

Revisiting the Breeder's Equation: Implications of our advancing understanding of trait genome-to-phenome relationships

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Plant breeders are expected to have a working knowledge of the Breeder's Equation. It is also expected that the Breeder's Equation will be used as a framework to help optimise the design of their breeding program. This was relatively straightforward when breeding was based predominantly on selection for trait phenotypes. Today, breeders either use, or aspire to use, genomic information in many ways to improve the effectiveness of their breeding programs. I will share my experiences in how this transition to use of genomic information has required me to think differently about the Breeder's Equation. The prediction-based approaches to be discussed are grounded in an iterative empirical-modelling cycle that operates across two complementary domains: empirical-experimental and mathematical-modelling. The research themes are underpinned by: (1) Two decades of experience breeding maize hybrids for yield and yield stability in the US corn-belt and research partnerships with many colleagues, (2) Advances in hierarchical Bayesian modelling methods that leverage prior genetic and physiological knowledge for genomic prediction, (3) Advances in crop models that can enhance our ability to test "multiple workable solutions" to improve crop yield and yield stability through breeding and improved agronomy. Further, two strong motivations for investigating such prediction-based approaches are: (1) the need to increase the scale of breeding programs beyond what we can currently achieve by empirical approaches alone, and (2) using the environments we can sample today it is difficult to empirically test, at the required scale, for many dimensions of the projected future Target Population of Environments, given projected climate change scenarios for the rest of this Century.