Developmental variation in branch architecture in tillering mutants of Setaria viridis

Background and Methods

Axillary branches in grasses, particularly tillers, serve critical roles in the accumulation of biomass and seed yield. In wild grasses, the regulation of branching patterns is a dynamic process governed by environmental cues. Within domesticated lineages these environmentally labile responses are selected against and often lost entirely. To better understand the manner in which developmental responses are regulated by environmental conditions we are using the wild grass and recently adopted model system Setaria viridis (line A10.1) in conjunction with N-nitroso-N-methylurea (NNU) mutagenized lines that have been characterized as bearing aberrant branching patterns. Through a combination of qualitative observation and quantitative data generated through the use of PlantCV (Fahlgren, et al., 2015) we are characterizing morphological patterns and developmental trajectories of various mutants compared to wild type S. viridis.

Results

Several screened mutants within the NMU_00919.3m_4 and NMU_01004.5m_4 backgrounds display distinctive branching phenotypes. Both mutants experience delays in flowering compared to A10.1 (Fig. 1 A, E, & I). In addition, NMU_00919.3m_4 has reduced tillering (Fig. 1: L & H), and an enlarged inflorescence akin to the the domesticated cultivar Setaria italica at maturity (Fig. 2: A). Although axillary branching is suppressed in NMU_00919.3m_4 until flowering, after flowering many of these formerly suppressed axillary buds are released and immediately transition into reduced inflorescences (Fig. 2). By contrast, NMU_01004.5m_4 is unable to suppress axillary bud growth so that a grade of branches is found along the primary axis. Along the tillers of L4 and L5 tertiary axes are also visible (arrows in Fig. 1: L). NMU_01004.5m_4 also has a dwarfed shoot phenotype, but not a reduced root system (Fig. 1: J, K, & L). The root system in NMU_00919.3m_4 is notably smaller than either wild type or its dwarfed counterpart (Fig. 1 G & K) and mutants within this background lodge with higher frequency.

Figure 1. Morphology of wild type A10.1 (A, B, C, & D) and the NMU lines NMU_00919.3m_4 (E, F, G, & H) and NMU_01004.5m_4 (I, J, K, & L). Whole plant images displaying shoot and root systems for A10.1 (A), NMU_00919.3m_4 (E), and NMU_01004.5m_4 (I). Shape data extracted from shoot and root systems of A10.1 (B & C), NMU_00919.3m_4 (F & G), and NMU_01004.5m_4 (J & K). Dissected plants displaying axillary branches and corresponding leaf blades of the primary axis for A10.1 (D), NMU_00919.3m_4 (H), NMU_01004.5m_4 (L).

Discussion

Both NMU mutant lines have distinctive phenotypes and are strong candidates for future study. Moreover, the phenotype of NMU_00919.3m_4 may be pleiotropic with correlated changes in both root architecture and the developmental fate of axillary buds. The lack of leaf initiation among these reduced axes further suggests that these axillary buds may have only briefly functioned as vegetative meristems before transitioning into an inflorescence fate. As such it appears that NMU_00919.3m_4 phenotype is one of enhanced apical dominance whereas the phenotype of NMU_01004.5m_4 is the inverse, with the repression mechanism of axillary buds being inactivated. Future studies are planned to identify the causative loci for both of these mutant backgrounds as well as to further characterize the phenotypes observed through qualitative and quantitative analyses.

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References