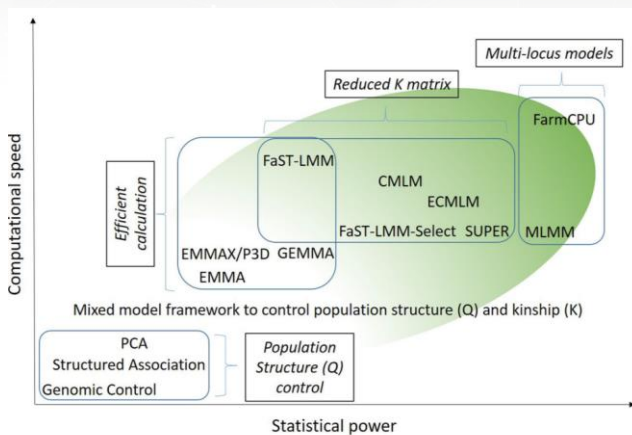


GWAS for complex traits

다양한 모델(방법론)을 적용하여 QTL 형질 연관 유전자, 마커 탐색의 효율을 높입니다.

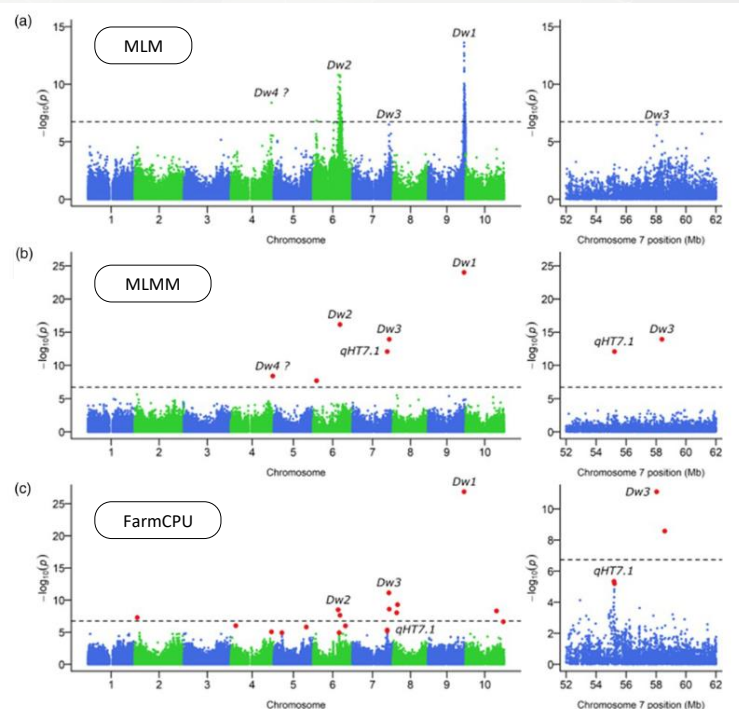
다양하고 복잡한 QTL 형질 연관 유전자 탐색을 위한 GWAS 모델들

- The development of the mixed model frame-work for GWAS dramatically reduced the number of false positives compared with naïve methods.



(Figure 1) Genome-wide association study methods for improving computational speed and statistical power.

*Laura Tibbs Cortes et al. Plant Genome.2021;14:e20077



(Figure 2) Genome-wide association studies of plant height in sorghum.

다양한 모델에 따른 위항병 GWAS 분석 결과 사례

- GLM (general linear model)
- MLM (mixed linear model)
- SUPER (settlement of mixed linear model under progressively exclusive relationship)
- ECMLM (enriched compressed mixed linear model)
- FarmCPU (fixed and random model circulating probability unification)
- MLMM (multi-locus mixed model)

