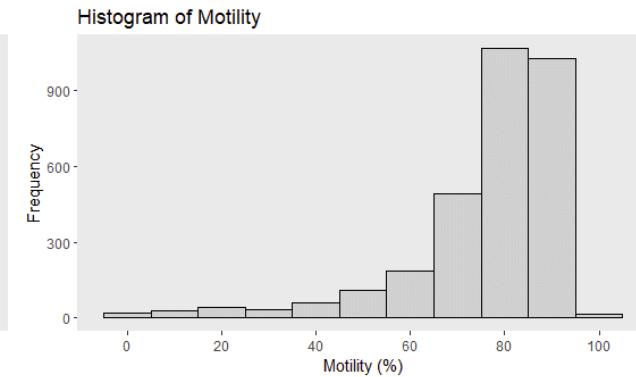
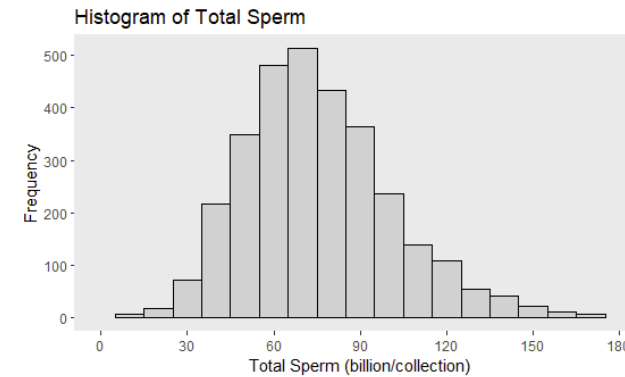


- Estimate **genomic parameters** (heritability, genomic correlations) of semen quality traits in Duroc and Large White US boars, and
- Perform a GWAS to **identify genomic regions** associated to these characteristics



Material and Methods

- 4,921 **semen doses**, analysed with CASA, from 1,638 **Large White** and **Duroc** boars selected from the cores of **Smithfield Premium Genetics**
- Boar age at semen collection 7 to 34 mo, from 2013 to 2023
- 813 boars **genotyped** with DNA chips of different density (48K, 50K, 60K, 80K)
- Only **SNP common to all 4 panels**, mapped in *Sus scrofa* reference genome (v. 11.1), in autosomes were retained (n = 29,021). A total of 27,350 SNP passed **QC** (SNP and individual call rate, MAF, and deviation from HW equilibrium)



Material and Methods

- **Genomic parameters** estimated with **BLUPF90+** (Misztal et al., 2002) according the following linear mixed model:

$$y_{ijklmn} = \underbrace{Breed_i + Year_j + Season_k + Stud_l}_{\text{Fixed effects}} + \underbrace{Age_m}_{\text{Linear covariate}} + \underbrace{Boar_ID_n}_{\text{Random effect } N(0, \mathbf{G}\sigma_a^2)} + \underbrace{e_{ijklmn}}_{\text{Random residual}}$$

- AI-REML used; **G matrix** constructed following VanRaden (2008)
 - **SNP effects** calculated with **POSTGSF90**; significance set at $P < 0.0001$; 'nearby' genes defined to be at most ± 0.1 Mb distant from the significant SNP
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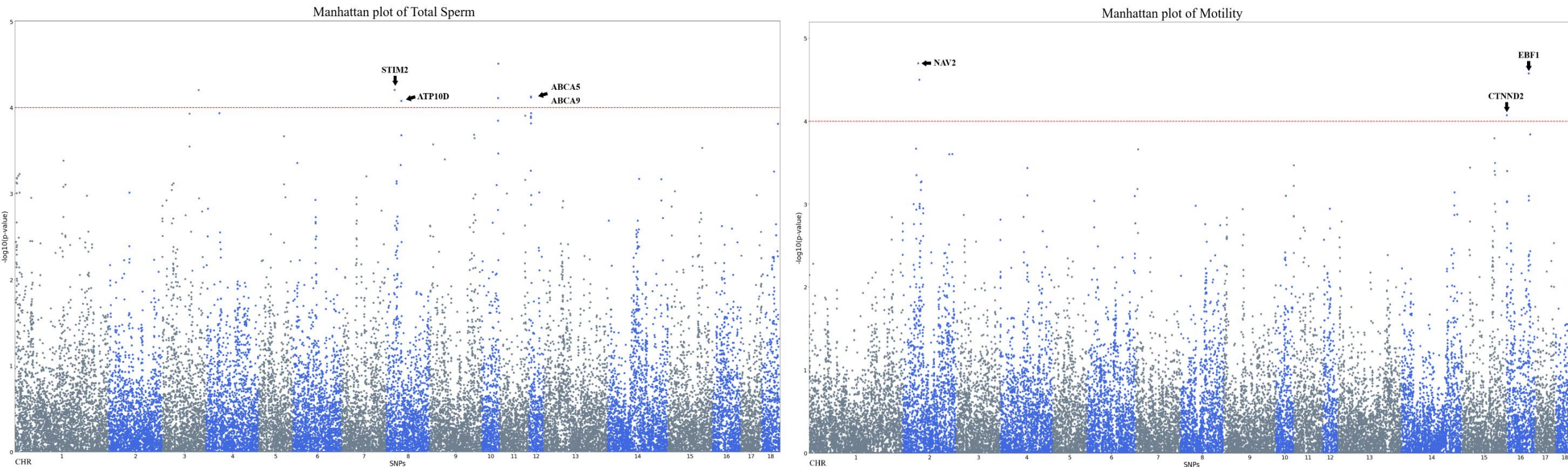
Results and Discussion

Trait	Mean (SD)	CV _a , %	Total sperm	Motility	Progressive motility	Normal morphology
Total sperm, bill/collection	71.57 (24.28)	10.84	0.12; 0.45	-0.06	-0.39	0.14
Motility, %	74.64 (17.80)	4.25	0.00	0.04; 0.39	0.78	0.96
Progressive motility, %	51.70 (18.33)	9.18	-0.01	0.84	0.08; 0.43	0.90
Normal morphology, %	87.43 (5.72)	2.89	-0.03	0.45	0.45	0.19; 0.57

- **Diagonal: Heritability** (SE range 0.04-0.06); Repeatability (SE range 0.02-0.03)
- **Below diagonal:** phenotypic correlations (SE range 0.01-0.03)
- **Above diagonal:** genomic correlations (SE range 0.19-0.88)



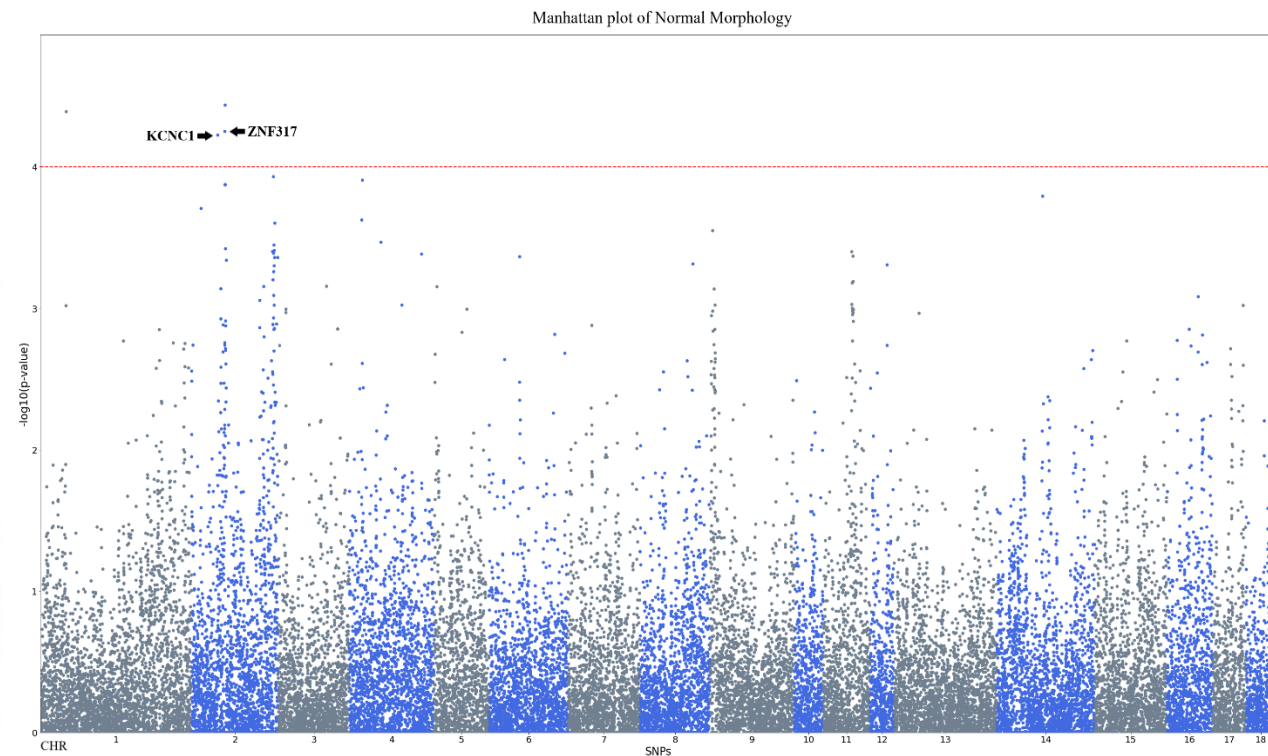
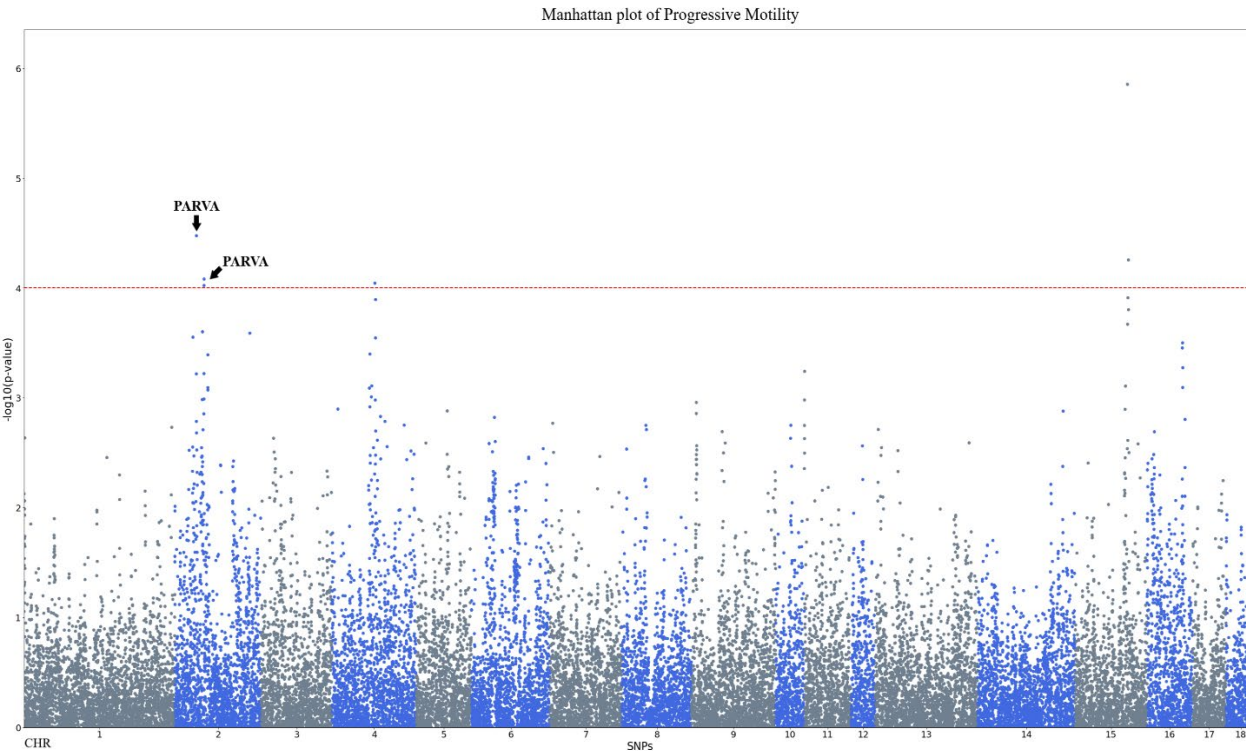
Results and Discussion



- **STIM2** gene involved in calcium channel regulation and regulates sperm physiology in mice (Darszon et al., 2012), **ABCA5** and **ABCA9** involved in lipid transport (Petry et al., 2006)
- **EBF1** lipogenic gene associated to fat deposition and circulating triglycerides (Taniguchi et al., 2014), while **CTNND2** negatively affect sperm motility in humans if altered (Pacheco et al., 2011)



Results and Discussion



- **PARVA** gene involved in actin binding, critical for structure and function of cellular cytoskeleton
- **KCNC1** gene involved in the formation ion channels, playing a key role in regulation of sperm function, such as volume, motility and morphology (Barfield et al., 2005)



Take at home message

- The present study confirm the **high complexity and polygenic nature** of semen quality traits
- Semen quality traits are **heritable** and some of them expressed **great genetic variability**, representing the basis for inclusion of this group of traits as a subindex to maximize **profitability** and make **informed decisions** in selection nuclei





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