

## Genomic Selection: A new approach for Crop Improvement

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Genomic selection (GS) was proposed in 2001 (Meuwissen et al., 2001). GS is a form of MAS (marker assisted selection), where the whole genome covered by genetic markers in a dense manner are used for estimating the breeding value of selection candidates for a quantitative trait (Goddard, 2009). By applying genomic selection, the selection cycle for selecting elite lines can be shortened and it results in greater gains/unit time and cost (Heffner et al., 2010). In GS estimations are based on more genotyping and less on phenotyping. In case of GS the main purpose of phenotyping is to estimate and re-estimate the marker effects (Heffner et al., 2009). In GS there are two populations (Heffner et al., 2009): Training population (TP) and Breeding population (BP). Based on markers having high breeding value, prediction would be made about BP

and lines having high breeding value will be selected for final evaluation in the field. Based on performance of these lines, line performing best could be released as variety. If not used for releasing variety then breeding lines selected based on breeding value could be used for germplasm improvement.

### References

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