Poster 27. Disruption of circadian clock caused by the earliness per se 3Am locus (Eps-3Am) contributes to early flowering in wheat (Triticum sp. L.).

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In temperate grasses, such as wheat and barley (*Hordeum vulgare* L.), earliness *per se* is understood as the intrinsic difference in flowering time of fully vernalized plants grown under long day conditions. In the current study, two einkorn wheat lines (*Triticum monococcum* L. x *T. boeoticum* Boiss.), RIL25 (early) and RIL71 (late) were selected from a RILWA1 population to generate a new F_2 population for fine mapping of the *Eps3A* locus. About 650 F_2 individuals were screened for genetic recombinations, and four new markers were added utilizing the physical map from barley chromosome 3H. This way, the locus could be delimited to approximately 350 kb and contained only two putative genes. Moreover, both genes were found to be deleted in the mutant parent of the RILWA1 population KT3-5 (*T. monococcum*) as well as in RIL25. The deletion of *TmLUX* (*lux arrhythmo*, an evening clock element) caused clock distortion and misexpression of circadian clock-related genes. Both effects were detectable by using delayed fluorescence measurements as well as a time-course qRT-PCR experiment on two key nuclear clock genes *TmTOC1* (*timing of CAB2 expression 1*) and *TmLHY* (*late elongated hypocotyl*). On the other hand, sequences of the *TmPUMILIO* (RNA-binding protein) and *TmLUX* were subjected to screen a barley TILLING population of the cultivar Barke, resulting in 34 confirmed mutations for *HvPUM* (including one nonsense mutation) and 39 putative mutations for *HvLUX*. Future analysis may reveal the phenotypes of the putative TILLING mutants in barley. The better candidate, *TmLUX* also was resequenced in a collection of 96 diploid and tetraploid wheats revealing a single A-genome-specific haplotype with a unique 21nt deletion found in the MYB domain. The Chinese cultivar Yunnan possessing this mutation was heading relatively early, thus supporting *TmLUX* as a sensible candidate for *Eps-3A*^{m}. Time course qRT-PCR on this accession as well as on transgenic putative knock-down lines will be performed to verify the *TmLUX*–circadian clock–earliness *per se* connection.

Poster 28. The pleiotropic effects of the master regulator Q and its homoeologous loci in polyploid wheat.

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The *Q* gene on chromosome 5A is of major importance because it governs the free-threshing character, and also pleiotropically affects many other traits associated with wheat development and domestication. To precisely investigate the function of *5AQ*, we developed three *Q* gene near-isogenic lines (NILs) in the background of the hexaploid wheat cultivar Bobwhite (BW), which consist of the BW wild type *5AQ*, an EMS-induced *5AQ* mutant (*5AQm*) with a premature stop codon, and the recessive *5Aq* allele from *Triticum turgidum* subsp. *dicoccoides*. Phenotypic analyses confirmed the previously identified traits controlled by the *Q* gene, such as spike shape, threshability, glume toughness, plant height, and flowering time. In addition, the grain yield per plant of the *5AQ* NIL was significantly higher than the *5AQm* and *5Aq* NILs due to differences in several yield component traits. Microscopic analysis of spike tissue revealed obvious differences in cell morphology among the NILs, which likely underlies the differences in glume toughness and rachis disarticulation attributed to *Q*. To investigate potential downstream genes of *5AQ* responsible for these traits, we analyzed the expression of wheat genes homologous to known development-associated genes, such as *AGAMOUS*, *FLOWERING LOCUS T* (*FT*), *CONSTANS*, and *SHATTERPROOF*. RT–PCR showed a dramatic change in the expression of