In vitro floral development in poplar: Insights into seed trichome and trimonoecy regulation

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Summary

Woody perennials including *Populus* spp. (poplars) have a juvenile phase that ranges from several years to decades in length. This and the year-long floral development process are major impediments to breeding and to fundamental research of reproductive traits. Here we report a CRISPR-empowered *in vitro* flowering system and demonstrate its application using three reproductive traits: sex, seed trichomes, and a previously undescribed potential for trimonoecy in poplar.

Main text

Several regulators of floral development, such as LEAFY (LFY) and FLOWERING LOCUS-T (FT), have been used to induce precocious flowering in annual models and fruit trees (Weigel & Nilsson, 1995; Callahan *et al.*, 2016). Translating these findings into the poplar system has met with various challenges, including dwarfism and sterility (Zhang *et al.*, 2010). Using heat-inducible promoters for *FT* expression has circumvented many of the developmental anomalies; however, repeated application of heat treatments over weeks or months can be detrimental to microsporogenesis (Hoenicka *et al.*, 2014). The method’s efficacy is also season- and genotype-dependent, limiting its widespread adoption (Zhang *et al.*, 2010; Hoenicka *et al.*, 2016).

Here we present an induction-free, *in vitro* flowering system by targeting a negative regulator of floral initiation, *CENTRORADIALIS* (*CEN*, also called *TERMINAL FLOWER*), for knockout (KO). *CEN* antagonizes FT and LFY to regulate meristem determinacy and flowering (Bradley *et al.*, 1997; Jaeger *et al.*, 2013). RNAi-silencing of *CEN* orthologs in poplar and pear (*Pyrus communis*) shortened their juvenile phase to under three years (Mohamed *et al.*, 2010; Freiman *et al.*, 2012), and CRISPR-KO of *CENs* in kiwi (*Actinidia chinensis*) reduced flowering time to under one year (Varkonyi-Gasic *et al.*, 2019). For the present work, we adopted CRISPR/Cas9 to edit the *CEN1/CEN2* paralogs in a female *Populus tremula × alba* INRA 717-1B4 hybrid (hereafter 717). *In vitro* flowering of rooted plantlets was observed under long-day tissue culture conditions within four months of *Agrobacterium* transformation. During vegetative propagation of the mutants, single flowers developed directly from axillary buds of subcultured stem segments and decapitated mother plants within 1-2 wk (Fig. 1a). Amplicon-sequencing confirmed all 17 flowering events as *cen1cen2* double-KOs (Data. S1). *In vitro* flowering was reproducible in nodal cultures where carpels with a cupular disk developed directly from axillary buds (Fig. 1b). This effectively fast-tracked multi-season floral organogenesis to a timeframe of days. We next asked whether both paralogs are involved in floral development as only *CEN1* transcripts are detected in shoot tissues (Fig. S1). We
generated 10 cen1 single-KO events with biallelic mutations (Data. S1) and observed in vitro flowering phenotypes similar to the cen1cen2 double-KOs (Fig. S2). The findings suggest that CEN1, but not CEN2, represses poplar floral development, as independently reported by another group (Sheng et al., 2022).

A female-specific, type-A response regulator (ARR17) gene was recently identified as the sole sex determinant in poplars with either the XY (most Populus spp.) or ZW (P. alba) system (Müller et al., 2020). ARR17-KO in an early-flowering female P. tremula triggered male flower development (Müller et al., 2020). Interestingly, 717 has a hybrid sex configuration (♀, XZ) derived from P. tremula (♀, XX) and P. alba (♂, ZZ), which is supported by detection of hemizygous ARR17 in the haplotype-resolved 717 draft genome (Phytozome). Monoallelic ARR17-KO is predicted to convert 717 from female to male, and this was tested using multiplex-editing of ARR17 and CENs to determine the sex-switch outcome in vitro. We observed male flowers in all eight arr17cen1cen2 events (Fig. 1c-d) and confirmed targeted mutations in all cases (Data. S1). Our results support ARR17-dependent sex switch in a XZ background. The fast-track flowering system is more time- and labor-efficient than the inducible-FT method (Zhang et al., 2010; Hoenicka et al., 2016; Müller et al., 2020) for studying floral traits in poplars.

Soil-transplanted female and male mutants (8-10 events per group) flowered in terminal as well as axillary buds after acclimation (Fig. 1e-f). The indeterminate-to-determinate meristem conversion resulted in cessation of vegetative growth, accelerated maturation with thickening and darkening of preexisting leaves, and following repeated cutbacks, prolific root suckers not seen in WT (Fig. S3).

Healthy suckers and sprouts grew vegetatively for several weeks before they terminated into flowers, whereas cutback triggered flowering from axillary buds within days (Fig. 1g-h). Unfertilized carpels still matured into seedpod-like capsules, which eventually opened and released cottony hairs (Fig. 1i-j). These phenotypes remained consistent across all mutant lines, over multiple rounds of transplanting, and for over a year.

To further exemplify utility of in vitro flowering in reproductive trait investigation, we asked whether a group of MYB transcription factors recently shown to be essential for leaf and stem trichome initiation (Bewg et al., 2022) also regulate seed trichome development. Seeds with tufted hairs are characteristic of poplars and willows, with the cottony trichomes facilitating wind dispersal of seeds. In urban and plantation forestry, seed hairs are carriers of airborne allergens representing a potential health hazard (Hu et al., 2008). Multiplex-KO of CENs and trichome-regulating MYBs produced 11 early-flowering (♀)
glabrous events (Fig. S4), with confirmed edits at all 12 (eight MYB and four CEN) target sites (Data. S1). We compared in vitro carpel development between trichome-bearing and trichomeless (♀) mutants. Ovules were already visible in the immature carpels of cen1cen2 we bisected (Fig. 1k). Intra-ovarian trichomes were not observed until carpels reached c. 2 mm in length and gradually filled the ovary during maturation (Fig. 1l-n). An abundance of trichomes remained attached to ovules which resembled comose seeds (Fig. 1m inset). In glabrous mutants, ovules but not intra-ovarian trichomes were observed throughout carpel development in all three events examined (Fig. 1o-r). The results suggest seed trichomes, like other aerial organ trichomes, are regulated by the same MYBs in poplar, and provide a molecular basis for engineering hairless seeds for genetic confinement or for reducing allergen spread in urban/plantation forestry.

Finally, monitoring of cen1cen2 nodal cultures revealed a remarkable diversity of sex morphs in 717 (♀, XZ), with male, female, and perfect flower development (trimonoecy) dictated by stem node position on the mother plant. In multiple cen1cen2 events, we observed male flowers with stamens only from subapical nodes (Fig. 2a-c), perfect flowers with carpels and stamens from upper nodes (Fig. 2d-f, see also Fig. 1m,n,p), female flowers only from middle nodes (Fig. 2g-i), and vegetative buds from older nodes (Fig. 2j-l). The unusual stamen appearance (♂ or ♀) was transient, limited to just a few nodes near the top. Such a developmental gradient is difficult to capture in soil-grown cen1cen2 mutants because of the pleiotropic phenotypes discussed above. Nevertheless, carpellate flowers with stamens or stamen-carpel chimeras were occasionally observed and always near the top of the (cutback) plant (Fig. S5), consistent with transient male organ development. The occasional appearance of perfect flowers has also been reported in the field (Boes & Strauss, 1994; Zhang et al., 2010). Overall, the data suggest a critical role for ontogenic regulation on poplar sex determination that warrants further research. In sum, the in vitro flowering system bypasses the multi-year reproductive phase transition in poplar and fast-tracks the year-long floral development process to days and weeks. It offers a facile model for investigating floral traits and holds promise for rapid-cycle breeding and genomic selection in perennial trees.

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Author contributions
C.-J.T. and R.Z. conceived the study, C.-J.T. and M.A.O. designed the experiments, M.S.S.C., M.O.A., W.P.B., R.Z. and B.S. conducted the experiments, C.-J.T. wrote the paper with contributions from M.A.O. and R.Z.

Declaration of interests
The authors declare no competing interests.

Figure legends
Figure 1. Rapid flowering of poplar mutants.
(a, b) In vitro female flowers of cen1cen2 from a decapitated plant (a), subcultured stems (a inset), or node cultures (b). (c, d), In vitro male flowers of arr17cen1cen2 from a decapitated plant (c) or nodes (d). (e-h) Female (e, g) and male (f, h) flowers in terminal (e-f) and axillary (f-h) buds following soil transplanting (e-f) or cutback (g-h). (i, j) Seedpod-like capsules with cottony trichomes (i) and their release (j). (k-n) Bisected in vitro carpels of cen1cen2 (k-m) or cen1 (n). Intra-ovarian trichomes were not observed in immature carpels (k) but abundant in later stages and remained attached to ovules causing their comose appearance (m inset). (o-r) Bisected carpels of cen1cen1myb glabrous mutants devoid of intra-ovarian trichomes. Insets are pre-bisected carpels. Independent events are labeled. Bars in (k)-(r), 1 mm. s, stamens.

Figure 2. Ontogenic regulation of sex morphs in cen1cen2 (♀) mutants.
(a-c) Male flowers with stamens (s) from subapical nodes. (d-f) Perfect flowers with stamens and carpels (c) from upper nodes. (g-i) Female flowers from middle nodes. (j-l) Vegetative buds (v) from lower nodes. Three independent events are shown. (m-p) Corresponding nodes from an arr17cen1cen2 (♂) mutant for reference. All images were acquired 5-7 d after node culture except (p) at 18 d. Bars, 1 mm.
References


Supporting Information

Table S1. gRNA, oligo, and synthetic fragment sequences.

Figure S1. Expression of CEN1 and CEN2 in various poplar tissues.

Figure S2. In vitro flowering of representative cen1 mutants.

Figure S3. Phenotypes of soil-grown mutants.

Figure S4. In vitro flowering of representative glabrous cen1cen2myb (♀) mutants.

Figure S5. Chimeric and abnormal male structure in cen1cen2 (♀) mutants.

Data S1. Summary of mutation patterns determined by amplicon sequencing.

Methods
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