

GENOMIC SELECTION IN WHEAT

Ali Zidi
(Incoming Fellow)

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Barcelona
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Scientific background



❖ **IAMZ-CIHEAM & UAB (MSc)**
Ruminant Research group

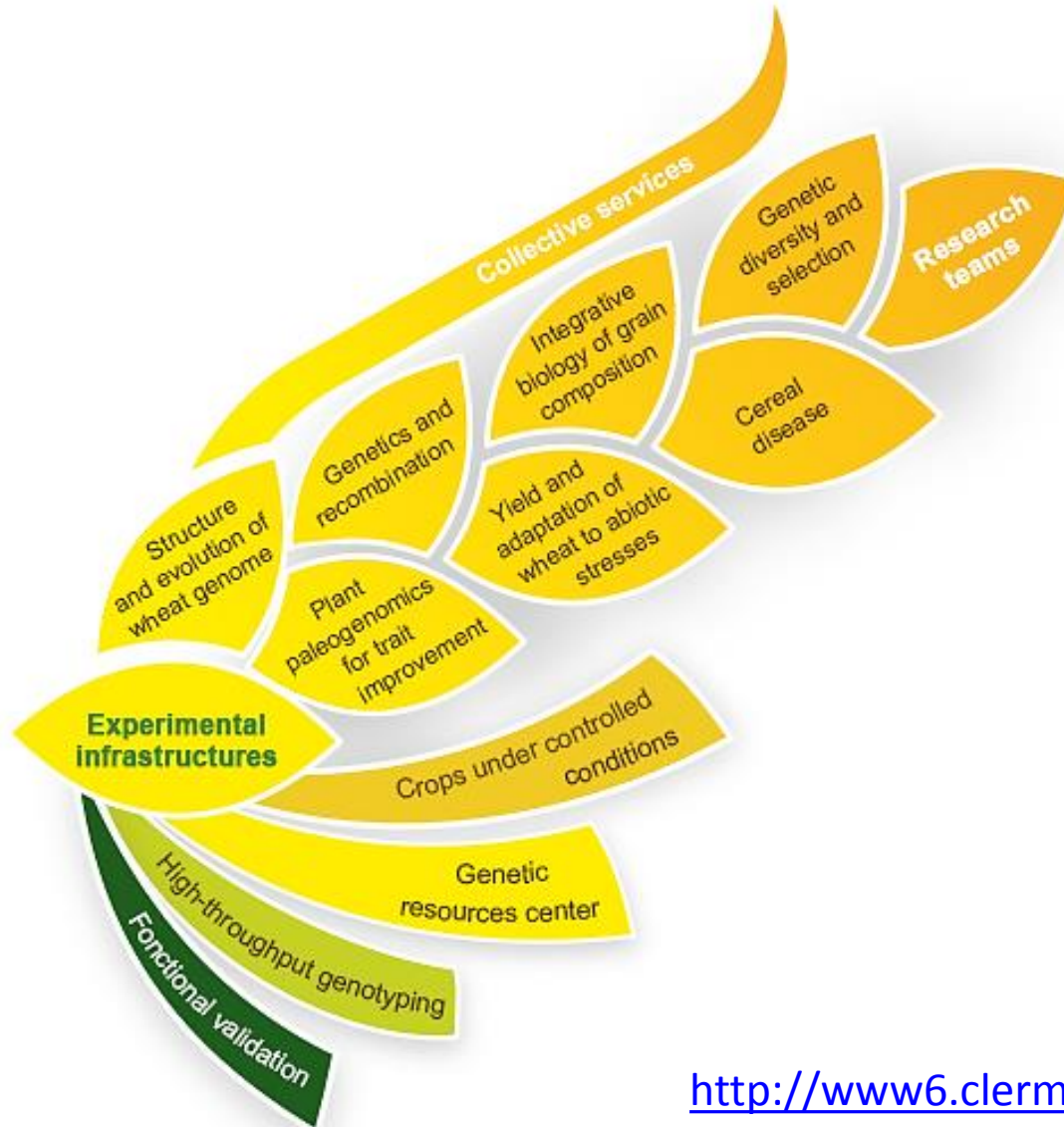
❖ **UAB (PhD)**
Animal Genetic Research group

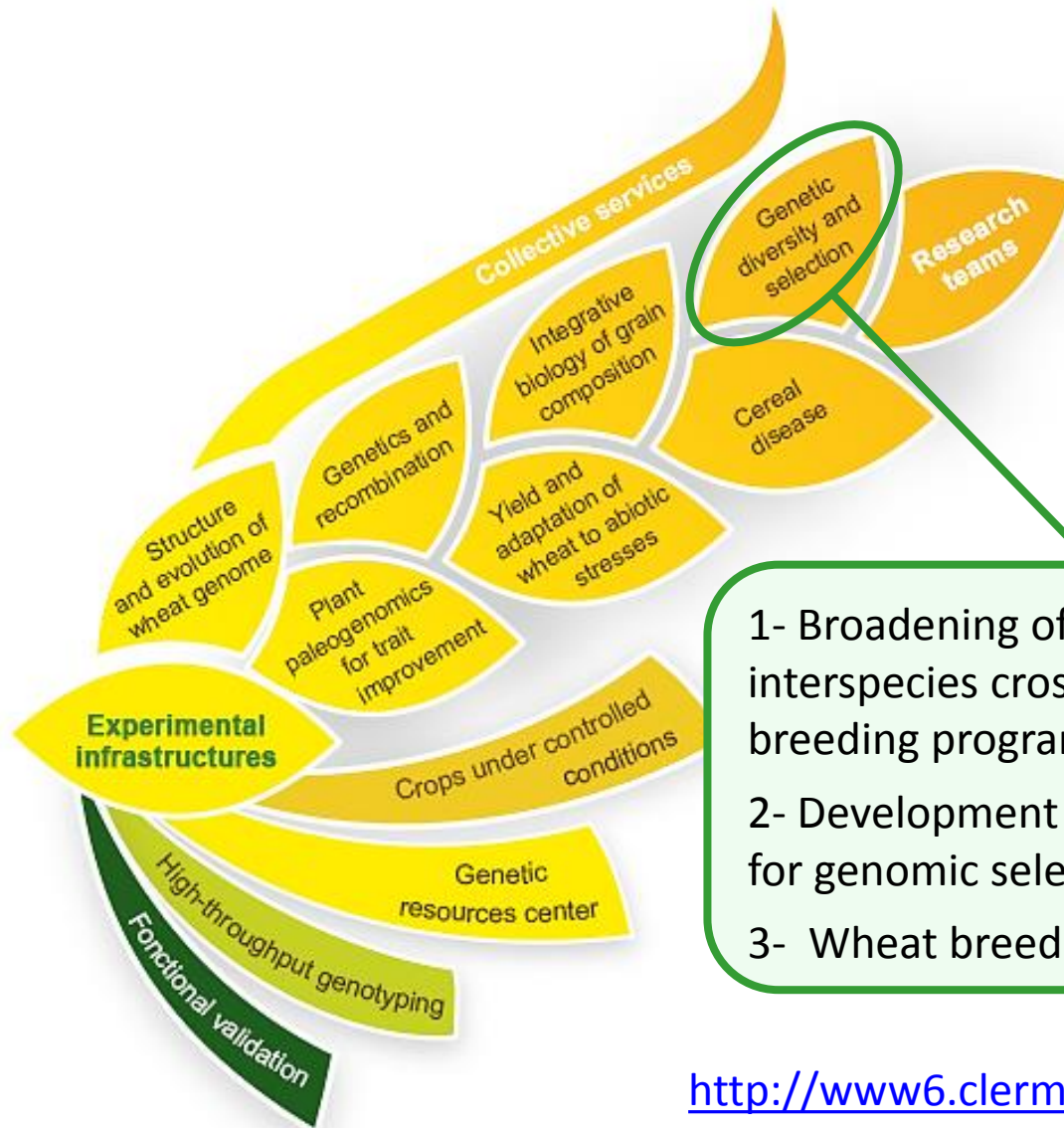
❖ **UAB (Post-Doc)**
Animal nutrition research group

❖ **CRAG (Post-Doc)**
Department of Animal Genetic

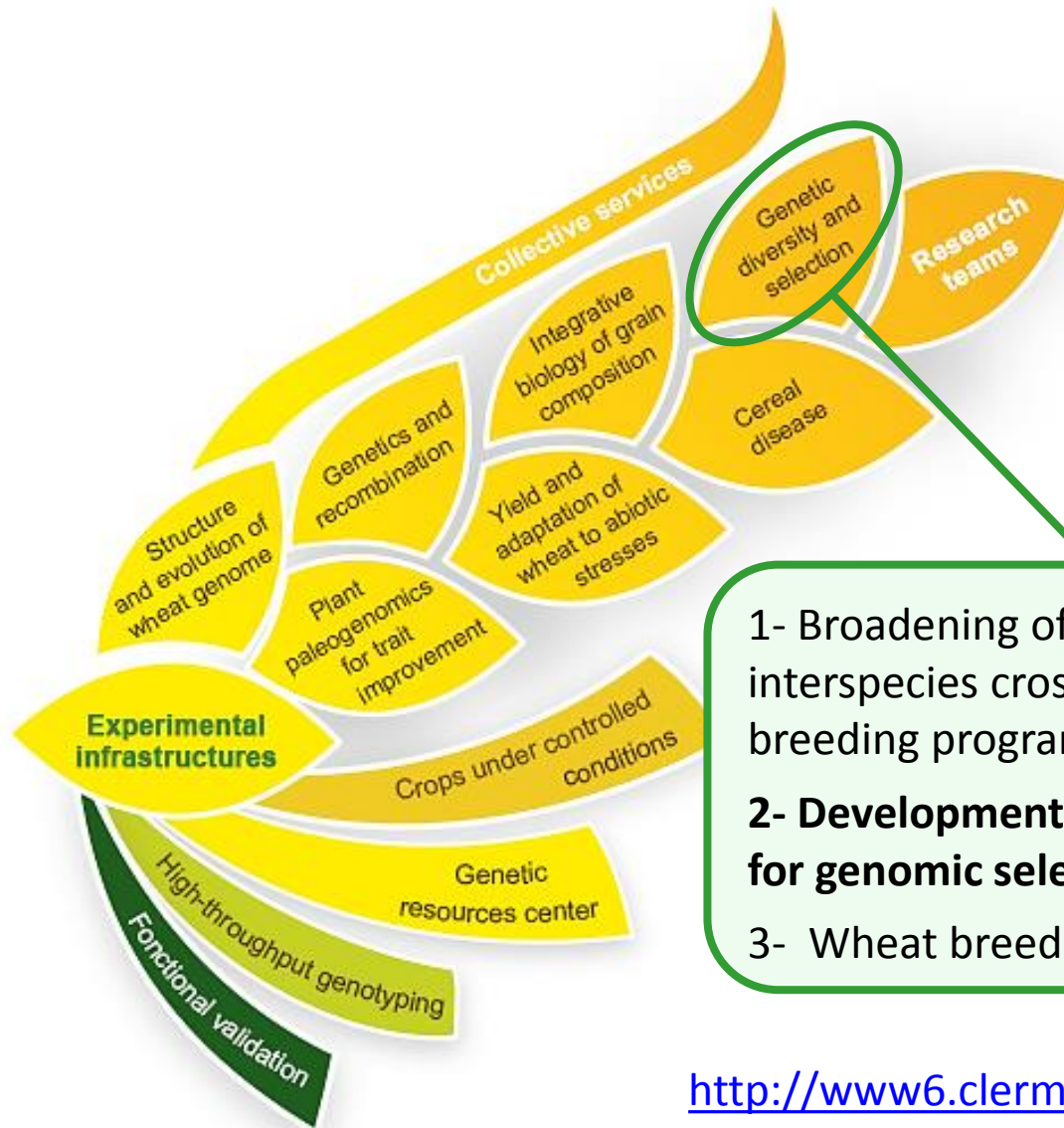
❖ **UCO (Post-Doc)**
Department of Animal Production

❖ **INRA, UMR GDEC (Post-Doc)**

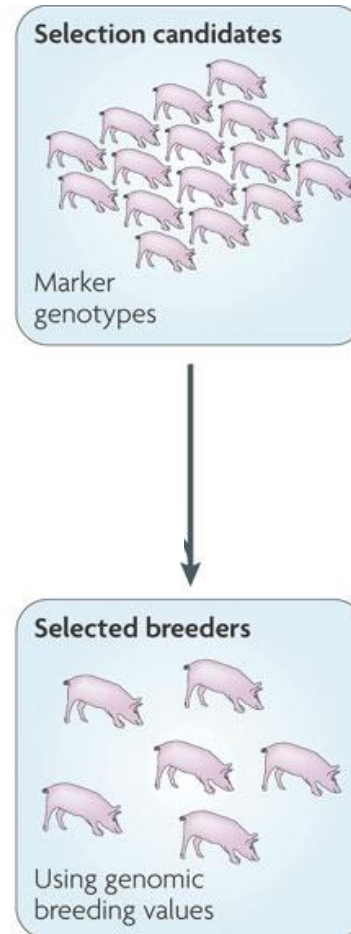




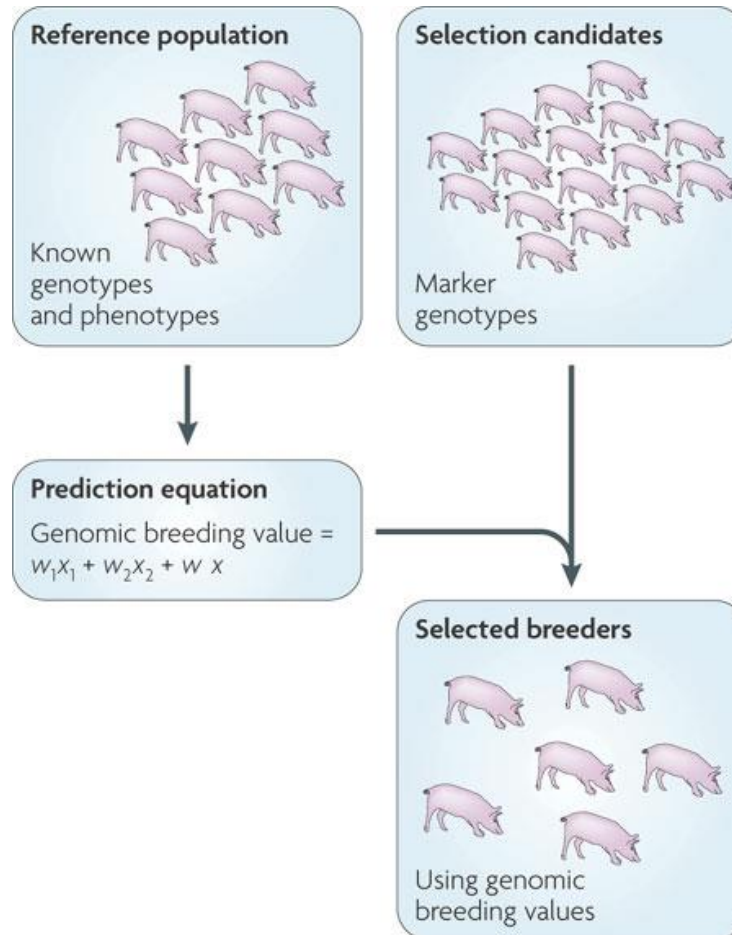
- 1- Broadening of diversity through interspecies crosses and pre-breeding programs.
- 2- Development of methodologies for genomic selection.
- 3- Wheat breeding program.

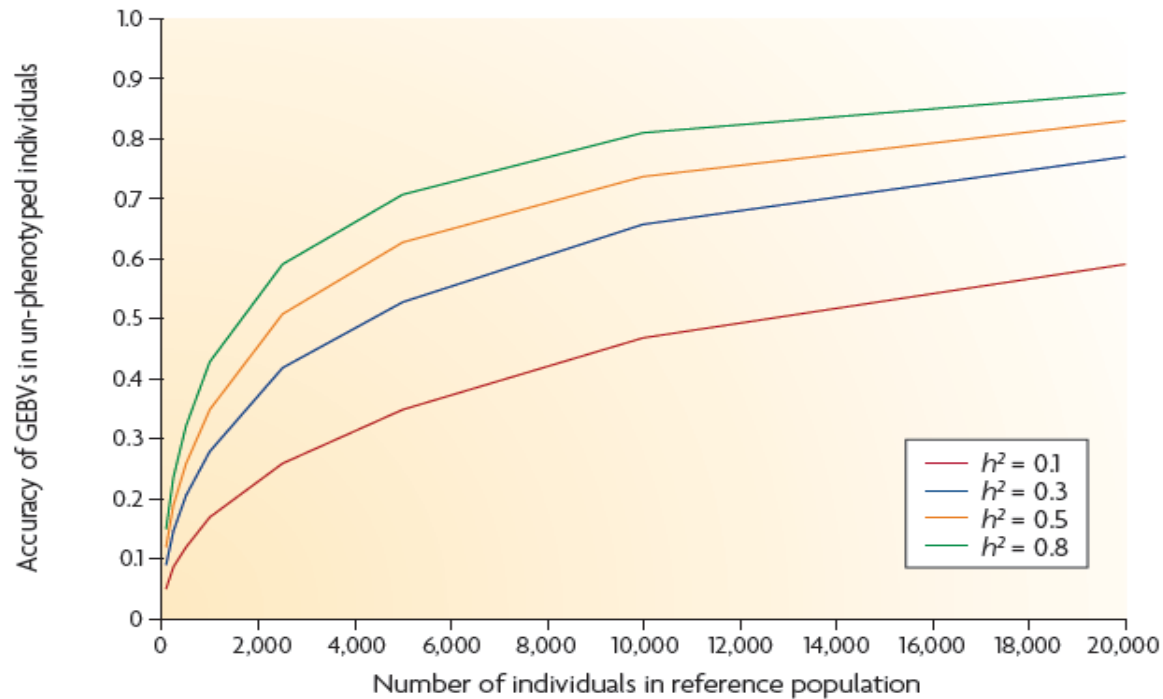


Genomic Selection



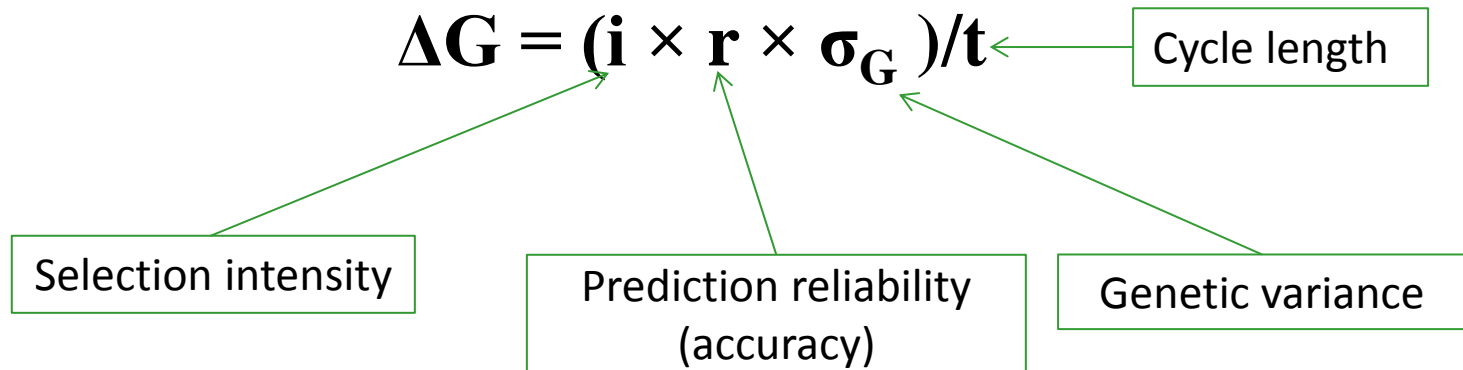
Genomic Selection





**Number of animals in a reference population
and accuracy of breeding values**

Genetic Progress



Accuracy = correlation (TBV, Prediction)

➡ Optimise the calibration set

Maximizing the Reliability of Genomic Selection by Optimizing the Calibration Set of Reference Individuals: Comparison of Methods in Two Diverse Groups of Maize Inbreds (*Zea mays* L.)

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ABSTRACT Genomic selection refers to the use of genotypic information for predicting breeding values of selection candidates. A prediction formula is calibrated with the genotypes and phenotypes of reference individuals constituting the calibration set. The size and the composition of this set are essential parameters affecting the prediction reliabilities. The objective of this study was to maximize reliabilities by optimizing the calibration set. Different criteria based on the diversity or on the prediction error variance (PEV) derived from the realized additive relationship matrix–best linear unbiased predictions model (RA–BLUP) were used to select the reference individuals. For the latter, we considered the mean of the PEV of the contrasts between each selection candidate and the mean of the population (PEVmean) and the mean of the expected reliabilities of the same contrasts (CDmean). These criteria were tested with phenotypic data collected on two diversity panels of maize (*Zea mays* L.) genotyped with a 50k SNPs array. In the two panels, samples chosen based on CDmean gave higher reliabilities than random samples for various calibration set sizes. CDmean also appeared superior to PEVmean, which can be explained by the fact that it takes into account the reduction of variance due to the relatedness between individuals. Selected samples were close to optimality for a wide range of trait heritabilities, which suggests that the strategy presented here can efficiently sample subsets in panels of inbred lines. A script to optimize reference samples based on CDmean is available on request.

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AMONG the different methods that use molecular markers for selection, genomic selection (GS) has received considerable attention in the last decade. The objective of this approach is to predict the breeding values of candidates based on their molecular marker genotypes. A prediction formula is developed using the genotypes and phenotypes of reference individuals forming a calibration set (Meuwissen

Objective

- ❖ CDmean takes all SNPs at the same level of importance and does not consider those SNPs with large effect on the trait under study.
- ❖ Rutkoski et al. (2014) reported that modeling selected markers as fixed effect leads to improve accuracy using genomic best linear unbiased prediction (GBLUP)

➡ Optimize (update CDmean) the composition of calibration set of the reference individuals

Expected Results

- ❖ We expect an increase of the accuracy of the genomic prediction by the optimization of the reference population considering major SNP in the algorithm of the optimization.

Cross validation prediction accuracies for adult plant stem rust resistance using different prediction models (Rutkoski et al., 2014)

	GBLUP	GBLUP-A	GBLUP-B
Accuracy	0,568	0,607	0,618

G-BLUP-A, genomic best linear unbiased prediction A, marker relationship matrix and fixed effects selected among all markers.

G-BLUP B, marker relationship matrix and fixed effects selected among candidate gene linked markers.

Thank you for your attention

