Barley Cytoplasmic Multi Parent Population (CMPP) for Studying Loss of Plasticity Under Domestication

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ABSTRACT

Although there is evidence that phenotypic plasticity can facilitate the evolution of fixed traits in general, it remains an open question whether it is stability or variability of the different characteristics that have adaptive value and therefore be selected? Besides, recent studies indicate the loss of DNA standing variation underlying interaction with a different environment in modern crops. It remains to explore how much of this left-behind variation is adaptive under current scenarios of climate change and in agricultural fields. To begin answering these questions, we have generated a new multi-parent population derived from reciprocal crosses between cultivated barley (*Hordeum vulgare* cv Noga) and ten different *H. vulgare* ssp. *spontaneum* wild barley ecotypes. Initially, we focus our phenotypic analysis on attributes of the circadian clock plasticity using newly developed high-throughput phenomics platform. Preliminary results indicate trends of lost plasticity of the clock in the transition from wild to the cultivated gene pool. We develop genetic models to allow genome scan for allelic variation driving environmental sensitivity, and testing role of cytoplasm and nuclear loci epistasis in providing thermal plasticity of the circadian clock. Combining these results with field experiments under thermal gradients, and evolutionary field studies (Evolve&Resequence), should assist us in questioning the possible pleiotropic effects of clock plasticity and robustness on fitness and agronomic traits. This study will explore hitherto unknown allelic variation controlling robustness and contribute to our understanding of the mechanisms underlying flexibility vs buffering under a significant ecological constraint

METHODS

Plant material: Four different populations with varying quality and quantity of wild alleles (nuclear and plasmotype) were used to asses plasticity of the circadian clock under domestication. The wild barley gene pool is including representatives for each of the Barley1K (B1K) micro-sites and encompassed 51 sites that from a broad genetic and ecogeographic adaptation niche (Hubner et al. 2009). The US Spring Two-Row Multi-Environment Trial (S2MET) panel, including 232 breeding lines (Neyhart et al., 2019), serves as representative for the cultivated gene pool. Finally, the interspecific multiparent barley population HEB-25, which include introduction of 25 wild barley accessions into the background of the cultivated Barke background (Maurer et al. 2015), is a partial wild material with expected 71.875% homozygosity for the cultivated genome (Maurer et al. 2015). Genotypes to test effects of the plamotype diversity on the phenotype includes reciprocal hybrids between Noga (H. vulgare) and B1K lines.

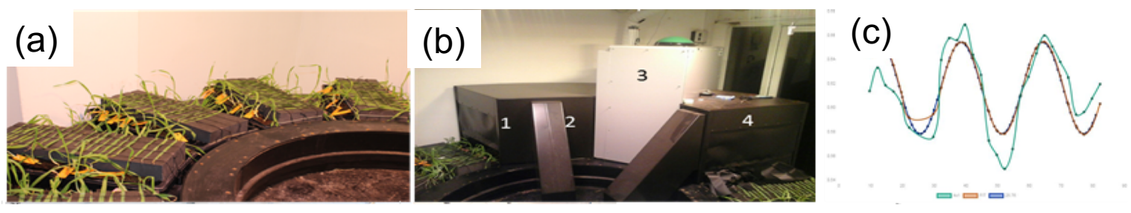

Figure 1: Clock Phenotype. The SensyPAM high-throughput platform is an upgrade for fluorescence-based measurement of the circadian clock rhythm (Dakhiya et al. 2017; Bdolach et al. 2019). It includes **(a)** a carousel which is spinning to the **(b)** imaging chamber and after three days the in continuous light **(c)** NPQlss ((Fm-Fmlss)/Fmlss) is calculated for following the circadian clock (period in h and amplitude) in the BioDare2 website (https://biodare2.ed.ac.uk).

RESULTS AND ONGOING WORK

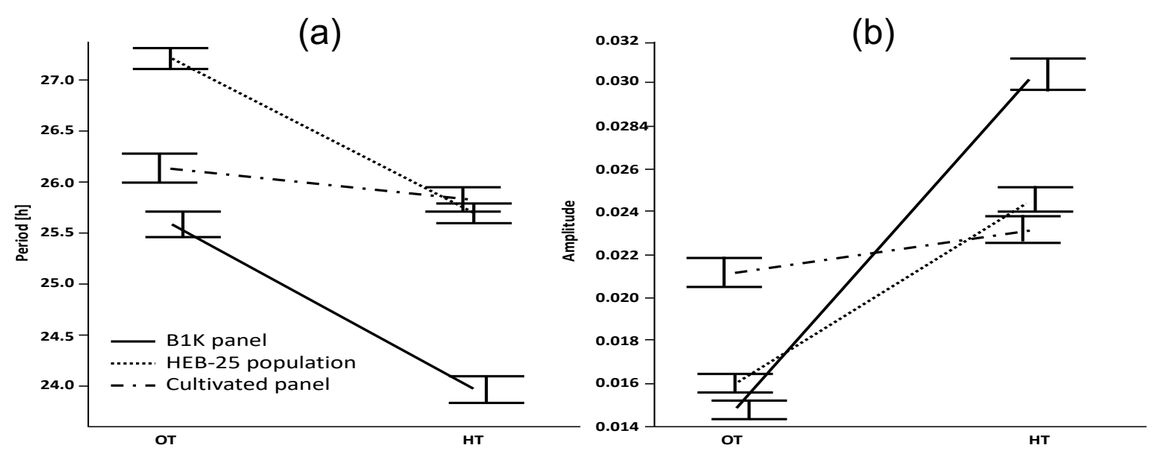

Figure 2: Reaction norms depicting the loss of circadian clock plasticity under domestication. On average, in transition from optimal to high temperature (OT to HT, 22˚C to 32˚C, respectively) the circadian clock is accelerating in wild (B1K) and interspecific (HEB) populations, whereas in the breeding cultivated material (S2MET) the period is maintained. Similarly and more pronounced, the amplitude of the clock is increasing by 50% or 100% in the HEB or B1K populations, respectively, while maintained in breeding material.

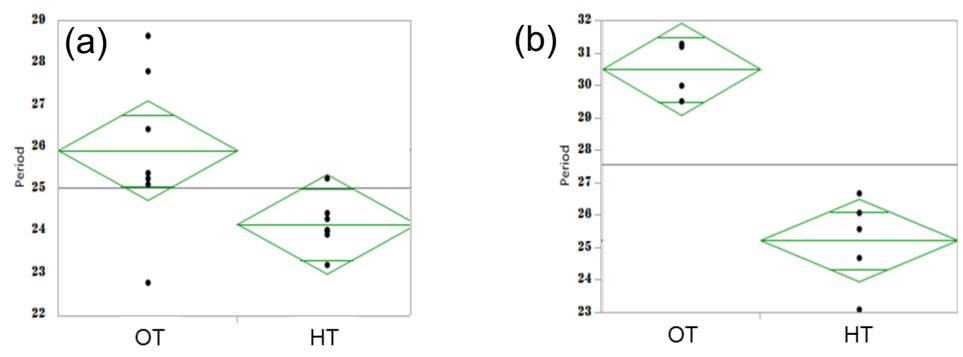

Figure 3: Comparison between reciprocal cultivated x wild F1 hybrids depict link between plamotype diversity and circadian clock plasticity . While **(a)** the cultivated plasmotype [NogaxB1K-03-09] was linked with mild clock acceleration under heat (delta Period; dPERIOD=-1.7 h), **(b)** the reciprocal [B1K-03-09xNoga] F1 hybrids accelerated their rhythms from period of 30.5 h under OT to to 25.2 h (dPeriod=-5.3 h) under HT.

Cytoplasm *Hordeum spontaneum*
Multi **P**arent **P**opulation [**CMPP**)

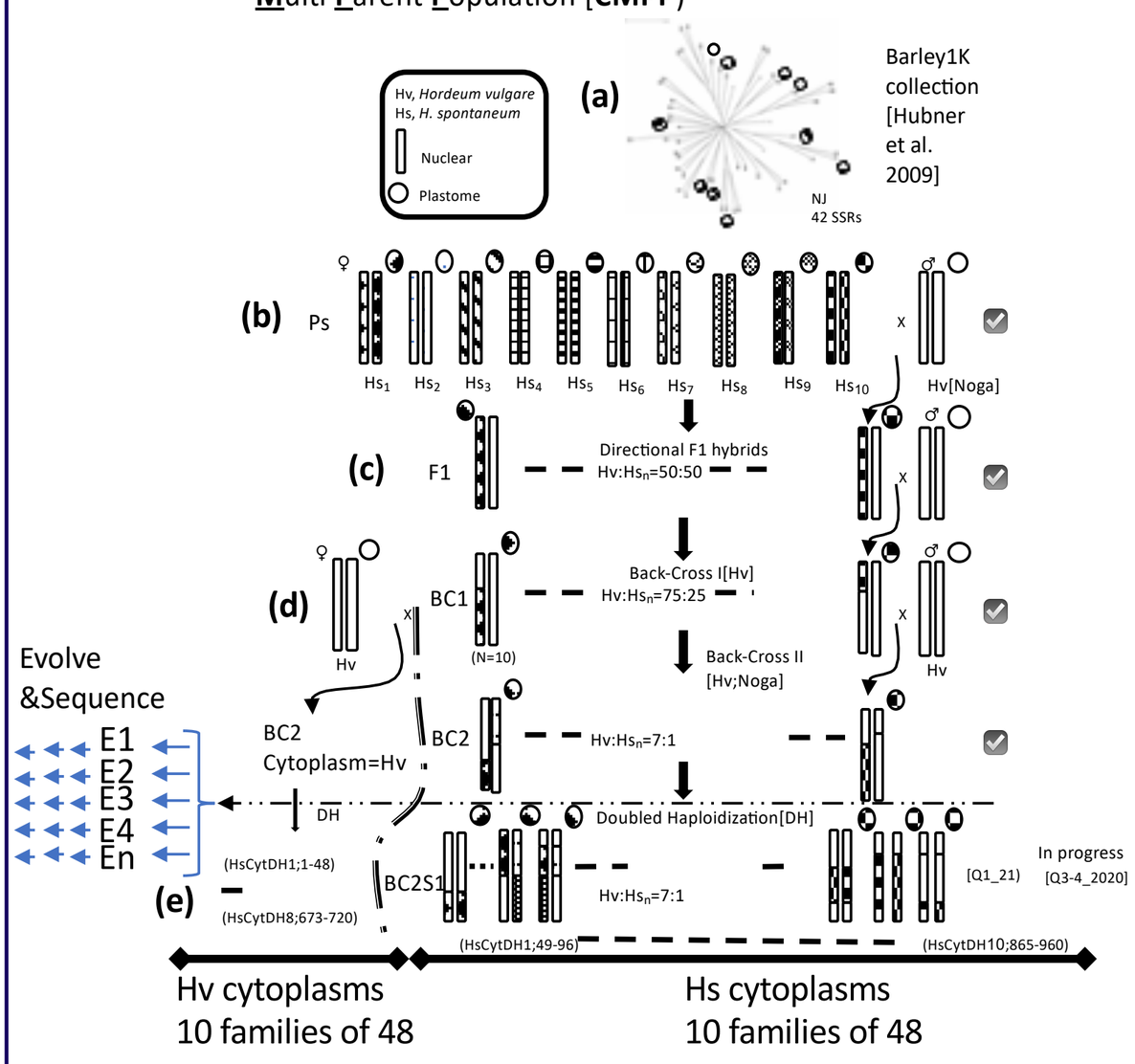

Figure 4: Cytoplasm multi-parent mapping population (CMPP) to dissect genetic sources for circadian clock plasticity, their consequences on adaptation (by QTL analysis) and vice verse, identifying possible selective advantages by E&R experiment. Ten *H. spontaneum* wild barley accessions originated from the Barley1K infrastructure (Hubner et al., 2009) were crossed as females to a common cultivated H. vulgare cv. Noga. The F1 hybrids were back-crossed once to Noga, and 12 of each BC_1 in each family were back-crossed again to Noga, either as female or male. These BC_2 progeny serve as starting material for Evolve&Resequence (ER) experiments under optimal and high-temperature regimes. Besides, these BC_2 serve as pollen donor for generating doubled haploids, either with cultivated or wild plasmotype.

CONCLUSIONS and PROSPECT

- This high-throughput circadian clock SensyPAM is a newly developed phenomics platform that allow high-resolution and large scale, non-invasive measurements of the circadian clock robustness.
- Performing these experiments in different thermal environments allow us to estimate and compare phenotypic plasticity
- Circadian clock plasticity is a hallmark of naturally-adapted wild germplasm and this feature seem to be lost under domestication and selection
- This plasticity is caused by both nuclear and cytoplasm (chloroplast or mitochondria) diversity
- Comparison of the clock and filed phenotype should allow to examine possible pleiotropic effects on fitness and agronomic traits
- These comparisons could be achieved in new CMPP population to possibly develop prediction models
- E&R experiments under optimal and high temperatures are complementary to the QTL approach and could validate selective advantage of specific cytonuclear interactions

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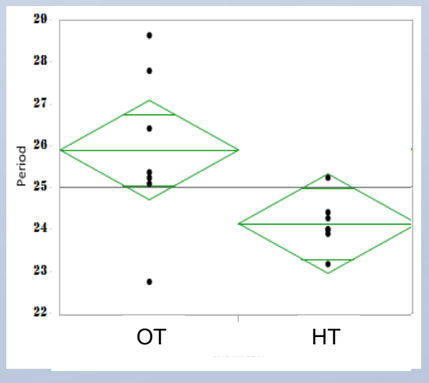
We wish to thank Royi Levav, Oded Anner and Elad Lifshin (SensyTIV, Israel) for the valuable design, construction and implementation of the SensyPAM hardware and software. The FACCE-ERA-NET (Grant # 406/14), ISF 1270/17, and CAPITALISE Horizon2020 grants to E.F support this research.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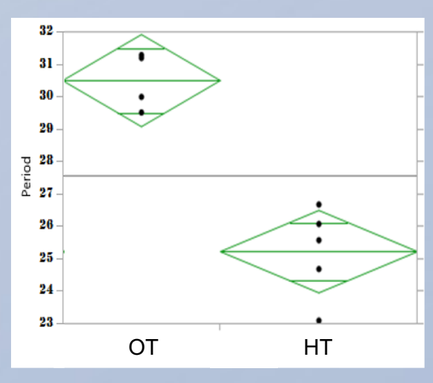
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