

Identification of key genomic segments related to grapevine early-ripening trait by dissecting the pedigree of Pearl of Csaba

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Introduction

The lack of early-ripening varieties with excellent berry quality resulted in the less flexible grapevine supplying marketing period, and limited the economic benefits of planter. Pearl of Csaba (PC) is a valuable backbone parent for early-ripening grapevine breeding, from which many excellent early-ripening varieties have been bred. However, it is largely unknown about the genetic basis of the stable inheritance of its early-ripening trait.

Experiment

The forty varieties from the pedigree of PC were re-sequenced, and combined published data of late-ripening varieties. Population genetic and identity-by-descent analysis were performed by high-quality SNPs to examine population structure and haplotypes. Subsequently, the key genomic segments were identified based on the combination analysis of haplotypes, selective signatures, known ripening-related QTLs and transcriptomic data.

Results & Discussion

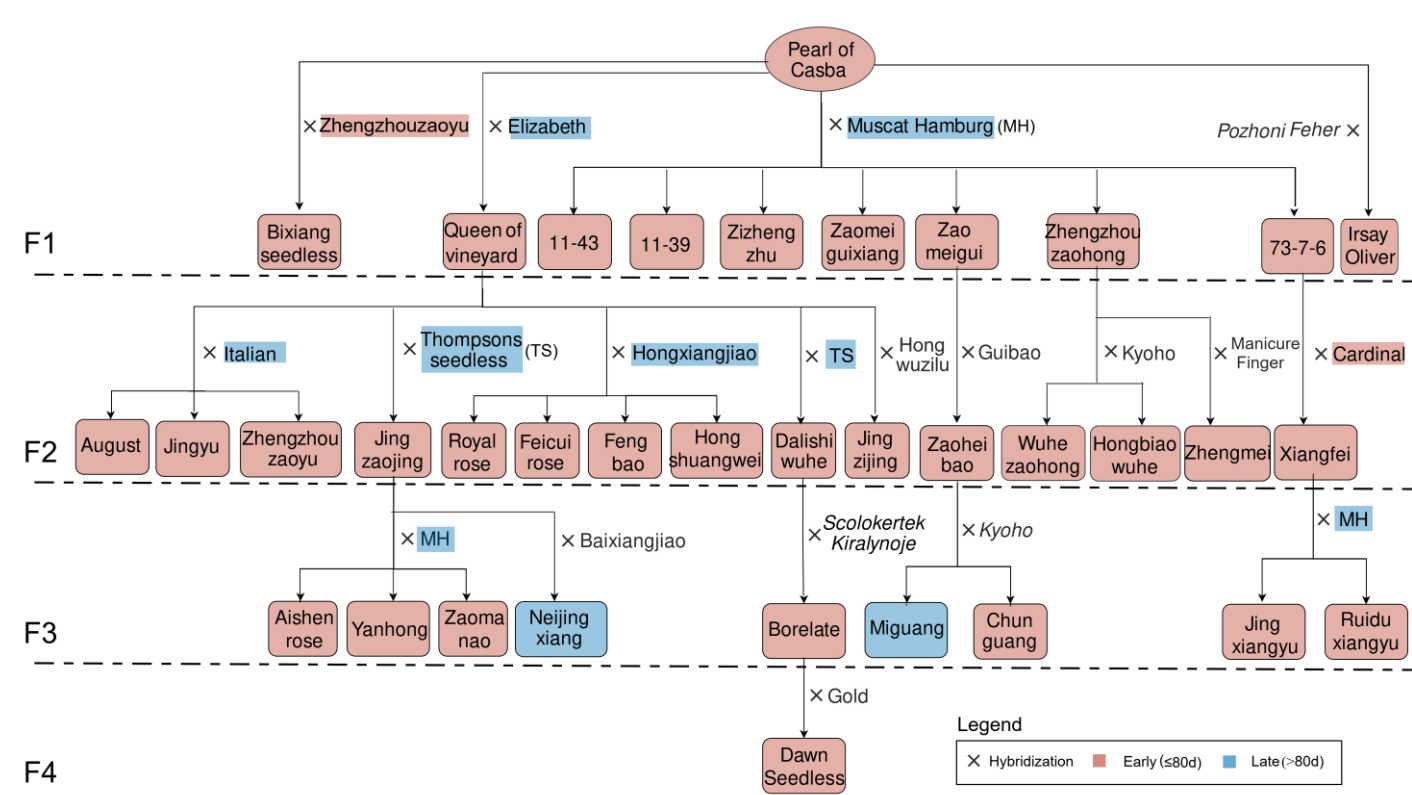


Figure 1. The four-generation pedigree chart of 'Pearl of Csaba'. Different berry ripening trait are represented by different colors.

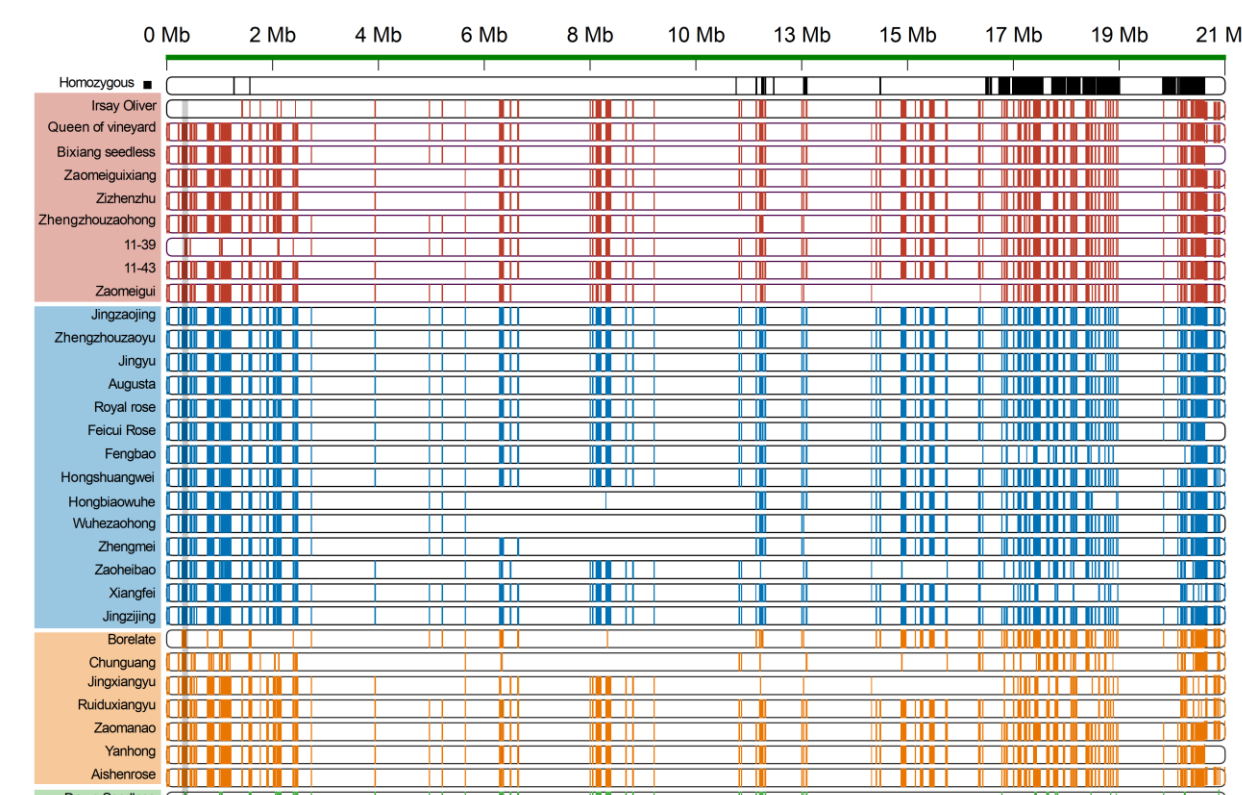


Figure 2. Transmission pattern of conserved haplotypes in the 'Pearl of Csaba' breeding. The transmission pattern of Chromosome 16 was showed.

The descendants of PC showed early-ripening trait with short BDP (Figure 1). The conserved haplotypes (CHs) transmitted in the pedigree were obtained with identity-by-descent analysis based on the pedigree phasing (Figure 2).

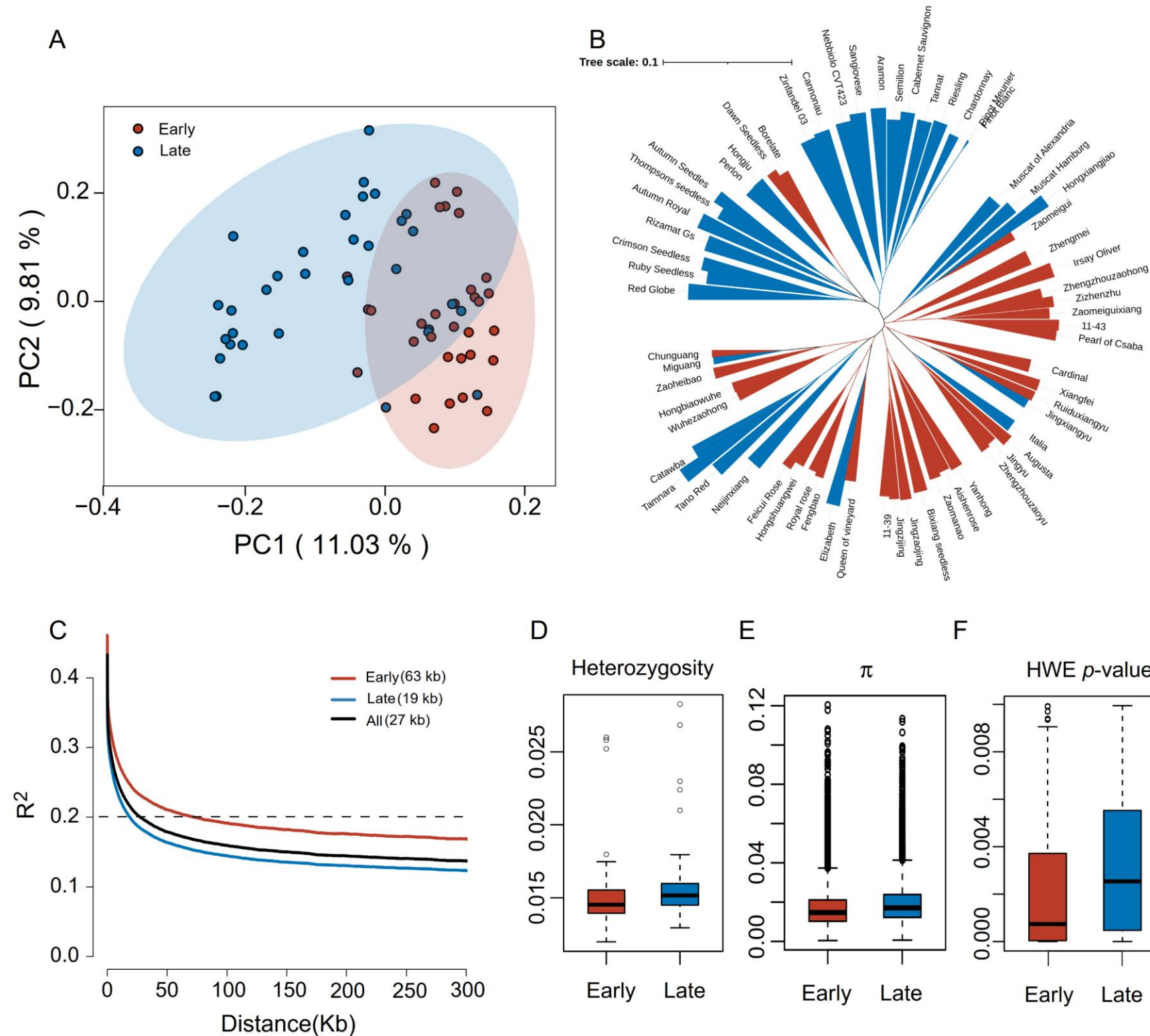


Figure 3. A, PCA plot of early (red) and late (blue). B, Unrooted neighbor-joining tree. C, LD decay. D, heterozygosity, E, nucleotide diversity, and F, Hardy-Weinberg Equilibrium.

The population genetic analysis (i.e. PCA, phylogenetic tree, and STRUCTURE) showed that these varieties could be distinguished clearly, and the early-pedigree was characterized by lower nucleotide diversity and stronger linkage disequilibrium than the late-cultivar.

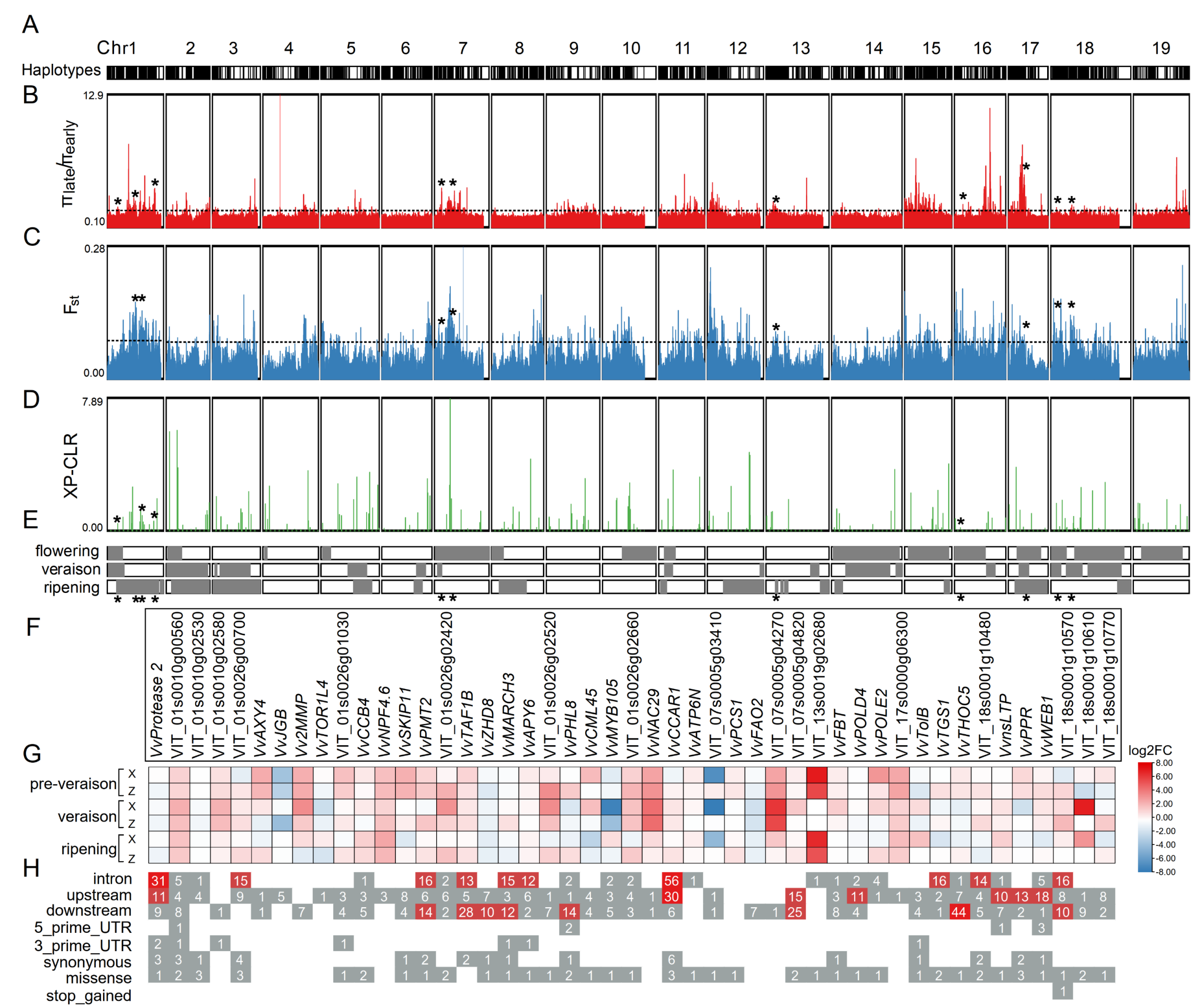


Figure 4. The genome-wide A, Conserved haplotypes, and selective sweeps of B, $\pi_{\text{early}}/\pi_{\text{late}}$, C, F_{st} and D, XP-CLR. E, ripening-related QTLs. F, 47 candidate gene related to early-ripening, and G, their $\log_2\text{FC}$ value at berry developmental stages, and H, their fixed SNPs (fisher-exact p value < 0.0001).

The 47 genes related to early-ripening trait were identified by the combination analysis of conserved haplotypes (Figure 4A), selective signatures (Figure 4B-D), known ripening-related QTLs (Figure 4E), RNAseq (Figure 4G) and fisher-exact test (Figure 4H).

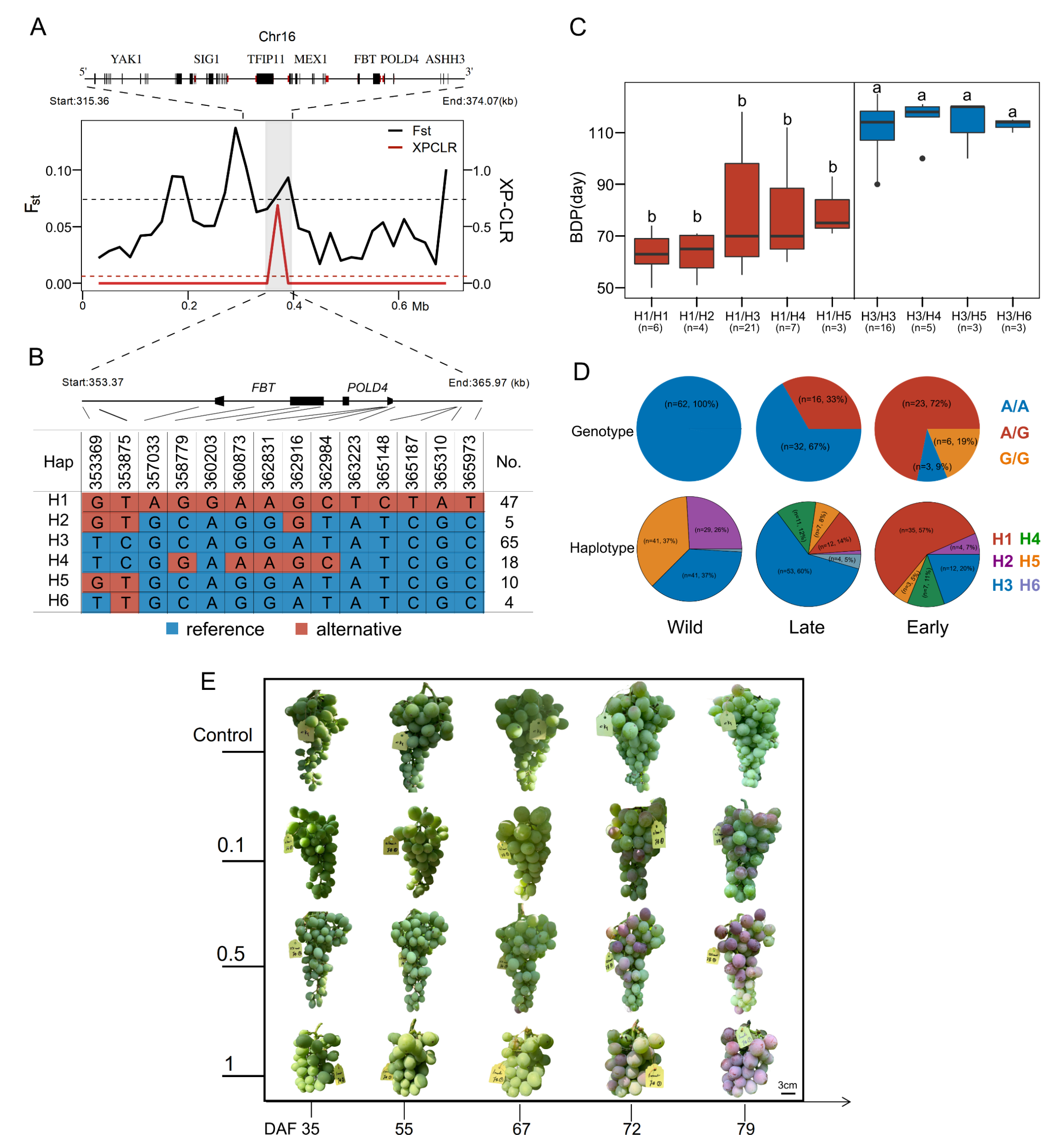


Figure 5. A, Conserved haplotype and F_{st} and XP-CLR overlapped the grey shade. B, The two genes were composed of six haplotypes. C, The association analysis of BDP (days) and haplotypes. D, Number and proportion of a missense SNP (chr16:360203), and haplotypes in different groups. E, The phenotype of exogenous 0.1, 0.5 and 1 mmol·L⁻¹ folate treatment advanced veraison of 'Kyoho'.

The superior haplotype, H1, which significantly exhibited the short berry development days, was focused. H1 encompassed VvFBT encoding folate transporter protein with a missense mutation, and VvFBT was specifically and highly expressed during grapevine berry development, particularly at veraison. Exogenous folate treatment advanced the veraison of 'Kyoho'.

Conclusion

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The core haplotypes and genomic segments related to the early-ripening trait of PC were uncovered based on the combination analysis of re-sequencing, haplotypes, selective signatures, known ripening-related QTLs and RNA-seq.