

Genomic selection—a breeder’s perspective

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All oat cultivars thus far are developed through conventional breeding, which includes the following steps: parent selection, generation advancement, selection based on breeder’s eye, and selection based on yield trial data. Selection based on breeder’s eye is highly dependent on the breeder’s experience and the selecting environment. Genomics has advanced to such a stage that it is time to explore its possibility to replace the breeder’s eye (genomic selection stage 1 or GS1) and eventually some yield trials (GS2) in making selection decisions. This is on the condition that highly predictive genomic selection models for key breeding objectives can be developed. The latter is dependent on four elements: 1) quality genome-wide molecular marker data of a representative genetic population, 2) phenotypic data of the genetic population from representative environments (representative locations across a number of years), 3) robust statistical modeling to associate the marker data with the phenotypic data, and 4) the predictability of the trait of interest by the markers. The process of building predictive models is referred to as pre-genomic selection (GS0). This presentation describes the relationship between conventional breeding and genomic selection and emphasizes the importance of “quality” phenotypic data in GS0.