

SCREENING OF A SUNFLOWER TILLING POPULATION BY SEQUENCING

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Cultivated sunflower (*Helianthus annuus* L.) is an important oilseed crop grown widely throughout the world. A characteristic trait of this species is solar tracking in which the floral heads track from east to west following the sun's relative position during the day. At night, the reverse happens, and the heads return to face east before dawn. This is one of the most conspicuous diurnal rhythms observed in plants and a crucial role could be played by circadian clock. Circadian clocks are timekeeping mechanisms that integrate environmental signals with internal cues in order to regulate many physiological processes. Eukaryotic circadian clocks consist of numerous interlocking transcriptional feedback loops that involve many genes. Despite the great importance of sunflower, little information is available about the mechanisms underlying the circadian clock in this crop.

Unlike other well-studied species, control of flowering time varies substantially in sunflowers and includes short-day, long-day and day-neutral photoperiodic responses. The components of the flowering-time gene regulatory network that likely contributed to adaptive evolution of flowering time plasticity in sunflower have been previously identified.

Since the circadian clock and flowering time impact agronomically important traits, the investigation of the roles of genes involved in these processes could be especially interesting. Several genetic resources for sunflower were developed in the last few years. Among these, TILLING (Targeting Induced Local Lesions IN Genomes) represents a powerful tool to identify and characterize genes involved in specific pathways.

A previously developed sunflower TILLING platform, sunTILL, is available for the study of genes involved in circadian rhythms and the flowering process. We identified 21 candidate genes possibly involved in these two processes in sunflower and we are now screening an M₂ population of 2,048 mutant lines through the use of next-generation sequencing. The identification of rare mutations in these genes will be useful in defining their roles in circadian clock regulation and in the flowering process in this important crop species.