

Low Cost Genomic Selection

M. Judge^{1,2}, F. Kearney^{2,3}, M.C. Mc Clure³, R. Sleator² and D.P. Berry¹

¹*Teagasc, Moorepark AGRIC, Fermoy Co. Cork, Ireland*

²*Cork Institute of Technology, Co. Cork, Ireland,*

³*Irish Cattle Breeding Federation, Highfield House, Bandon, Co. Cork, Ireland.*

Low density genotype panels for dairy & beef

❑ Cost of genotyping hampering uptake on farm

❑ The cost of genotyping is a function of the number of SNPs

❑ Reduce the number of SNPs without reducing accuracy of genomic predictions



Panel Development

- ❑ Illumina Bovine50 beadchip genotypes 6,369 HF
 - Validation population (youngest animals + pedigree n=750)
 - Not within two generations of valid. pop (n=1,267)
 - Imputation reference population (n= 1,249)
- ❑ 40,483 SNPs remained
- ❑ External validation in beef
 - Illumina HD genotypes on 4,727 beef animals
 - 1) Reference population (800 Limousin & 800 Charolais)
 - 2) Validation population (148 Limousin & 117 Charolais)
- ❑ Varying panel densities
 - 384, 1,000, 2,000, 3,000, 6,000, 12,000 SNPs

Algorithms

- ❑ Random

- ❑ Uniform

- ❑ Machine learning

- ❑ Blocks

- High MAF + strong LD within blocks

- ❑ Chromosomal genomic architecture

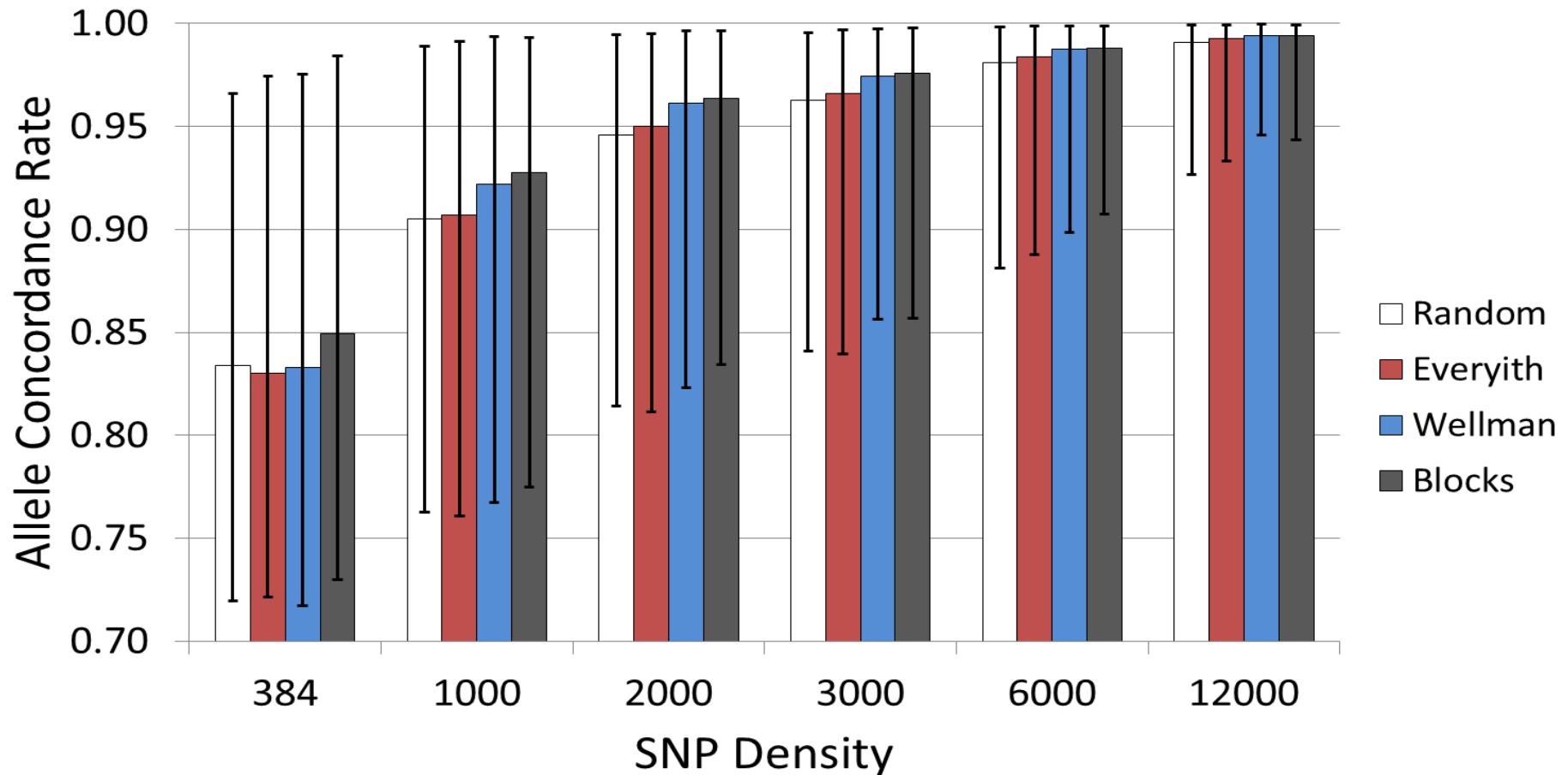
- Wellman et al (2013)
 - $f(\text{MAF}, \text{genomic position/LD})$

Results

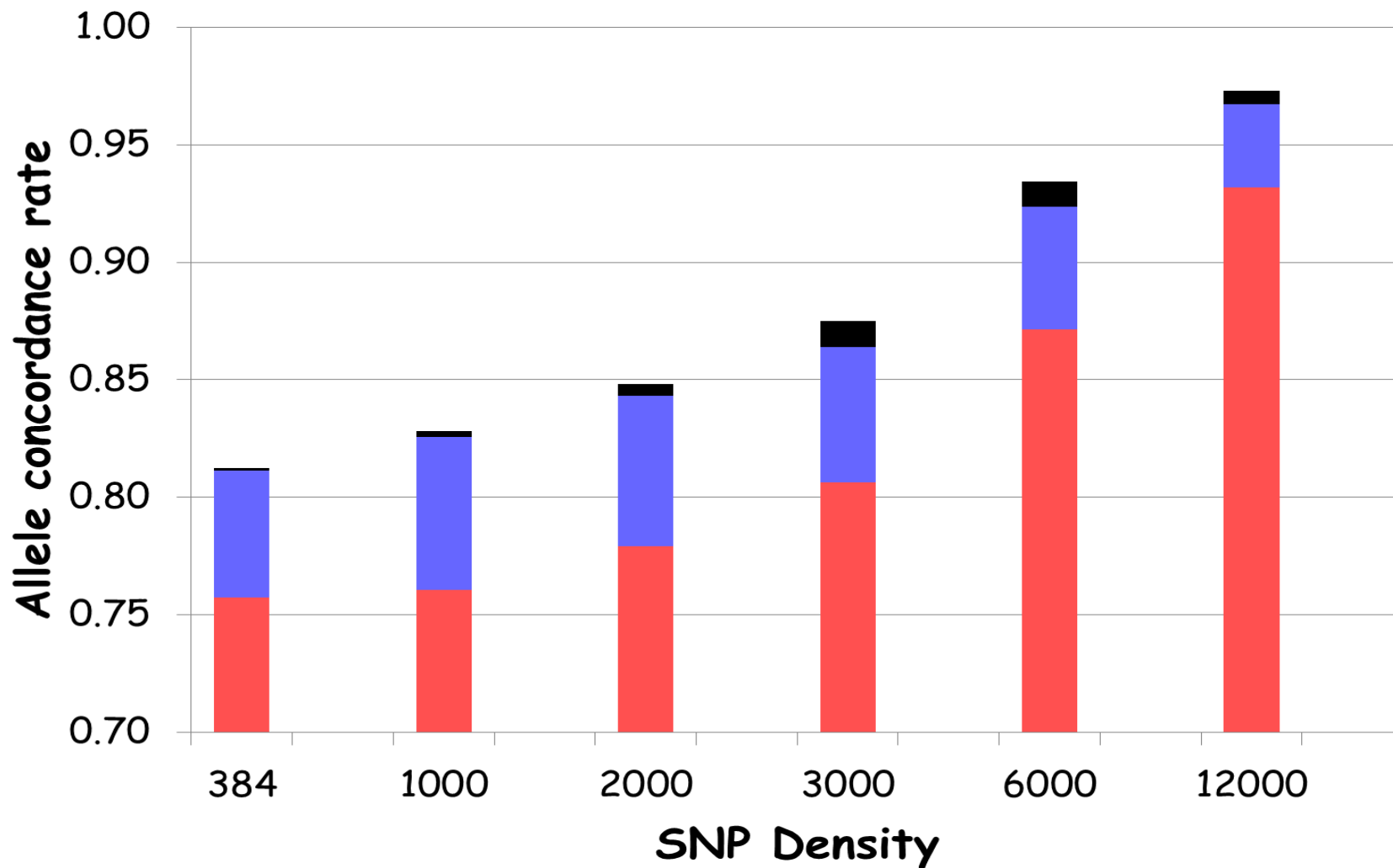
- ❑ Accuracy: FImpute $\approx$ Beagle
- ❑ Speed: FImpute $\lll$ Beagle



Allele concordance rate



Beef Data



Conclusion

- 3,000 SNP density panel
- Block method of SNP selection
- FImpute as imputation method

Acknowledgements

Research Stimulus Fund (MultiGS & GENOTRACE)



Department of
**Agriculture,
Food and the Marine**

An Roinn
**Talmhaíochta,
Bia agus Mara**