Meuwissen *et al.* on Genomic Selection

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ORIGINAL CITATION

WHEN Meuwissen *et al.* published this landmark article in 2001, most agricultural genomics research was focused on detecting quantitative trait loci (QTL) using experimental crosses or existing family relationships. Around this time the human genome was nearing its completion, but no livestock or crop genomes were yet available. Genomic markers in livestock were mainly microsatellites, complemented by Amplified Fragment Length Polymorphisms in crops, with Diversity Arrays Technology markers on the horizon. Such genomic information was intended to be used in artificial selection mainly via Marker-Assisted Selection and Marker-Assisted Introgression. In these methods, selection decisions are made based on only a few markers that individually show association with the relevant trait.

So it required considerable foresight by Meuwissen *et al.* (2001) to develop a new approach that required a sufficiently high marker density such that every QTL affecting a relevant trait would be in linkage disequilibrium with at least one marker. Meuwissen *et al.* (2001) argued that decisions to select for breeding could be based on the joint merit of all markers across the genome. Before this, breeders used a combination of polygenic effects and genotypes of painstakingly selected and validated QTL. The concept introduced by Meuwissen *et al.*, now known as "genomic selection," has allowed unprecedented advances in commercial breeding in the past 15 years, including a doubling of dairy cattle improvement per generation compared to traditional selection.

Meuwissen *et al.* explored these concepts using a simulated data set with a mere 1010 genetic markers and 1000 putative QTL. They applied different statistical modeling approaches: linear regression, Best Linear Unbiased Selection (BLUP), and two Bayesian approaches, dubbed BayesA and BayesB. The Bayesian approaches have been extensively tweaked and revised by other researchers, with many improvements related to the prior distributions of QTL effect [giving rise to the "Bayesian Alphabet" coined by Dan Gianola (Gianola *et al.* 2009; Gianola 2013)]. It is notable that despite many years of methods development BayesB is still among the gold standards for evaluating new approaches, while a modified implementation of the BLUP approach (GBLUP) is used in many practical applications of genomic selection (reviewed by de los Campos *et al.* 2013 and Daetwyler *et al.* 2013).

At the time of publication the work in Meuwissen *et al.* was hailed as a breakthrough by the breeding communities, but the tools needed for implementation were not yet available. So for the next few years genomic selection was just a proposal. However, after 2006, when medium-density SNP chips were becoming routinely available for the main livestock species, genomic selection suddenly became a hot research topic (Figure 1).

Since then, industry uptake of the method, both in terms of speed and magnitude, has been remarkable. In dairy cattle breeding, genomic selection has all but replaced the traditional selection based on progeny testing, with unparalleled results. Other livestock species are following suit. Maize and wheat are at the forefront of genomic selection in crops, not the least because of large international efforts by the International Maize and Wheat Improvement Center (CIMMYT).

So it is fair to say that Meuwissen *et al.* changed selective breeding for many, if not most, agriculturally important species within 15 years of publication. The principles of genomic selection are now also increasingly being applied in studies of
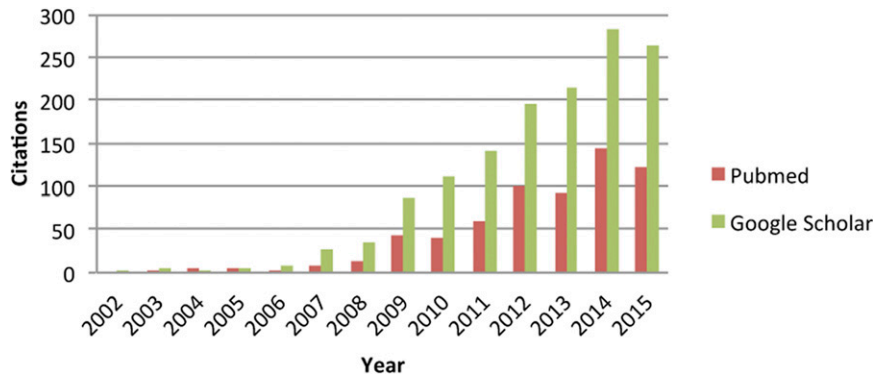
Figure 1 Citations to Meuwissen *et al.* (2001) according to PubMed and Google Scholar.

human disease. Researchers in this area, not the least Theo Meuwissen, Ben Hayes, and Mike Goddard, continue to refine the applications of genomic selection including the optimal use of whole-genome sequence information.

The Genetics Society of America journals *GENETICS* and *G3:Genes|Genomes|Genetics* have special collections on genomic selection, which currently has >50 papers (http://www.genetics.org/collection/genomic-selection). This collection includes reviews, methods, tools, and applications, including access to valuable data sets for comparison and benchmarking of new approaches.

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