

Population genomics and epigenomics provide insights into the evolution of facultative asexuality in plants

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Abstract

Many organisms, particularly plants, can reproduce both sexually and asexually but with varying frequencies. Because variations in the reproductive system profoundly affect fitness and genomic diversity, natural selection should act on changes between sexual and asexual types of propagation. However, the genomic evidence of natural selection driving switches between reproductive systems remains scarce, and the evolutionary consequences of such switches on the genomic and epigenomic diversity remain controversial. Here, by analyzing population genomes and epigenomes of *Spirodela polyrhiza* (L.) Schleid., a facultatively asexual angiosperm, we show that while the genomic diversity and DNA methylation levels are very low, they vary among populations. These variations are associated with both the demographic history and the frequency of sexual reproduction in each population. A genome-wide scan revealed that multiple genes involved in flowering and embryogenesis were under positive selection, consistent with the hypothesis that natural selection drove the evolution of asexuality in this plant. Together, these results provide new insights into the evolution of plant reproductive systems and suggest that natural selection can drive the evolutionary changes of asexuality, which in turn alters the levels of genomic and epigenomic diversity.

Introduction

Understanding the evolution of sexual reproduction has long been at the centre of evolutionary biology. Theories suggest that asexual reproduction is beneficial for the short term but costly for the long term, mainly due to accumulations of deleterious mutations and low effective population size^{1–5}. Facultative asexuality, where organisms can reproduce both sexually and asexually depending on environmental conditions, should be optimal for one individual's lifespan^{6,7}. While rather few animals such as aphids (aphidoidea)⁸, water fleas (cladocerans)⁹, and rotifers¹⁰ reproduce facultatively asexually, up to ~ 80% of the flowering plants, including important crops and keystone species, can reproduce both sexually and asexually¹¹. Asexual reproduction in plants involves different types of vegetative reproduction (e.g. runners, tubers, bulbs, corms, suckers, plantlets), as well as apomixis, the formation of seeds without fertilization¹². Because changes between sexual and asexual reproduction profoundly affect fitness, natural selection might act on the genetic controls of sexual and asexual reproduction in facultative asexual organisms, which in turn can alter the levels of genomic diversity, heterozygosity and effectiveness of selection in the population^{2,5,13–15}. However, direct evidence supporting this prediction remains scarce, mainly due to the lack of a suitable facultative asexually reproducing system in which the signature of selection can be detected at genomic levels.

Evolutionary changes in sexual and asexual reproduction might also affect the maintenance and dynamics of epigenetic markers, i.e., DNA methylations. In plants, cytosine methylation can occur in three sequence contexts: CpG, CHG, and CHH (H = A, T, or C), which are controlled by different mechanisms and have different dynamics during reproduction¹⁶. Typically, CpG and CHG methylation are maintained by methyltransferases1 (*MET1*) and CHROMOMETHYLASE3 (*CMT3*), whereas CHH

methylation is mostly maintained by *CMT2* or the RNA-directed DNA methylation (RdDM) pathway¹⁷. However, *CMT3* was found to also play a role in the maintenance of CHH methylation, as well as *de novo* methylation¹⁸. During sexual reproduction, DNA methylations are highly dynamic¹⁹. In both male and female gametogenesis, the megaspore mother cell and its male analogue experience dramatic chromatin changes during cell specification, such as heterochromatin decondensation and an enlarged nuclear volume^{20,21}. During male gametogenesis, sperm DNA is highly methylated in the CpG and CHG context but has low CHH methylation in retrotransposons^{19,22,23}. During female gametogenesis, CpG and CHH methylation remains largely steady²⁴. After fertilization, CHH methylation increases during embryogenesis and can approach 100% at individual cytosines, which then decreases likely through a passive mechanism after germination^{25–27}. In contrast, during vegetative reproduction, DNA methylation is likely steady since meiosis and embryogenesis are lacking^{28–30}. Although a recent study comparing DNA methylations among 34 angiosperm species suggested that clonally propagated species often have low CHH methylation³¹, the extent to which asexual reproduction affects genome-wide methylation levels remains unclear.

Here, we investigated the population genome and epigenome of a facultatively asexual flowering plant, *Spirodela polyrhiza* (the giant duckweed; Lemnaceae), which has a global distribution. This species, like other duckweeds from the genera *Spirodela*, *Landoltia* and *Lemna*, is characterized by leaf-like fronds derived from fused stems³² and, with multiple roots on each frond³³ and with a highly reduced vascular system³⁴. *Spirodela polyrhiza* reproduces vegetatively via budding under normal conditions but rarely switches to sexual reproduction under unfavourable conditions^{35,36}. Recent studies showed that despite its global distribution in diverse habitats, the genomic diversity, spontaneous mutation rates and DNA methylation levels in *S. polyrhiza* are very low^{37–42}, which might be associated with its overall low frequency of sexual reproduction. DNA methylation profiling of two genotypes suggests that DNA methylation in *S. polyrhiza*, which is substantially lower than in other plants, likely due to the loss of the RdDM pathway, varied between genotypes⁴¹. Further insights into the evolutionary origin and consequences of asexuality on genomic and epigenomic variations in *S. polyrhiza* are required to understand the demographic history and to identify the footprint of selection on the genome.

Results

Low genomic variations in *S. polyrhiza*

We sequenced the genomes of 131 globally distributed *S. polyrhiza* genotypes with an average of ~ 25 X coverage. Together with previously published samples^{1,2}, we analysed the genomic diversity of 228 *S. polyrhiza* individuals across five continents (Supplementary Data 1). We identified 1,241,981 high-quality biallelic single-nucleotide polymorphisms (SNPs) and 166,075 short insertions and deletions (INDELs, less than 50 bp of length). Based on an updated genome annotation of *S. polyrhiza* (see Section 1.1 of the Supplementary Information), we found that most of the SNPs (70.3%) are in the intergenic regions (Supplementary Fig. 1). Of all the SNPs located in the protein-coding regions, 61,039 were identified as

nonsynonymous and 44,287 as synonymous (Supplementary Data 2). Consistent with our previous study, the genome-wide nucleotide diversity at neutral sites is 0.0013 (Supplementary Table 1), the lowest among multicellular eukaryotes. The species-wide efficacy of selection (π_N/π_S ratio) is 0.39, the highest among studied organisms⁴³, indicating relatively weak purifying selection in *S. polyrhiza*, despite its large effective population size^{1,2}.

In addition to SNPs and small INDELs, we also characterize the genome-wide structural variations (SVs, ≥ 50 bp in length) in *S. polyrhiza* (see Section 1.2 of the Supplementary Information). We identified 3,205 high-quality SVs, including 2,089 deletions, 291 duplications, and 825 insertions. The abundance of the SVs is substantially lower than all reported multicellular organisms^{44,45}. Among all identified SVs, 155 duplications and 169 deletions affected protein-coding genes (Supplementary Table 2). Interestingly, in comparison to the genome-wide average, the MADS-box genes (see Section 1.3 of the Supplementary Information) showed a higher tendency to overlap with SVs (permutation tests; $P = 0.063$). In addition, we also observed a significant overrepresentation of small INDELs in the MADS-box genes (permutation tests; $P = 0.008$). These results indicate that MADS-box genes might be under positive or relaxed purifying selection in *S. polyrhiza*.

Population structure and demographic history of *S. polyrhiza*

Because *S. polyrhiza* is facultatively asexual, genotypes collected from the geographic proximity can be derived from the same clonal family. Using a previously established grouping threshold that was developed in *S. polyrhiza*², we identified 159 likely clonal families (Supplementary Data 3).

Population structure and principal component analyses revealed four populations in *S. polyrhiza* (Fig. 1a and 1b). Consistent with our previous study, the four populations are largely concordant with their geographic origins, namely America, South East Asia (SE-Asia), Europe, and India (Supplementary Fig. 2), with a few exceptions that can be due to recent migration events or artefacts during long-term duckweed maintenance.

We inferred the population history with a Maximum Likelihood (ML) phylogeny combined with Approximate Bayesian Computation (ABC). Using *Colocasia esculenta* (from the Araceae family) as an outgroup, the maximum likelihood phylogeny of all 228 genotypes indicated an early split of the American population from the other populations and subsequent splits of the Indian and European populations from SE-Asia (Fig. 1c). The European population constitutes the most recent split (Fig. 1c-d). Here, genotypes collected from the transcontinental region (e.g. Russia) showed intermediate features of SE-Asian and European populations, suggesting this as a likely migration route. Furthermore, the Indian population possibly originated via Thailand and Vietnam, as genotypes from these countries show intermediate features between Indian and SE-Asian populations.

We modelled the demographic history using an ABC modelling approach to further validate the evolutionary history of the four populations in *S. polyrhiza*. Three plausible demographic scenarios were

simulated, allowing for either the SE-Asian, American or an additional putative population to function as the ancestral population (Supplementary Fig. 3). We found that the scenario, in which the American population and Asian population were derived from an additional putative ancestral population, constituted the most supported model (Fig. 1d). While the American population was separated from other populations around 1 million generations ago, the European population was derived from the SE-Asian population only 12,000 generations ago (see Section 1.4 of the Supplementary Information).

Determinants of genomic diversity among populations

Among the four populations, nucleotide diversity (π) and the efficacy of selection (π_N/π_S ratio) varied among populations (Fig. 2b). While the SE-Asian population has the highest π and lowest π_N/π_S ratio, the American population has the lowest π and highest π_N/π_S ratio. Interestingly, while the European population has a much smaller π compared to the SE-Asian population, the π_N/π_S ratio of the European population remains similar to the latter, likely due to its recent split from the SE-Asian population.

Using genome-wide SNPs, we found that linkage disequilibrium (LD) is comparable to *Arabidopsis thaliana*⁴⁶, suggesting considerable historical sexual reproduction in *S. polyrhiza*. However, the extent of LD decay varied substantially among populations (Fig. 2b and Supplementary Fig. 4). While the Asian population showed the most rapid LD decay (about 12 kb at $r^2 = 0.2$), the European population had very long LD blocks (> 100 kb). The Indian and American populations had intermediate LD decay. This pattern is further supported by the recombination rates calculated for all four populations, where the Asian population had the highest recombination rate compared to the other three (Fig. 2b). Different LDs and recombination rates found among populations indicate that the frequencies of sexual reproduction varied among populations. In addition, we found that the variations of heterozygosity in *S. polyrhiza* showed a similar pattern with the genomic diversity and recombination rate among four populations (Fig. 2 and Supplementary Fig. 5).

Interestingly, the changes in genomic diversity and levels of heterozygosity are associated with two SVs involving MADS-box genes that are involved in sexual reproduction. One SV is an 84 bp insertion at the last coding sequence (CDS) of gene SpGA2022_005278, a homolog of *AGL62* from the Ma subclade of MADS-box genes (Supplementary Fig. 6). In *A. thaliana*, *AGL62* is a transcription factor that suppresses endosperm cellularization by activating the expression of a putative invertase inhibitor, *InvINH1*, in the micropylar region of the endosperm^{47,48} (Supplementary Fig. 7). The insertion likely disrupted the function of the *AGL62*-like gene, thus reducing the suppression of endosperm development, which is likely required for sexual reproduction (Fig. 2a). Consistently, we found the insertion was at a higher abundance in the SE-Asian population (87.5%) than in other populations (Fig. 2c and 2d). In addition, the insertion positively correlates with heterozygosity within the European population (Supplementary Table 3 and Supplementary Fig. 8). Another SV is a 69 bp deletion at 1.8 kb upstream of *SOC1* (SpGA2022_007306, Supplementary Fig. 5), the ortholog of which is a positive regulator of the flowering process in *A. thaliana*⁴⁹ (Fig. 2a). The deletion was exclusively found in the Indian population with the

alternate allele frequency of 73% (Fig. 2c). It is plausible that the deletion, due to its disruption potential at the *cis*-regulatory region, reduces the ability of the *SOC1*-like gene to respond to the upstream floral activators (e.g. *CO*) in *S. polyrhiza*, thus reducing the frequency of sexual reproduction in the Indian population (Fig. 2d). Consistently, this deletion negatively correlates with heterozygosity in the Indian population (Supplementary Table 3, Supplementary Fig. 9).

Population epigenomic diversity in *S. polyrhiza*

As changes in sexual reproduction can also alter epigenomic dynamics, we further investigated the patterns of population epigenomic diversity in *S. polyrhiza*. We selected five individuals from each population and quantified their shoot DNA methylation levels at single-base resolution using whole genome bisulphite sequencing. Similar to a recent study⁴⁰, we found that only 1.5% of cytosines are methylated in *S. polyrhiza* (7.2% of CpG, 2.2% of CHG, and 0.1% of CHH; see Supplementary Table 4), and the average species-wide methylation levels are much lower than all other investigated angiosperm species (Supplementary Fig. 10)^{31,50}. The hierarchical clustering of 20 methylomes in CpG, CHG, and CHH contexts show high consistency with their genetic similarity (Supplementary Fig. 11–13). Few discrepancies were mostly found within the same population or between the recently diverged SE-Asian and European populations, which indicates that population demography can strongly affect epigenomic variations in *S. polyrhiza*.

We then compared the genome-wide weighted methylation level (wML) among populations. For CpG methylation, the four populations did not differ at genome-wide levels (Fig. 3a). However, CpG methylation level in gene bodies (but not in TEs) was higher in the American population than the other three populations (Fig. 3d, g). For CHG, the Indian population had the lowest genome-wide methylation level among all four populations (Fig. 3b, 3e and 3h). Interestingly, for CHH, the American population had the lowest genome-wide methylation level ($P < 0.01$, pairwise Wilcoxon test; Fig. 3c), while the European and Indian populations showed a gradual reduction of methylation in comparison to the SE-Asian population. The pattern was the same for both gene bodies and TEs ($P < 0.01$, pairwise Wilcoxon test; Fig. 3f and 3i). The genome-wide reduction of CHH methylation is consistent with the hypothesis that clonal reproduction reduces CHH methylation, and the effects gradually accumulate over clonal generations⁵¹.

The footprint of selection on the genome

To identify the genomic signature of selection at the species level we performed genome-wide scan. To reduce false positives, we used the μ -statistics from RAI^{SD}⁵², the composite likelihood ratio CLR statistic from SweeD⁵³, and the T statistic from LASSI⁵⁴. We found 69 genes showed strong signature of selection using all three methods (Supplementary Fig. 14). Manual inspection indicated that several orthologs of these genes are related to gametogenesis (e.g., *NOTCHLESS*) and embryogenesis (e.g., *NUP214*, *CPSF*, *CDK*, *AGP*, and *ACR4*) in *Arabidopsis thaliana*^{55–59}. Further enrichment analysis indeed showed that embryo lethal genes were enriched in these 69 genes ($P = 0.016$, χ^2 test). In addition, the *A.*

thaliana orthologs of several genes under selection are also associated with controlling sexual reproduction, including floral development (*DRMY1* and *ACR4*)^{55,60}, flowering time (*NF-Y AT2G27470*, *NF-YAT1G72830*, and *CPSF*), pollen development (*EFOP3*, *ELMOD*, and *CLC*)^{57,61–65}, seed development (*NUP214*, *NF-Y AT2G27470* and *NF-YAT1G72830*, and *Transducin/WD40*)^{56,61,66}. Furthermore, among these 69 genes, we also found several genes involved leaf development and vascularity (*SECA2*, *RbgA*, *PHABULOSA/PHAVOLUTA*)^{67–69}, light signaling (*NF-Y*, *CCR4-NOT*, and *PPP*)^{61,70,71}, root development (*GEND1*, *WAVY*, and *ACR4*)^{55,72,73} and DNA damage repair (*ATM* and *Xrcc3*)^{74,75} (Supplementary Data 4).

To further understand the selection that drove the evolution within individual populations, we identified the signature of positive selection in a three-population tree using patterns of linked allele frequency differentiation and calculating the corresponding composite-likelihood ratio (CLR, see Methods). In total, we found 1,883 genes on the SE-Asian branch, 593 genes on the Indian branch and 401 genes on the European branch (Fig. 4a; see Section 1.5 of the Supplementary Information) which showed strong signatures of selection (top 1% of CLR values).

We found that genes under positive selection in the European branch are enriched with reproduction and development-related GO terms (Supplementary Fig. 15). Among these, SpGA2022_013448, in chromosome 9, is an ortholog of FLOWERING LOCUS KH DOMAIN (*FLK*) that delays flowering by up-regulating *FLC* family members in *A. thaliana*⁷⁶. This gene showed a strong signature of selection in the European branch but not in other branches (Fig. 4c and d). Similarly, SpGA2022_006111, on chromosome 3, is an ortholog of the *A. thaliana* BIG BROTHER (*BB*) that negatively regulates floral organ size and is also under selection in Europe⁷⁷ (Fig. 4c).

In the SE-Asian population, we found that gene SpGA2022_051517, a CHROMOMETHYLASE3 (*CMT3*) homolog in *A. thaliana*, is involved in maintaining CpG, particularly CHG methylation¹⁷. This is consistent with the higher CpG and CHG methylation levels observed in the SE-Asian population when compared to the European and Indian populations (Fig. 3a and 3b). Within the Indian population, we found that five MADS-box genes have been under selection exclusively along this branch. Given that there are 43 MADS-box genes in the genome, the fact that five of them have been targeted by selection, constitutes a significant enrichment of such genes under selection ($P = 0.0075$, Fisher's Exact test). For example, SpGA2022_013078 is an ortholog of AGAMOUS-LIKE6 (*AGL6*), which is involved in flower and meristem identity specification in rice⁷⁸; SpGA2022_052274, a homolog of APETALA3 (*AP3*), is involved in the petal and stamen specification in *A. thaliana*⁷⁹; and SpGA2022_006905 belongs to the SHORT VEGETATIVE PHASE (*SVP*-group) which controls the time of flowering and meristem identity⁸⁰.

We found 77 genes under positive selection (top 1% CLR values) in both the European and Indian populations (Fig. 4b), significantly more genes than expected by chance ($P < 2.2e-16$, Fisher's Exact Test). Among these, gene SpGA2022_055195, a homolog to *CYP78A9* of cytochrome P450 monooxygenases in *A. thaliana*, belongs to a highly conserved gene family CYP78A. Previous studies in *A. thaliana* and other species found that *CYP78A9* plays a critical role in promoting cell proliferation

during flower development and further impacts seed size^{81–83}. Overall, these data consistently suggest that genes involved in reproduction and development were under selection in Indian and European populations, which might have led to reduced sexual reproduction in these two populations.

Discussions

Here, we characterized the genomic and epigenomic diversity, as well as the demographic history of a facultative asexual flowering plant, *S. polyrhiza*. We found that among populations of *S. polyrhiza*, demographic history and reproductive system jointly determine the population's genomic and epigenomic diversity. Analyses on the footprint of selection suggest that natural selection drove the reduced vascular system and increased asexuality in *S. polyrhiza*.

Theory predicts that asexual reproduction reduces genomic diversity and the efficiency of purifying selection⁸⁴. Consistent with this prediction, at the species level, we found that *S. polyrhiza* has very low genomic diversity and reduced purifying selection (seen as an increased π_N/π_S ratio), when compared to a wide range of spermatophyte plants⁴³. Within species, the SE-Asian population, which has the highest frequency of sexual reproduction based on the estimated recombination rate, has the highest genomic diversity, the lowest π_N/π_S ratio and the highest heterozygosity (Fig. 2b), supporting the theoretical prediction^{2,5,13–15}. The low π_N/π_S ratio found in the European population, which has the lowest sexual reproduction and genomic diversity, is most likely due to its migration history. The demographic model suggested that the European population derived from the SE-Asian population very recently (Fig. 1d). It is likely that the π_N/π_S ratio in the European population remained the same as its ancestral population and has not reached an equilibrium level yet.

While there are fewer genome-wide SVs in *S. polyrhiza* compared to other species^{44,45}, we found these variants and small INDELs are in tendency enriched in MADS-box genes. This indicates that the loss-of-function of MADS-box genes, many of them involved in flower development and sexual reproduction, is under natural selection. The results are consistent with the observation that the number of functional MADS-box genes was dramatically reduced in *S. polyrhiza*⁸⁵.

Single-base resolution methylomes of 20 individuals showed that the overall CpG, CHG and CHH methylation levels in *S. polyrhiza* shoots are very low, consistent with previous studies^{40,86}. The low levels of DNA methylation might be associated with reduced sexual reproduction: while CpG and CHG methylations in plants are important for controlling cross-overs during meiosis⁸⁷ and are increased during male gametogenesis, CHH methylation is highly accumulated during embryogenesis^{19,25–27}. In facultative asexual plants, due to reduced sexual reproduction and meiosis, the selection of genetic mechanisms maintaining or increasing the CpG, CHG and CHH methylation is reduced or absent, which might have led to the reduced CpG, CHG and CHH methylation levels. Consistently, a recent study suggests that *S. polyrhiza* has lost several genes in the RdDM pathway⁸⁶. Interestingly, within species, the methylation profile of the 20 individuals correlates with their genetic distance (Supplementary

Fig. 11–13), indicating a gradual evolution of DNA methylomes in *S. polyrhiza*. For example, the Indian and European populations, which diverged from SE-Asian populations around 51,000 and 12,000 generations ago, gradually decreased their DNA methylations (Fig. 3a-c).

At the species level, using a genome-wide scan approach, we found a strong signature of natural selection on genes involved in flower and seed development. indicating that the evolution of reproduction, likely, an increased clonal propagation in *S. polyrhiza*, was driven by natural selection. This is consistent with the pattern that many aquatic organisms reproduce clonally⁸⁸. In addition, several genes related to vascularity, root development and DNA damage repair were also under strong selection, suggesting the reduced root and vascular development and low mutation rate in *S. polyrhiza* were likely also driven by natural selection.

Among populations, we found strong positive selection on genes involved in sexual reproduction and development in Indian and European populations, two recently evolved populations that showed reduced genomic recombination. These results suggest that natural selection favours clonal reproduction in *S. polyrhiza* during the recent colonization process, a pattern was frequently found in many invasive species^{89,90}. However, despite strong selection favouring clonal reproduction, substantial recombination in the *S. polyrhiza* genome, mostly in the SE-Asian population, remained, reflecting that sexual reproduction is essential to overcome the costs involved in clonal reproduction in long term.

Taken together, population genomes and epigenomes of *S. polyrhiza* suggest that natural selection acting on the mating system and organ development can shape genome-wide genomic and epigenomic variations.

Methods

DNA sample preparation and sequencing

We sequenced 131 genotypes that were primarily collected from Asia and Europe (Supplementary Data 1). These samples were cultivated in N-medium⁹¹ until DNA isolation using a CTAB method. Library preparations were carried out following the protocol described in Xu *et al.* (2019)³⁷. All libraries were sequenced either on Illumina HiSeq X Ten or Illumina HiSeq 4000 platforms for paired-end sequencing with a read size of 150 bp. Low-quality reads and adapter sequences were trimmed with AdapterRemoval (v2.033)⁹². On average, 33.8 million reads per genotype were obtained. The clean reads were aligned to the *S. polyrhiza* reference genome^{93,94} using BWA-MEM (<https://github.com/lh3/bwa>) with default parameters. Reads without alignment hits or with multiple alignment positions were removed. SAMtools “rmdup” function was used to remove PCR duplicates⁹⁵.

Single nucleotide variant calling

We filtered SNPs using GATK⁹⁶ (v4.1.4.1, Java 11) with options: "QD < 2.0 | QUAL < 30.0 | SOR > 3.0 | FS > 60.0 | MQ < 40.0 | MQRankSum < -12.5 | ReadPosRankSum < -8.0". Then, VCFtools (v0.1.13)⁹⁷ was used to remove SNPs that have the following features: 1) non-biallelic; 2) minor allele frequency (MAF) less than 0.01; 3) mean sequencing depth greater than eight or less than 41; 4) missing genotypes greater than 20%; 5) located in small SNP clusters (more than two SNPs in a ten base-pair window). SnpEff (version 5.0c)⁹⁸ was used to annotate SNPs and INDELs.

We estimated genome-wide nucleotide diversity and genome-wide π_N/π_S ratios using SNPgenie (v2019.10.31)⁹⁹. The genome-wide heterozygosity for each individual was calculated using VCFtools (v0.1.13)⁹⁷. We estimated the genetic associations between heterozygosity and the SVs of AGL62 and SOC1 using RVTESTS¹⁰⁰ with single variant Wald test.

Population structure and linkage disequilibrium (LD)

We grouped genetically similar genotypes by defining clonal genotype pairs that have no more than 0.01% different homozygous sites and no more than 2% different heterozygous sites. These thresholds were previously adopted by Ho *et al.* (2019)³⁸.

Prior to the population structure analysis, we removed SNPs that 1) deviated from Hardy-Weinberg Equilibrium (Fisher exact test, $P < 0.01$) or 2) linked loci (each pair of SNP have correlation coefficient $r^2 > 0.33$ in a sliding window with a size of 50 SNPs and step of 5 SNPs), using VCFtools (v0.1.13)⁹⁷ and Plink (v1.9)¹⁰¹.

Principal component analysis (PCA) and population structure analysis were carried out using Plink (v1.9)¹⁰¹ and fastStructure (v1.0)¹⁰², respectively. The simple mode (as default) from fastStructure was used for the population structure analysis. The K value was estimated using a heuristic function in fastStructure.

For each of the 159 clonal families, we selected the least missingness genotype (i.e. the genotype with the highest sequencing coverage of that clonal family) as the representative genotype. SNP information from all 159 representative genotypes was used to estimate the linkage disequilibrium decay for each of the four populations. PopLDdecay (v3.41)¹⁰³ was used to measure LD decay. For each population, we used the following filters: SNP of missing allele > 20% and MAF < 0.05. The allele frequency correlation (denoted as r^2) of pairwise SNPs within 100 kb physical distance was calculated.

Phylogenetic tree reconstruction

We used BLAST + version 2.9.0¹⁰⁴ to identify orthologous fragments between the genomes of *S. polyrhiza* and *Colocasia esculenta* (Araceae). For each SNP from the core set, the reference allele and its flanking 300 bp (upstream 150 bp and downstream 150 bp, respectively) sequences were extracted from the *S. polyrhiza* genome and then aligned to the *C. esculenta* reference genome¹⁰⁵. The hit thresholds

were set as 1) alignment identity > 70%; 2) e-value > $1e - 6$; 3) minimum aligned sequence length ≥ 50 (the aligned sequence must cover SNP position); 4) keep the best hit; and 5) ignore short deletions from *C. esculenta*. The orthologous alleles from *C. esculenta* were used as the outgroup genotype. We identified only 13,120 SNPs that have orthologous fragments in the *C. esculenta* genome. Those data were further used to infer the maximum-likelihood (ML) phylogenetic tree using RAXML-ng (v1.0.1)¹⁰⁶. The best hit model was estimated to be 'TVM + G4' using Modeltest-ng (0.1.6)^{107,108}. The bootstrapping converged after 700 iterations of the ML tree search. ITOL v5¹⁰⁹ and the Python package ETE2¹¹⁰ were used for tree visualization.

Selection analysis

Genome-wide scans of selection were performed on all 20 chromosomes of all sampled populations. Selective sweeps were inferred by three programmes: RAI^{SD}⁵², SweeD⁵³ and LASSI⁵⁴. RAI^{SD} uses the μ statistic, which provides information on the SFS, LD, and genomic diversity to evaluate the presence of positive selection⁵². SweeD calculates the traditional composite likelihood ratio (CLR) to infer loci under selection⁵³. LASSI employs the T statistic, which uses a likelihood model based on the haplotype frequency spectrum to detect hard and soft sweeps⁵⁴. As recommended by the authors of LASSI, we selected the top 5% T scores as candidates for selection. For RAI^{SD} and SweeD we selected the top 1% scores. After finding the common genes under selection according to all three programmes, we reported the genes that have orthologs in *A. thaliana*. The embryo lethal genes from *A. thaliana*¹¹¹ were used for the enrichment analysis.

To test for population/branch-specific signals of selection, we ran a composite likelihood ratio (CLR) approach as implemented in 3P-CLR¹¹². Briefly, this method uses three-population trees coupled with genomic data as input, from which patterns of linked allele frequency differentiation are calculated. By doing this, this algorithm can tell apart signals of selection that happened in either branch of the tree or in the ancestral lineage, as well as outputting the loci with the highest CLR¹¹². In our case, we used either a North America-Asia-Europe, or a North America-Asia-India population tree as input, and 3P-CLR output the CLR across windows along each chromosome in the *S. polyrhiza* genome. We then selected the top 1% windows for each branch of the input tree and reported the genes that are present in each window. To further validate the evidence of positive selection on the regions with the highest CLR, we ran scans of Tajima's D and genomic diversity along the same windows and contrasted them with the same signal along the other population branches. We expect negative Tajima's D and low genomic diversity values along the populations with high CLR values.

DNA methylation in *S. polyrhiza*

We selected five genotypes from each of the four populations (America, India, SE-Asia, Europe) for single-base whole-genome bisulphite sequencing (WGBS). The genotypes originated from distinct clonal families, except for two European genotypes that came from the same clonal family. (Supplementary Table 5).

FastQC (v0.11.5, <https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>) was used to summarize statistics of the sequencing reads. Trimmomatic (Version 0.36)¹¹³ was used to filter out low-quality reads with the parameters “SLIDINGWINDOW: 4:15, LEADING:3, TRAILING:3, ILLUMINACLIP: adapter.fa: 2: 30: 10, MINLEN:36”. Bismark (version 0.16.3)¹¹⁴ was used to align bisulphite-treated reads to the *S. polyrhiza* reference genome^{93,94}. Identical reads aligned to the same genomic regions were deemed as duplicated reads and thus were removed. Cytosines covered by less than five sequencing reads were excluded from the study. Only after applying these filters the sequencing depth and coverage were then summarized. The sodium bisulphite non-conversion rate was calculated as the percentage of non-converted cytosines to all cytosines in the reads that mapped to the chloroplast genome¹¹⁵ (GenBank: JN160603.2). For each cytosine site, a binomial test was performed to determine if the cytosine was methylated. If the methylation frequency at the site was lower than the background, which was estimated as the non-conversion rate, then the site was considered unmethylated, and the reads supporting methylation at this site were excluded¹¹⁶.

We calculated two different methylation parameters: the proportion of methylated cytosines (mC methylation) and weighted methylation level (wML)¹¹⁶. For both parameters, only cytosines covered by more than four sequencing reads were involved in the calculation. Those cytosines with low reads supporting methylation but not passing the binomial test were considered as un-methylated cytosines. The mC proportion was calculated by dividing the number of methylated cytosines by the total number of cytosines. Genomic regional wML was calculated using the methylKit (v1.17.5)¹¹⁷ and the regioneR (v1.28.0)¹¹⁸, with input based on the cytosine report generated with the Bismark pipeline. Line plots that show the wML patterns across the gene body and transposable elements, as well as their 2 kb flanking regions, were generated using ViewBS (v0.1.11)¹¹⁹. The hierarchical clustering, based on the methylation profiles' similarity, was done using methylKit. The comparison between the genetic phylogenetic tree and hierarchical clustering based on the methylome was made using the R packages ggtree (v3.4.4)¹²⁰, treeio (v1.20.2)¹²¹, ape (v5.6.2)¹²², and phytools (v1.2.0)¹²³.

Declarations

Data availability

The raw genomic and bisulfite sequencing reads involved in this study can be retrieved from NCBI under Accession numbers Bioproject PRJNA701543 and Bioproject PRJNA934173. The scripts for the data analyses are deposited in https://github.com/Xu-lab-Evolution/Great_duckweed_popg. The authors declare that the data and corresponding computational codes supporting the conclusions of this study are available within the article, its Supplementary Information files, or upon request.

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Author contributions

Y. W., P. D. and S. X. performed data analysis. A. C. performed the experiments. K. J. A., H. Z., A. W., K. S. S., and S.X. contributed to the giant duckweed collections and resources. S. X. and M.H. conceived and supervised the project. S. X., Y. W., and P. D. wrote the manuscript. All authors contributed to the final version of the manuscript.

Competing interests:

The authors declare no competing interests.

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Figures

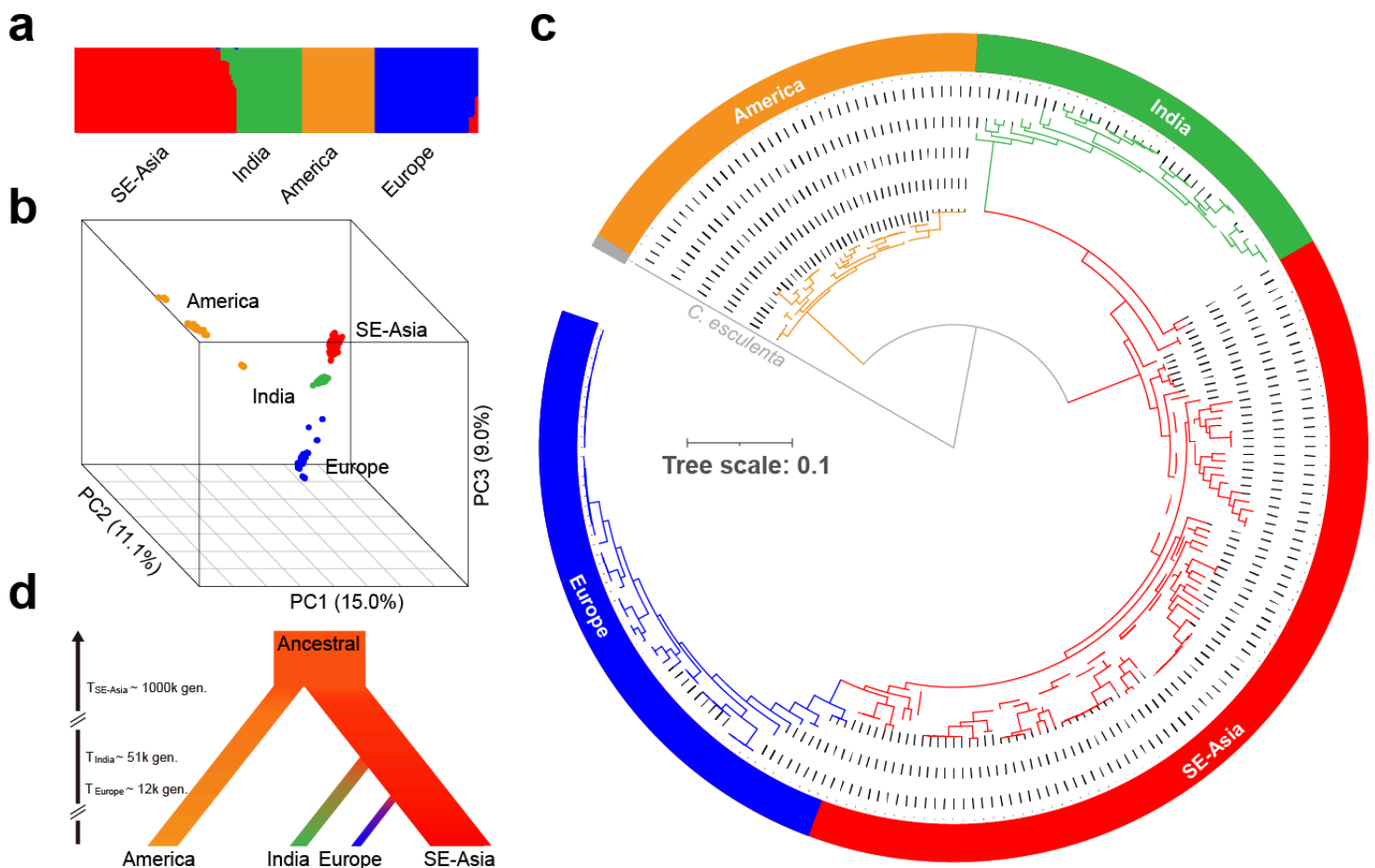


Figure 1

Phylogeny, population structure and demographic model of 228 *S. polyrhiza*.

a The population structure of 228 *S. polyrhiza* genotypes. **b** The principal component (PC) analysis of the SNPs from 228 *S. polyrhiza* genotypes. The three coordinates indicate the first three PCs. **c** The Maximum Likelihood phylogenetic tree of 228 *S. polyrhiza* genotypes. The grey branch represents the outgroup - *C. esculenta*. Dashed branches represent internal nodes with supporting values lower than 0.75 (the max is 1). **d** The demographic model of *S. polyrhiza* populations. “ $T_{\text{population}}$ ” indicates the estimated divergence time in generations.

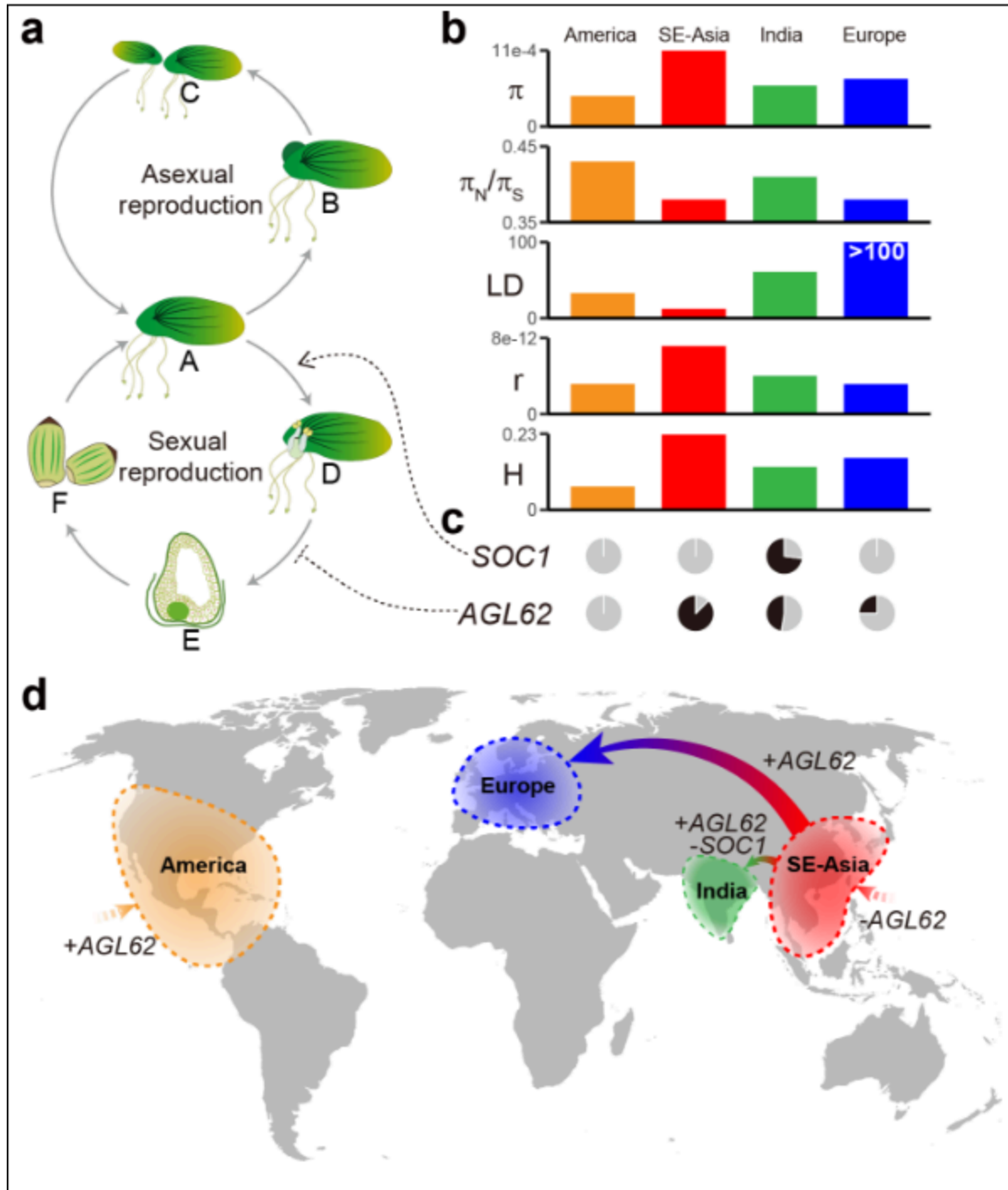


Figure 2

Genomic diversity variation among four populations might result from the switching between sexual and asexual propagation in *S. polyrhiza*.

a Scheme of asexual and sexual propagation cycles in *S. polyrhiza*. **A)** Vegetative stage of *S. polyrhiza*; **B)** Budding; **C)** Offspring from clonal propagation; **D)** *S. polyrhiza* flowering; **E)** Putative schematic of ovule at endosperm cellularization stage; **F)** Putative schematic of seeds. **b** Bar plots show the differences among the four populations in terms of “ π ”: genome-wide nucleotide diversity; “LD”: the physical extent (in kb) of pairwise SNPs at r^2 of 0.2 (Europe does not yet reach $r^2=0.2$ at 100 kb, Supplementary Fig. 4); “ π_N/π_S ”: the efficacy of linked selection; “ r ”: genome-wide recombination rate; “ H ”: the median of per population genome-wide heterozygosity rate. **c** Two panels of pie charts indicate the allele frequencies of the functional allele of *SOC1*-like and *AGL62*-like genes among populations. Grey: functional allele frequency; Black: SVs allele frequency. **d** The distribution and migration world map of the four *S. polyrhiza* populations. “+” suggests the increased functional allele frequency, while “-” suggests the decreased functional allele frequency.

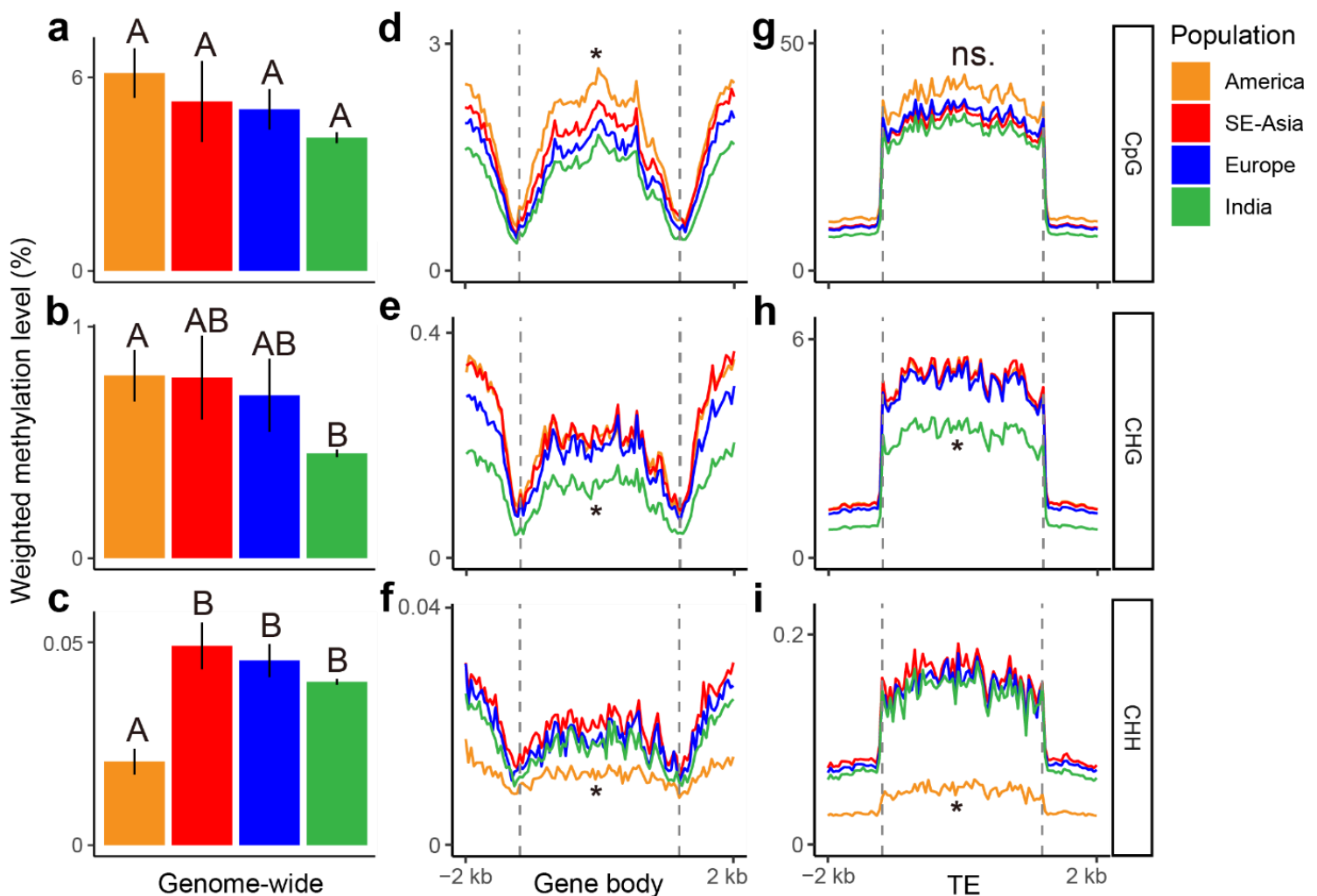


Figure 3

Weighted methylation level (wML) among four populations.

a-c Bar plots of genome-wide weighted methylation level (wML) in (a) CpG, (b) CHG, and (c) CHH context. Black vertical lines indicate the standard error of the mean of each population's wML. Uppercase letters indicate statistical differences among populations. **d-f** wML in the gene body and its flanking 2 kb regions in (d) CpG, (e) CHG, and (f) CHH context. **g-i** wML in TE and its flanking 2 kb regions in (g) CpG, (h) CHG, and (i) CHH context. The asterisks indicate significant differences between populations ($P < 0.01$; Wilcoxon test), while "ns." indicates no significant difference.

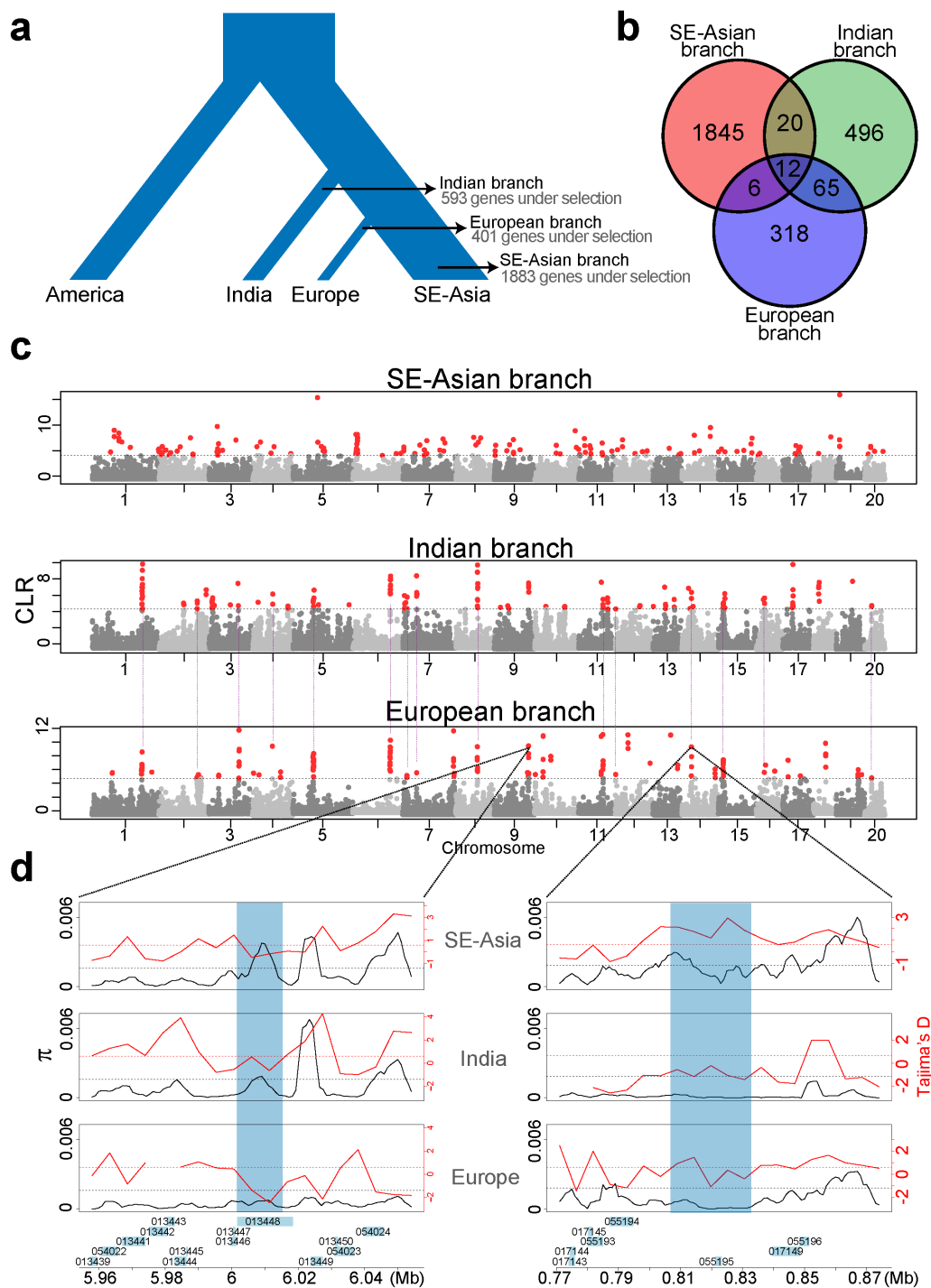


Figure 4

Branch-specific selection signature scans.

a Population tree is used for the population-specific selection analyses. Input consists of an “outgroup” population (America) and two “ingroup” populations (India and SE-Asia, or Europe and SE-Asia). We present the number of genes in the ingroup populations belonging to the top 1% CLR scores reported by 3P-CLR. **b** Venn diagram showing the genes under selection that are common between the populations of SE-Asia, India, and Europe. **c** Branch-specific genome-wide scan of selection: each dot represents a chromosomal locus picked by 3P-CLR for which a CLR score is calculated; loci on the top 1% CLR are shown in red. The dashed purple lines between European and Indian panels indicate common peaks of selection detected at the same genomic regions in both populations. **d** Genomic diversity as depicted by p (solid black lines) and Tajima’s D (solid red lines) for two selected loci: the *FLK* (left) and the *CYP78A9* (right). *FLK* shows a signature of selection (low p and negative Tajima’s D) in the European population, while *CYP78A9* shows a signature of selection in both Europe and India. Dashed lines indicate genome-wide averages for p (black) and Tajima’s D (red).

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [Supplementarydata.zip](#)
- [Supplementaryinfo6.docx](#)