

A new dairy cattle mating advice tool for Ireland which incorporates genomic information

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Introduction

- Mating advice tool
- Best combination of potential mating
 - » Maximise long-term genetic gain
 - » Minimise closely related mating
 - » Homogenous herd
- Incorporate genomics into mating advice



Objectives

- Incorporating genomic information into mating advice tools
- Handle un-genotyped animals in a population
- Achieve more homogenous herd

Handling non-genotyped animals

Genotypes data

- 45,147 Holstein-Friesian animals
 - Imputed to Illumina BovineSNP50
- 545 females had genotyped Sire, Dam, and Maternal-grandsire
 - Genotypes were masked



Predicting Allele Dosage

- Allele dosage was predicted following Genglers gene drop method

$$q_x = \left(1 \quad A_{xy}A_y^{-1} \right) \begin{pmatrix} \mu \\ q_y - 1\mu \end{pmatrix}$$

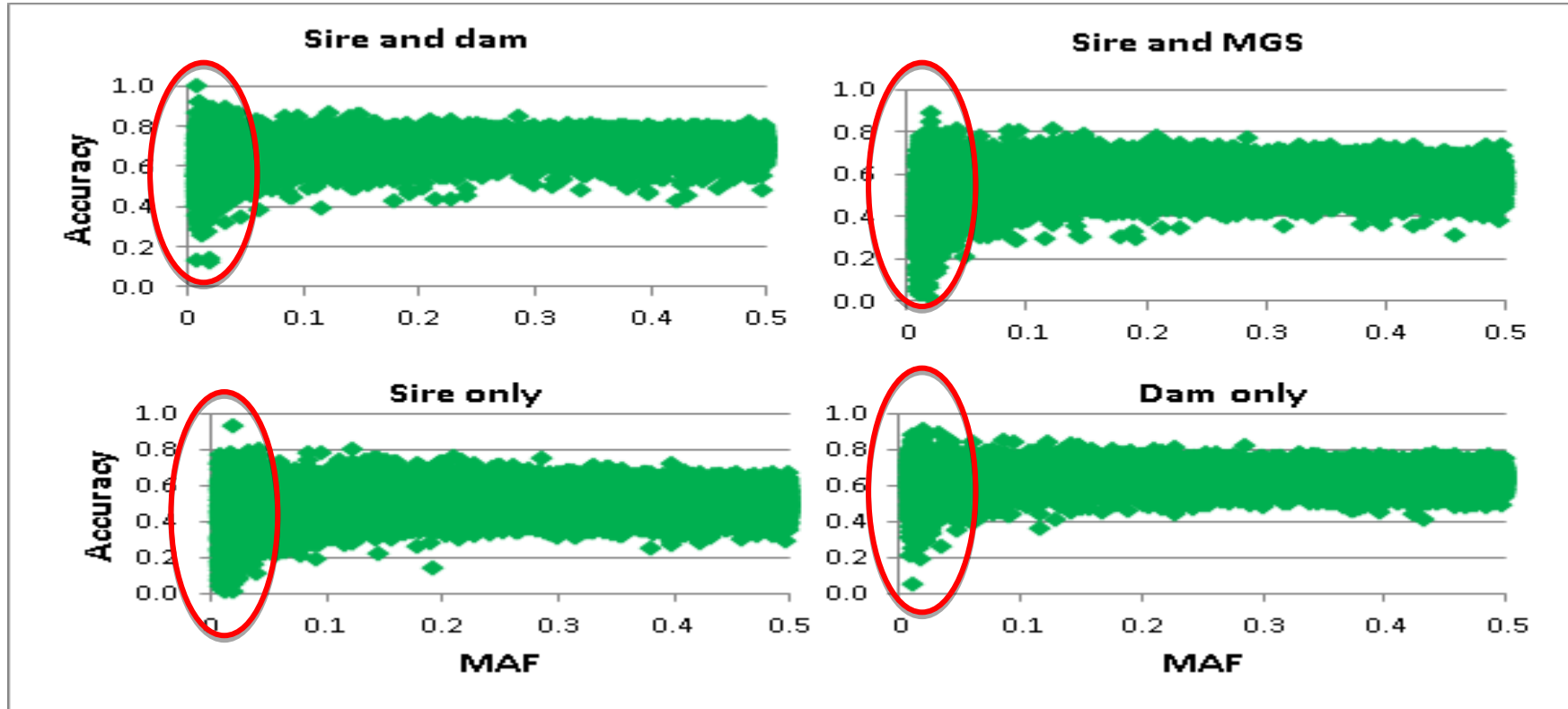
- Accuracy was determined as the correlation between the true allele dosage and the predicted allele dosage

Prediction Accuracy

Scenario	Animal
SireDam	0.69
SireMGS	0.57
Sire	0.49
Dam	0.63

Accuracy was highest when both the sire and dam were genotyped

SNP prediction accuracy



Estimation of relationships

Estimation of co-ancestry

- Genomic relationships

$$a_{jk} = \frac{1}{N} \sum_i^n \frac{(x_{ij} - p_i)(x_{ik} - p_i)}{2p_i(1 - p_i)}$$

- Pedigree relationships
- Predicted genomic relationship

Prediction of genomic relationships

	Correlation	Regression coefficient
Pedigree	0.66	0.60
Predicted allele dosage with sire and dam genotypes	0.91	0.99
Predicted allele dosage with sire and maternal-grandsire genotypes	0.89	0.99
Predicted allele dosage with sire genotypes	0.89	1.02

Mating allocation

Proposed mating index

$$I_{ij} = \sum \left(\frac{EBI_{ij} - \omega f_{ij}}{EBI_{sd_{pop}}} \right) + \sum \left(\frac{Trait_{ij}}{Trait_{sd_{herd}}} - \frac{|Trait_{avg} - Trait_{ij}|}{Trait_{sd_{herd}}} \right) - 1 \frac{|Milk_{ij} - Fertility_{ij}|}{var_{sd_{pop}}}$$

Index maximised in the herd
using linear programming

Maximise sub-index while
accounting for
inbreeding depression

penalise animals that
are too far from the
mean

Maximise sub-index while
penalising animals that
are too far from the
mean

Mating scenario

100 cows herd



10 AI Bulls



Mating scenario

100 cows herd

10 AI Bulls

	Random	Breeding Value	Proposed Index
Mating allocation	Randomly	Sequentially on expected progeny breeding value	Maximise proposed index in the herd

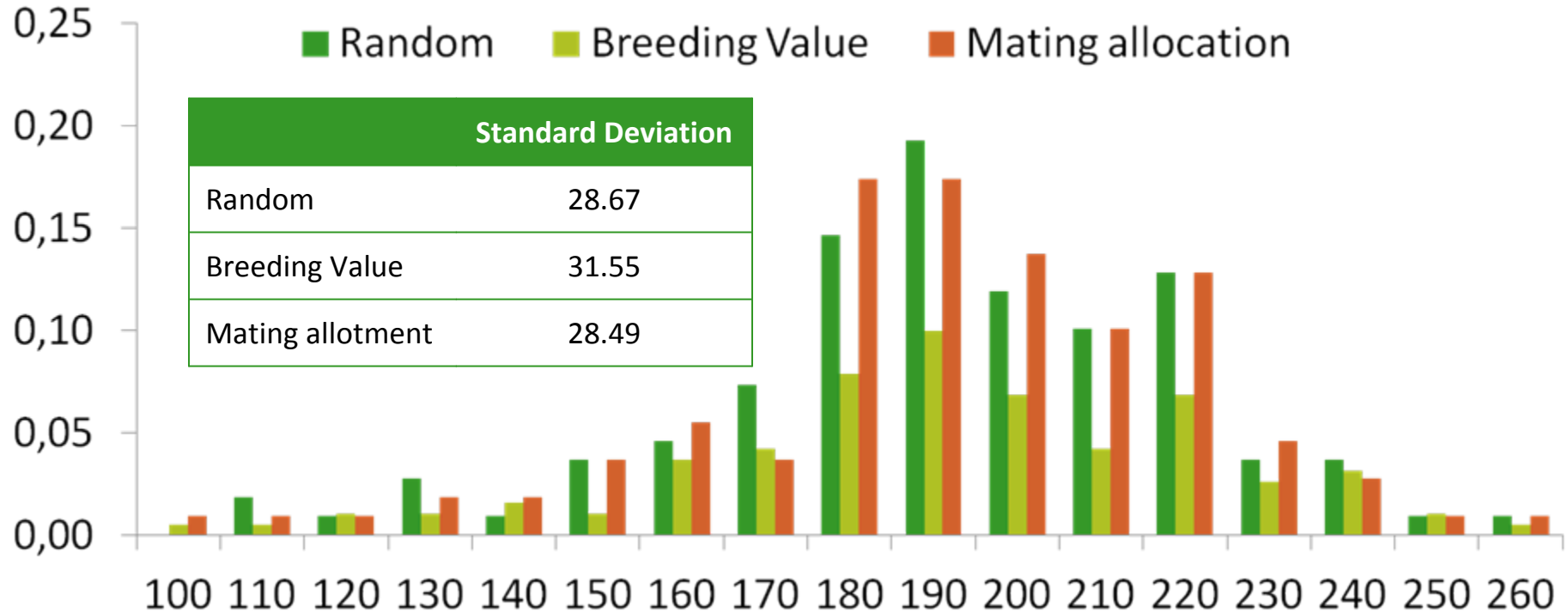
Mating allocation

- Three methods of co-ancestry were used
 - Pedigree
 - Genomic
 - Predicted genomic (with sire and dam)
- Parameters examined
 - Expected progeny inbreeding (pedigree and genomic)
 - Variance in the herd

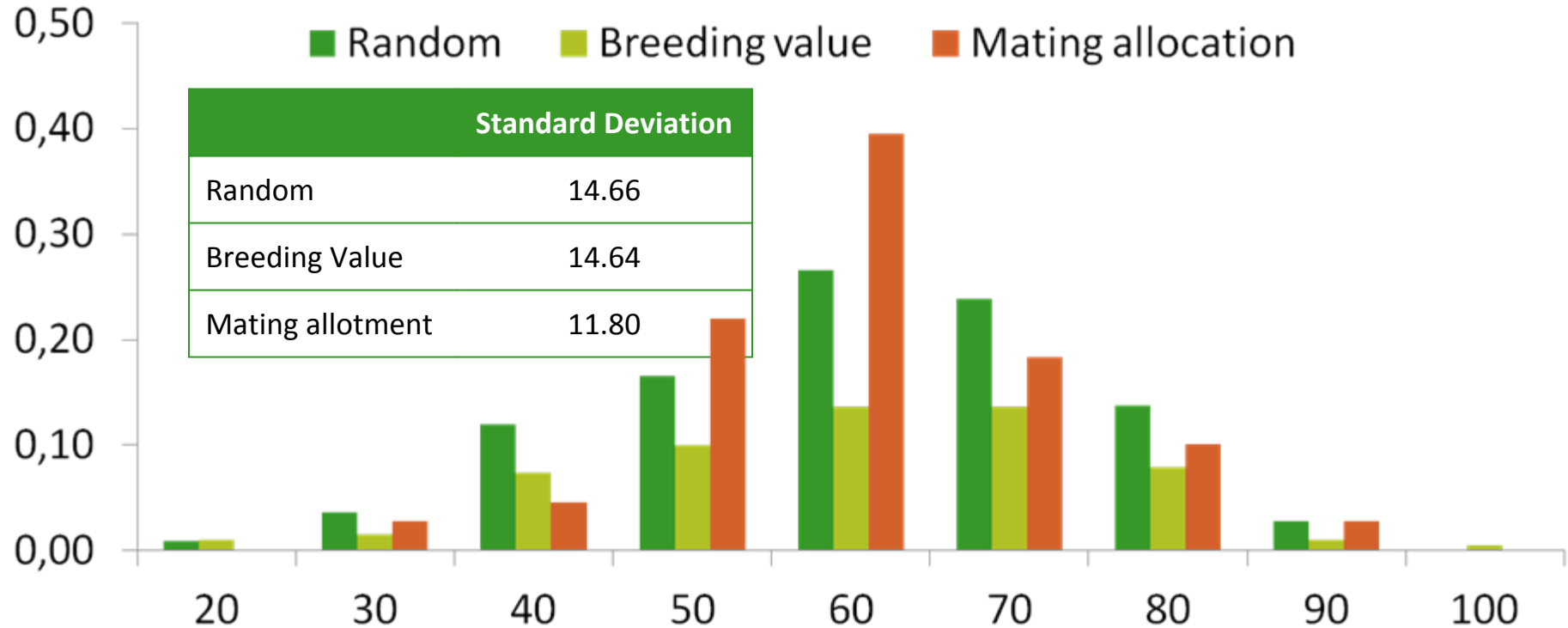
Effects on future progeny inbreeding

Method	Pedigree inbreeding (%)	Genomic inbreeding (%)
Random	4.01	-0.20
Breeding Value		
Pedigree	3.99	-0.36
Genomic	4.25	-0.08
Predicted genomic	4.25	-0.07
Mating allocation		
Pedigree	3.39	-1.06
Genomic	3.60	-1.68
Predicted genomic	3.54	-1.45

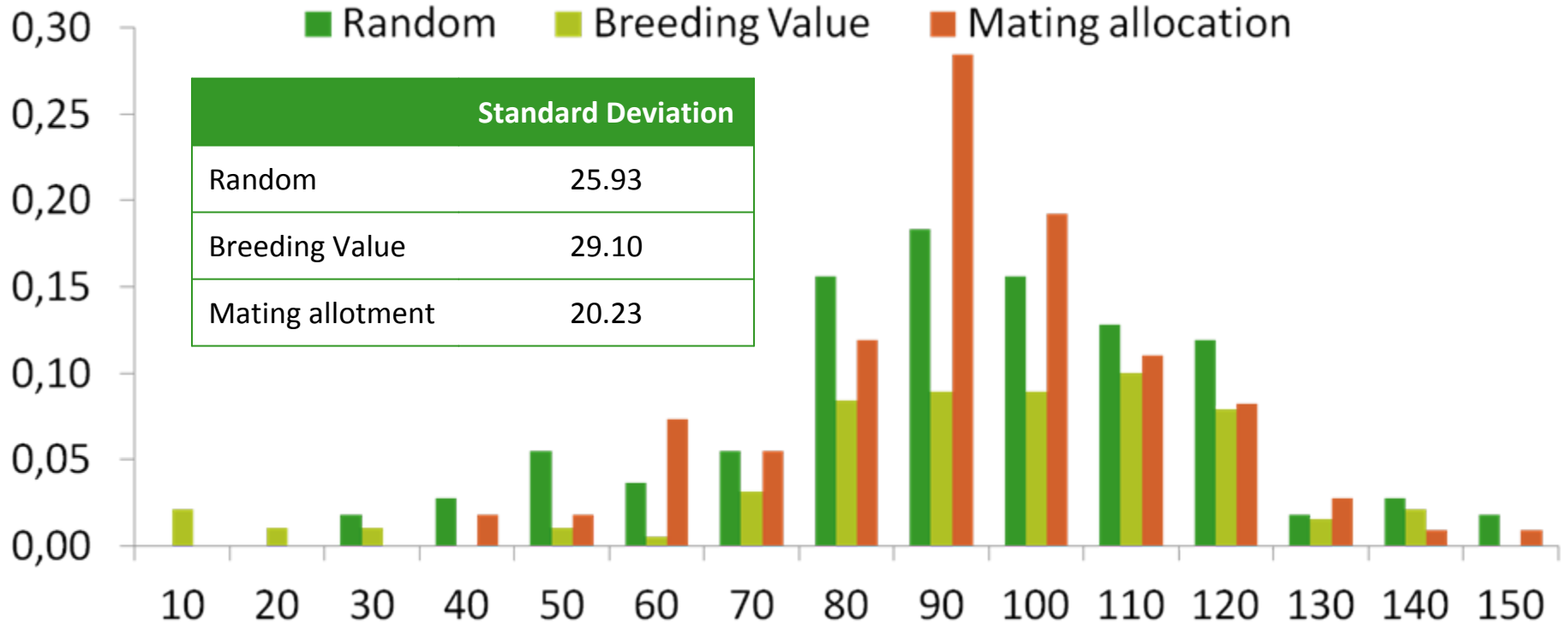
Overall Breeding Value



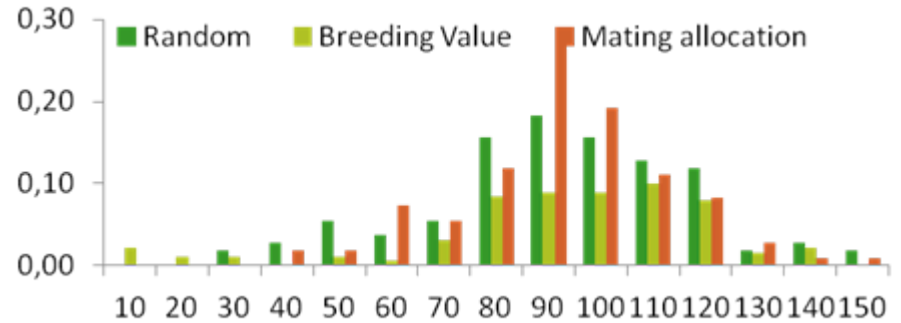
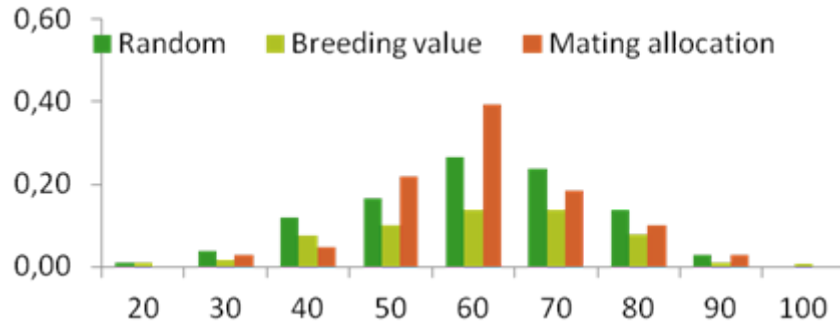
Milk Sub-index



Fertility Sub-index



Difference between the milk and fertility sub-index



	Mean	Standard Deviation
Random	41.44	29.16
Breeding Value	43.15	23.91
Mating allotment	34.63	20.32

Conclusion

- Prediction of un-genotyped animals is possible
 - More relative information the better the prediction
 - Prediction of the minor allele in low MAF SNPs needs a close relatives
- The new mating index
 - Reduces herd variance within and between traits
 - Reducing future progeny inbreeding

Conclusion

- New mating advice program will be launched based on results presented here
 - Includes the new mating index
 - Include genomic inbreeding
 - » Revert to pedigree when genotypes are not present
- A cross-breeding version to maximise heterosis is also available



Acknowledgements



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