

In Two Lowland Switchgrass Populations, Qtls for Spring Green-Up, Plant Vigour, and Plant Biomass were Mapped

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Opinion

At the turn of the twentieth century, Darwin and Mendel's foundational discoveries laid the scientific foundation for plant breeding and genetics. Similarly, the recent integration of biotechnology, genomic research, and molecular marker applications with traditional plant breeding procedures has laid the groundwork for molecular plant breeding, an interdisciplinary field that is transforming crop development in the twenty-first century. Although molecular plant breeding technologies continue to evolve and are a hot issue among plant breeders and crop scientists, the majority of plant biologists involved in basic scientific research have paid little attention to them. The goal of this Editor's Choice article for a series on future advances in crop biotechnology is to review key historical developments in molecular plant breeding, key principles influencing current molecular plant breeding practise, and factors influencing molecular plant breeding adoption in crop improvement programmes. We also underline how molecular plant breeding is now contributing to the discovery of genes and their activities, which opens up new paths for fundamental plant biology research [1].

Due to its high potential for cellulosic bioenergy feedstock production, switchgrass (*Panicum virgatum L.*) is an important perennial C4 plant. Understanding the genetic basis and applying marker-assisted selection (MAS) in switchgrass breeding requires the identification of quantitative trait loci (QTL) influencing crucial developmental features. This study used one F1 hybrid population generated from NL94 (♀) × SL93 (♂) and one S1 (first-generation selfed) population from NL94. For the three characteristics tested, plant vigour, spring green-up, and plant biomass, both populations revealed substantial genotype and genotype by environment interactions. In both populations, plant vigour demonstrated high and positive associations with plant biomass. In the hybrid and selfed populations, broad-sense heritability estimates for plant vigour varied from 0.46 to 0.74 and 0.45 to 0.74, respectively [2]. Heritability estimates for spring green-up were 0.42–0.78 in the hybrid population and 0.47–0.82 in the selfed population. The hybrid population had a heritability of 0.54–0.64 while the selfed population had a heritability of 0.64–0.74. In the hybrid population, fifteen QTLs for spring green-up, six QTLs for plant vigour, and three QTLs for biomass yield were found, whereas the selfed population had four QTLs for spring green-up, four QTLs for plant vigour, and one QTL for biomass yield. To speed up the switchgrass breeding programme, markers associated with these QTLs can be employed in MAS. This research added to our knowledge of the genetic control of biomass components and indicated significant heterotic vigour, which may be used to develop hybrid switchgrass cultivars [3].

Abiotic pressures such as moisture stress (drought, waterlogging), temperature stress (hot, cold), and salinity stress, which are all key variables impacting maize yield, are all exacerbated by global climate change. Many quantitative trait loci (QTL) have been identified to develop abiotic stress tolerance in maize, but only a few have been successfully used in breeding programmes. In this case, a meta-QTL

study of the reported QTL will allow the identification of stable/real QTL, paving the way for a reliable method of introgressing these QTL into elite cultivars using marker-assisted selection. In this study, 542 QTL for tolerance to various abiotic stimuli in maize were compiled from 33 published publications to conduct meta-QTL analysis using BiomeqV4.2.3. Only 244 significant QTL with more than 10% phenotypic variance were preferred for meta-QTL analysis [4]. Over a wide range of genetic and environmental backgrounds, 32 meta-QTL containing 1907 candidate genes were discovered for various abiotic stressors. Different stress-related features for combined abiotic stress tolerance are controlled by the MQTL2.1, 5.1, 5.2, 5.6, 7.1, 9.1, and 9.2. For varied stress tolerances, candidate genes for essential transcription factor families such as ERF, MYB, bZIP, bHLH, NAC, LRR, ZF, MAPK, HSP, peroxidase, and WRKY have been discovered. Future climate-resilient maize breeding programmes and functional validation of candidate genes studies will benefit from the found meta-QTL, which will help us better grasp the complexity of these abiotic stresses [5].

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