

1 **TITLE: Recent origin of an XX/XY sex-determination system in the ancient plant**
2 **lineage *Ginkgo biloba***

3

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38 ABSTRACT

39 Sexual dimorphism like dioecy (separate male and female individuals) have evolved
 40 in diverse multicellular eukaryotes while the molecular mechanisms underlying the
 41 development of such a key biological trait remains elusive (1). The living fossil
 42 *Ginkgo biloba* represents an early diverged lineage of land plants with dioecy.
 43 However, its sex-determination system and molecular basis have long been
 44 controversial or unknown. In the present research, we assembled the first and largest
 45 to date chromosome-level genome of a non-model tree species using Hi-C data. With
 46 this reference genome, we addressed both questions using genome resequencing data
 47 gathered from 97 male and 265 female trees of ginkgo, as well as transcriptome data
 48 from three developmental stages for both sexes. Our results support vertebrate-like
 49 XY chromosomes for ginkgo and five potential sex-determination genes, which may
 50 originate ~14 million years ago. This is the earliest diverged sex determination region
 51 in all reported plants as yet. The present research resolved a long-term controversy,
 52 lay a foundation for future studies on the origin and evolution of plant sexes, and
 53 provide genetic markers for sex identification of ginkgo which will be valuable for
 54 both nurseries and field ecology of ginkgo.

55

56 MAIN TEXT

57 Dioecy (separate male and female individuals) and sex chromosomes are common in
 58 animals, but rare in plants (2). Plants appear to have sex-determination systems
 59 developed at different evolutionary timelines, whereas the best studied animal
 60 systems are ancient. The repeated independent evolution of sex chromosomes in
 61 plants provide a unique system studying the time course of evolutionary events in sex
 62 chromosomes (3). Sex chromosomes in most flowering plants (angiosperm) are
 63 cytologically homomorphic or have very small non-recombining sex-determination
 64 regions on homomorphic sex chromosomes (4-6). Remarkable progresses have been
 65 achieved on understanding sex-determination in plants by applying genomic
 66 approaches in papaya (*Carica papaya*), cucumber (*Cucumis sativus*), and white
 67 campion (*Silene latifolia*) (2). In contrast, sex chromosomes are heteromorphic in all
 68 the six known species (0.6%) from three families (Cycadaceae, Ginkgoaceae and
 69 Podocarpaceae) in gymnosperm (plants with naked seeds), possibly reflecting an

70 ancient evolutionary history (3). Unfortunately, the confirmation of sex chromosomes
71 and reconstruction of their evolutionary history remain to be explored in the sister
72 lineage of flowering plants.

73 The dioecious maidenhair tree, *Ginkgo biloba* (ginkgo), a long-lived tree species
74 which represents one of the four gymnosperm lineages, provides an ideal model for
75 the origin of dioecy in seed plants. Ginkgo is an ancient lineage present in the Jurassic
76 period 170 million years ago (7). The discovery of multiflagellated swimming sperm
77 from a male ginkgo tree in 1896 hinted at a striking example of convergent evolution
78 (8). Its sex-determination system, XX/XY (9, 10) vs. ZW/ZZ (11, 12), remains
79 controversial and was based on previous work using optical microscope or
80 Fluorescence *in Situ* Hybridization (FISH) approaches, which may suffer unreliability
81 or ambiguity (9-11, 13). Thus, the genetic basis of the sex determination of ginkgo has
82 remained poorly explored (2, 9, 11, 12, 14) largely due to its large and complex
83 genome (15).

84 We used three-dimensional proximity information obtained by chromosome
85 conformation capture sequencing (Hi-C) to order and orient the draft genome
86 assembly of *Ginkgo biloba* (15) (**fig. S1**), generating 12 chromosomes spanning 9.03
87 Gb (~94% of the whole genome) (**tables S1, S2**). The chromosome-level assembly
88 was well supported by the inter- and intra-chromosome contact matrices of the Hi-C
89 data, and revealed an anti-diagonal pattern within a chromosome and clear separations
90 between chromosomes (**fig. S2a**). Moreover, chromosome sequence lengths were
91 highly correlated with the physical length of chromosomes described in a previous
92 karyotype study (13) ($R^2=0.98$, **fig. S2b**), further supporting the high quality of our
93 assembly.

94 We performed a genome-wide association study (GWAS) of ~1.5 million SNPs in 97
95 male and 265 female specimens sequenced at an average depth of ~8× (**table S3**;
96 described in our parallel study (16): Zhao *et al.*, submitted simultaneously). A ~4.6
97 Mb region on chromosome 2 (Chr2: 380.00 Mb–384.60 Mb) was identified as a
98 candidate sex-determination region (SDR) due to its significant association with sex
99 (**Fig. 1A** and **fig. S3**, corrected *P*-value < 0.05). We computed the fixation index (F_{ST})
100 (17) between the males and females in the whole genome, showing substantially
101 higher differentiation on the similar region of chromosome 2 (**Fig. 1B**). Finally, the

linkage disequilibrium (LD) of this region was substantially stronger than for other regions (**Fig. 1C** and **fig. S4**), consistent with the previous reports of enhanced LD on sex chromosomes in other species(18). To further validate this region as an SDR, six randomly-selected SNPs were sequenced in 24 males and 24 females using PCR and Sanger sequencing, revealing a high correlation between the SNPs and sexes (**fig. S5**). One SNP for PCR validation matched amplification products in 70.83% males with no product in all females (**Fig. 1D**). Using 19,164 SDR-associated SNPs, 97 males and 265 females were completely clustered into two distinct groups, and the remaining 183 sequenced ginkgo individuals with unknown sex information were classified into the two sex clusters, i.e., 75 males and 108 females (**Fig. 1E**).

Four male and five female accessions of ginkgo were resequenced at higher sequencing depth (~30×). Mapping the reads back to the reference genome continued to support the SDR (**figs. S6 and S7**). Males and females showed similar mapping depth (~32×) at both ends of the SDR (S1: 380.00–381.46 Mb and S3: 383.52–384.60 Mb) (**Fig. 2A**). The mapping depth in the middle of SDR (S2: 381.46–383.52 Mb) for males was ~17× (**Fig. 2A**), which was about half of that of females in S2 and also of males at the whole-genome level, indicating a higher divergence between males in S2. We observed notably higher SNP polymorphism in the S1 and S3 regions in males (97 males and 265 females) (**Fig. 2B**), and substantially higher heterozygosity ($P = 5.84 \times 10^{-66}$) in the S1 and S3 regions in the specimens subjected to deeper resequencing (~30×, four males and five females) (**Fig. 2C**). A ubiquitous feature of species with heteromorphic sex chromosomes (e.g. males with an X and a Y chromosome, females with two X chromosomes, as observed in mammals and fruit flies), is the presence of only one X chromosome in the male(1). Contrasting male and female, the copy number of S2 was one in males and two in females (**Fig. 2D**). The copy number of flanking regions (including S1 and S3) were two in both sexes(19). Collectively, we provide multiple lines of evidence of a classic XX/XY sex-determination system in ginkgo in which males harbor one allele (X) identical to the female alleles and one differentiated allele (Y; manifested by substantial divergence in SDR S2).

The origin of dioecy and sex chromosomes in ginkgo was inferred based on the three SDRs (S1, S2 and S3). We anticipated the highest difference between X and Y alleles

134 in S2 because only the X allele could be assembled and reads from the Y allele could
135 not be mapped back to this region. For S1 and S3, we had genotype data of both X
136 and Y alleles, thus we calculated the pair-wise distances between four males and five
137 females and estimated the divergence times of S1 and S3 to be 14.18 (11.04–16.64)
138 million years ago (MYA) and 9.44 (4.48–11.42) MYA, respectively (**table S4**).
139 Considering the higher difference among X and Y alleles in S2, the divergence time of
140 the associated SDR in ginkgo could be more ancient than 14.18 MYA. We were not
141 able to reconstruct the most divergent part of the Y allele, possibly because of the
142 inherent high complexity of the ginkgo genome. The emergence timing of ginkgo
143 SDR, ~14 MYA, substantially precedes that for the known flowering plants, e.g., ~1.5
144 MYA for *Rumex hastatulus* with an XY sex-determination system, 5–10 MYA for
145 *Silene latifolia*, and ~7.3 MYA for *Carica papaya*(20). Despite the oldest origin of
146 ginkgo sex chromosomes in the known land plants to date, their timing as recent as
147 ~14 MYA is in contrast to the ancient origin of ginkgo lineage and reproductive
148 organs. Ginkgoalean and *Ginkgo* genus may have originated 320 MYA (21, 22) and
149 170 MYA (7), respectively. The timing for the origin of the extant species, *Ginkgo*
150 *biloba*, was estimated 56–58 MYA (23). Fossils of ginkgo-like pollen and ovulate
151 organs have long been known from the Upper Triassic and the Palaeozoic,
152 respectively (22). Such a contrast again suggests a young origin of sex chromosomes
153 in seed plants despite ancient origin of dioecy.

154 A critical property of an SDR is the presence of genes, typically transcription factors,
155 associated with sexually dimorphic gene expression and traits (1). There were 16
156 protein-coding genes located in the ginkgo SDR (**Fig. 3A, Table 1** and **table S5**),
157 among which five genes (*Gb_15883*, *Gb_15884*, *Gb_15885*, *Gb_15886*, and
158 *Gb_28587*) were functionally annotated to be related to floral meristem development
159 and sex determination. *Gb_15883* and *Gb_15884* were homologs of response
160 regulators 12 and 2 (RR12 and RR2), proteins which respond to cytokinins and have
161 been reported to be involved in the sex determination of kiwifruits (24). *Gb_15885*
162 was a homolog of early flowering 6 (ELF6), a H3K4 demethylases gene which
163 regulates flowering time (25, 26). *Gb_15886* was similar to Brassinosteroid-related
164 AcylTransferase1 (AtBAT1) which regulates sex determination in maize (27).

165 *Gb_28587* was a homolog of AGAMOUS-like 8, a member of a transcription factor
 166 family which specifies sex organ identity during development (28).

167 To further determine the candidate sex-determination genes in ginkgo, we sequenced
 168 32 transcriptomes from two tissues (cones and leaves, **Fig. 3B**) at various
 169 developmental stages in each of three males and females (**table S6**). Comparison
 170 between male and female specimens resulted in the identification of 5,831 and 132
 171 differentially expressed genes (DEGs), respectively, in cones (reproductive organs)
 172 and leaves between male and female individuals (P -value < 0.001 ; **fig. S8a, b**). Of
 173 these 249 were uniquely expressed, specifically expressed genes (SEGs), in either
 174 male or female cones (**fig. S9** and **table S7**), while only two SEGs were found in
 175 leaves. Then, we focused on 5,774 genes which showed differential gene expression
 176 only in cones (**fig. S8c**). Five DEGs were located in the SDR, of which *Gb_15886*
 177 was exclusively expressed in female cones (**Fig. 3C**). To identify genes of S2 Y allele,
 178 we *de novo* assembled and contrasted the transcriptomes of males and females. This
 179 effort revealed five transcripts with significant divergence from the S2 X allele (~20%
 180 identity) which can be considered candidate Y allele-derived gene products. To
 181 understand the co-expression relationships between ginkgo genes, we performed
 182 weighted gene co-expression network analysis (WGCNA) (29) on male and female
 183 cone samples. This unsupervised and unbiased analysis identified a co-expression
 184 module significantly correlating 11 of 16 genes in the SDR with sex (**fig. S10** and
 185 **table S8**, P -value = 1×10^{-6}). These genes (*Gb_15886*, *Gb_28585* and *Gb_30343*) were
 186 hubs, genes with the most connections with other genes in the network (**Fig. 3D**),
 187 further strengthening the identified SDR. Regulatory variants (SNPs) can also
 188 influence gene expression and provide a proxy of gene function (30).

189 We phased the X and Y haplotypes using the SNPs, resulting in 12,425, 2,067 and
 190 4,672 SNPs phased in the S1, S2 and S3 with the average interval distances of 83 bp,
 191 988 bp and 303 bp, respectively (**fig. S11** and **table S9**). Of these 19,164 phased SNPs,
 192 17,533 were located in the intergenic regions and 1,361 in introns (**Fig. 3A**). Only 270
 193 SNPs in 11 (out of 16) genes were located in the protein-coding exons. *Gb_15885* and
 194 *Gb_15884* specifically expressed Y allele genotypes, while the others nine genes
 195 expressed the X-allele or both X and Y alleles (**Fig. 3E** and **Table 1**). The
 196 allele-specific expression of *Gb_15885* and *Gb_15884* in male ginkgo might suggest

197 that these genes have a critical role in sex determination analogous to *SRY* in
198 mammals (31, 32).

199 In the present research, we identified the sex-determination region (SDR) of ginkgo
200 and resolved its sex-determination system (XX/XY type). Our data revealed a
201 gradually evolving and differentiating Y allele which originated approximately 14
202 MYA older than that in angiosperm. We provided evidence of a complex
203 sex-determination process, including the expression of male and female sex-specific
204 genes. Our genome and transcriptome data set offers an unprecedented resource for
205 research on dioecy and sex chromosome evolution. In addition, we provided genetic
206 markers for sex identification in vegetative stages of ginkgo (e.g., seedlings, juvenile
207 trees, and non-flowering trees), which will be remarkably valuable for the selection of
208 preferred sexes in nursery and for the identification of unknown sexes in field
209 ecology.

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211 REFERENCES AND NOTES

- 212 1. T. M. Williams, S. B. Carroll, Genetic and molecular insights into the
213 development and evolution of sexual dimorphism. *Nature Reviews Genetics* **10**, 797
214 (2009).
- 215 2. R. Ming, A. Bendahmane, S. S. Renner, Sex chromosomes in land plants. *Annual*
216 *Review of Plant Biology* **62**, 485-514 (2011).
- 217 3. D. Charlesworth, Plant sex chromosome evolution. *Journal of Experimental*
218 *Botany* **64**, 405-420 (2013).
- 219 4. M. Westergaard, The mechanism of sex determination in dioecious flowering
220 plants. *Advances in Genetics* **9**, 217-281 (1958).
- 221 5. Z. Liu *et al.*, A primitive Y chromosome in papaya marks incipient sex
222 chromosome evolution. *Nature* **427**, 348-352 (2004).
- 223 6. T. Akagi, I. M. Henry, R. Tao, L. Comai, A Y-chromosome-encoded small RNA
224 acts as a sex determinant in persimmons. *Science* **346**, 646-650 (2014).
- 225 7. Z. Zhou, S. Zheng, The missing link in *Ginkgo* evolution. *Nature* **423**, 821-822
226 (2003).

- 227 8. P. Del Tredici, Wake up and smell the ginkgos. *Arnoldia*. **66**, 11-21 (2008).
- 228 9. E. H. Newcomer, The karyotype and possible sex chromosomes of *Ginkgo biloba*.
229 *American Journal of Botany* **41**, 542-545 (1954).
- 230 10. E. G. Pollock, The sex chromosomes of the maidenhair tree. *Journal of Heredity*
231 **48**, 290-294 (1957).
- 232 11. R. Y. Chen, W. Q. Song, X. L. Li, Study on the sex chromosomes of *Ginkgo*
233 *biloba*. *Plant Chromosome Research* **381-86** (1987).
- 234 12. T. Y. Lan *et al.*, Microdissection and painting of the W chromosome in *Ginkgo*
235 *biloba* showed different labelling patterns. *Botanical Studies* **49**, 33-37 (2008).
- 236 13. Y. Nakao, T. Taira, S. Horiuchi, K. Kawase, Y. Mukai, Chromosomal difference
237 between male and female trees of *Ginkgo biloba* examined by karyotype analysis and
238 mapping of rDNA on the chromosomes by fluorescence *in situ* hybridization. *Journal*
239 *of the Japanese Society for Horticultural Science* **74**, 275-280 (2005).
- 240 14. B. Vyskot, R. Hobza, Gender in plants: sex chromosomes are emerging from the
241 fog. *Trends in Genetics* **20**, 432-438 (2004).
- 242 15. R. Guan *et al.*, Draft genome of the living fossil *Ginkgo biloba*. *GigaScience* **5**,
243 49 (2016).
- 244 16. Y. Zhao *et al.*, Resequencing 545 ginkgo genomes across the world reveals
245 evolutionary history of the living fossil *Ginkgo biloba*. (submitted simultaneously).
- 246 17. B. S. Weir, C. C. Cockerham, Estimating *F*-statistics for the analysis of
247 population structure. *Evolution* **38**, 1358-1370 (1984).
- 248 18. M. Slatkin, Linkage disequilibrium--understanding the evolutionary past and
249 mapping the medical future. *Nature Reviews Genetics* **9**, 477-485 (2008).
- 250 19. H. Nakanishi *et al.*, A novel method for sex determination by detecting the
251 number of X chromosomes. *International Journal of Legal Medicine* **129**, 23-29
252 (2015).
- 253 20. D. Charlesworth, Plant sex chromosomes. *Annual Review of Plant Biology* **67**,
254 397-420 (2016).
- 255 21. N. Hohmann *et al.*, *Ginkgo biloba*'s footprint of dynamic Pleistocene history

256 dates back only 390,000 years ago. *BMC Genomics* **19**, 299 (2018).

257 22. Z.-Y. Zhou, An overview of fossil Ginkgoales. *Palaeoworld* **18**, 1-22 (2009).

258 23. Z.-Y. Zhou, C. Quan, Y.-S. Liu, Tertiary ginkgo ovulate organs with associated
259 leaves from north dakota, U.S.A., and their evolutionary significance. *International*
260 *Journal of Plant Sciences* **173**, 67-80 (2012).

261 24. T. Akagi *et al.*, A Y-encoded suppressor of feminization arose via lineage-specific
262 duplication of a cytokinin response regulator in kiwifruit. *Plant Cell* **30**, 780-795
263 (2018).

264 25. B. Noh *et al.*, Divergent roles of a pair of homologous jumonji/zinc-finger-class
265 transcription factor proteins in the regulation of *Arabidopsis* flowering time. *Plant*
266 *Cell* **16**, 2601-2613 (2004).

267 26. Q. Hu, Y. Jin, H. Shi, W. Yang, *GmFLD*, a soybean homolog of the autonomous
268 pathway gene *FLOWERING LOCUS D*, promotes flowering in *Arabidopsis thaliana*.
269 *BMC Plant Biology* **14**, 263 (2014).

270 27. T. Hartwig *et al.*, Brassinosteroid control of sex determination in maize.
271 *Proceedings of the National Academy of Sciences of the United States of America* **108**,
272 19814-19819 (2011).

273 28. K. H. Ng, H. Yu, T. Ito, AGAMOUS controls *GIANT KILLER*, a multifunctional
274 chromatin modifier in reproductive organ patterning and differentiation. *PLoS Biology*
275 **7**, e1000251 (2009).

276 29. P. Langfelder, S. Horvath, WGCNA: an R package for weighted correlation
277 network analysis. *BMC Bioinformatics* **9**, 559 (2008).

278 30. L. Tian *et al.*, Genome-wide comparison of allele-specific gene expression
279 between African and European populations. *Human Molecular Genetics* **27**,
280 1067-1077 (2018).

281 31. M. A. Wilson, K. D. Makova, Genomic analyses of sex chromosome evolution.
282 *Annual Review of Genomics and Human Genetics* **10**, 333-354 (2009).

283 32. F. Veyrunes *et al.*, Bird-like sex chromosomes of platypus imply recent origin of
284 mammal sex chromosomes. *Genome Research* **18**, 965-973 (2008).

285 33. S. S. Rao *et al.*, A 3D map of the human genome at kilobase resolution reveals

- 286 principles of chromatin looping. *Cell* **159**, 1665-1680 (2014).
- 287 34. N. Servant *et al.*, HiC-Pro: an optimized and flexible pipeline for Hi-C data
- 288 processing. *Genome Biology* **16**, 259 (2015).
- 289 35. N. C. Durand *et al.*, Juicer provides a one-click system for analyzing
- 290 loop-resolution Hi-C experiments. *Cell Systems* **3**, 95-98 (2016).
- 291 36. O. Dudchenko *et al.*, *De novo* assembly of the *Aedes aegypti* genome using Hi-C
- 292 yields chromosome-length scaffolds. *Science* **356**, 92-95 (2017).
- 293 37. Y. Tang *et al.*, GAPIT Version 2: An enhanced integrated tool for genomic
- 294 association and prediction. *Plant Genome* **9**, (2016).
- 295 38. H. Li, R. Durbin, Fast and accurate short read alignment with Burrows-Wheeler
- 296 transform. *Bioinformatics* **25**, 1754-1760 (2009).
- 297 39. H. Li *et al.*, The Sequence Alignment/Map format and SAMtools. *Bioinformatics*
- 298 **25**, 2078-2079 (2009).
- 299 40. P. Danecek *et al.*, The variant call format and VCFtools. *Bioinformatics* **27**,
- 300 2156-2158 (2011).
- 301 41. S. Purcell *et al.*, PLINK: a tool set for whole-genome association and
- 302 population-based linkage analyses. *American Journal of Human Genetics* **81**, 559-575
- 303 (2007).
- 304 42. S. Kumar, G. Stecher, K. Tamura, MEGA7: Molecular Evolutionary Genetics
- 305 Analysis version 7.0 for bigger datasets. *Molecular Biology and Evolution* **33**,
- 306 1870-1874 (2016).
- 307 43. S. M. E. Sahraeian *et al.*, Gaining comprehensive biological insight into the
- 308 transcriptome by performing a broad-spectrum RNA-seq analysis. *Nature*
- 309 *Communication* **8**, 59 (2017).

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 331 supporting the findings of the study are available in this article, in the Extended Data,
 332 or from the corresponding authors upon request.

333

334 SUPPLEMENTARY MATERIALS

335 Materials and Methods

336 Figs. S1 to S11

337 Tables S1 to S9

338 References (33–43)

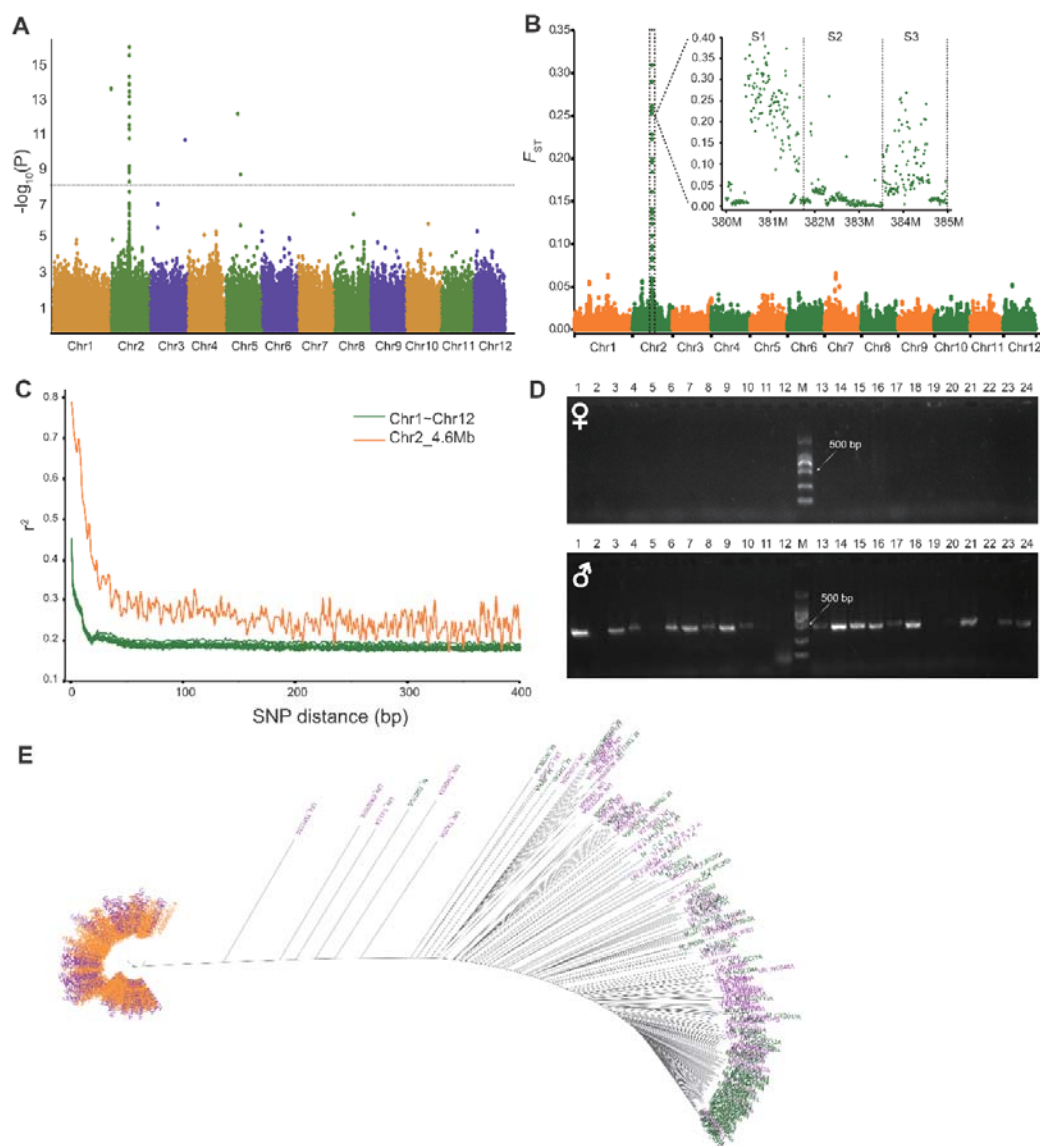


Fig. 1. 4.6 Mb region on chromosome 2 is a candidate ginkgo sex-determination region. (A) Manhattan plot of a genome-wide association study (GWAS) for SNPs associated with sex on 97 male and 295 female specimens. Negative log₁₀ P-value from linear mixed model (y-axis) are plotted against SNP positions (x-axis) on each of the 12 ginkgo chromosomes. The genome-wide significant P-value threshold (10⁻⁸) is indicated by a horizontal line. (B) The 4.6 Mb region on Chr2 is highly differentiated between ginkgo sexes, indicated by high population differentiation (F_{ST}) values (x-axis). Ginkgo chromosomes are shown on the y-axis. (C) SNPs spanning the 4.6 Mb region on Chr2 constitute a linkage disequilibrium (LD) block. Average genotypic association coefficient r^2 (y-axis) is presented as a function of inter-SNP distance (x-axis) between 4.6 Mb region and whole genome. (D) Gel photograph of PCR

351 amplicons. Validation of PCR amplification using specific designed primes for SNP
 352 on Chr2: 383,550,476 of 24 males and 24 females. **(E)** A neighbor-joining (NJ) tree
 353 constructed using 19,164 SNPs in the sex-determination region clusters 545 ginkgo
 354 specimen by sex. Specimens with known sex classification are labeled in orange
 355 (female; $n=265$) and green (males, $n=97$); specimens with unknown information
 356 ($n=183$) in purple.

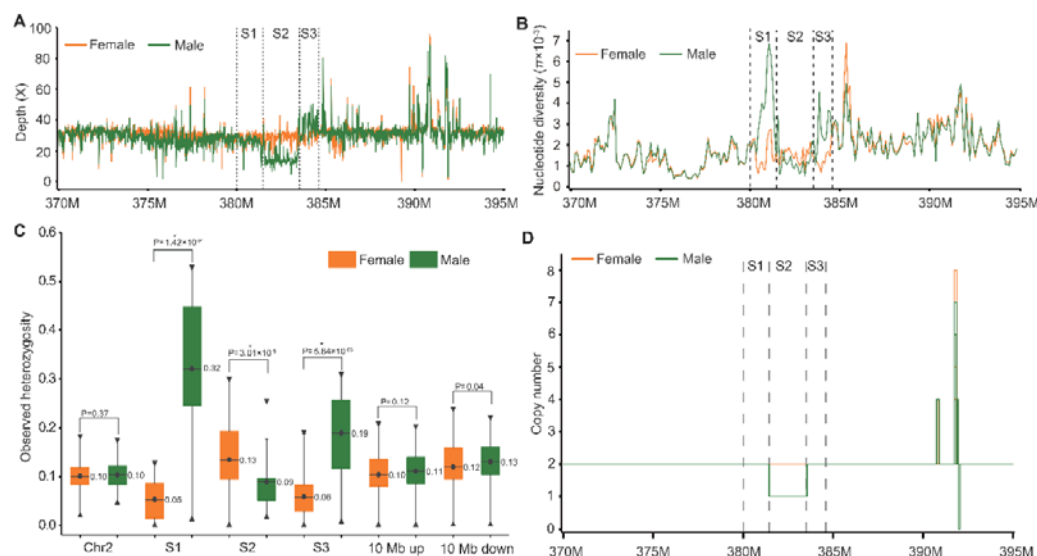


Fig. 2 Further dissection of the ginkgo sex-determination region. Four males and five females were sequenced at high depth (~30×). (A) Sequencing depth in the sex-determination region is similar in both ends (sex-determination region 1, S1, Chr2:380.00-381.46 Mb; sex-determination region 3, S3, Chr2:383.52-384.60 Mb) but lower in males in the middle (sex-determination region, S2, Chr2:381.46-383.52 Mb). Average mapping depth of males and females are shown in 10-kb window. Depth on the y-axis, chromosome 2 region on the x-axis. **(B)** Nucleotide diversity (π) in the males are in the sex-determination region (especially in S1 and S3 regions). Examined using a 100-kb window size. Nucleotide diversity (π) on the y-axis, chromosome 2 region on the x-axis. **(C)** Observed heterozygosity in sex-determination regions S1 to S3 and chromosomal other regions in ginkgo sexes. Heterozygosity on the y-axis, chromosome region on the x-axis. **(D)** Estimated copy number is two for the S1 and S3 regions and one for the S2 region. Copy number on the y-axis, chromosome 2 region on the x-axis.

node size reflect the number of connections for each node. Three genes in the sex-determination region (Gb_15886, Gb_28585 and Gb_30343) were identified as hub genes (the most connected, or central genes). **(E)** A heat map showing the expression of 11 genes in sex-determination region with phased SNP haplotypes. 18 male samples are shown (8 cones, 8 leaves). Gene expression (TPM) shown on as a colour gradient: white being no expression detected; blue and red low and high Y haplotype expression, respectively.

389 **Table 1. Genes in the ginkgo sex-determination region (SDR).** For each gene, the
390 top-candidate ortholog, the associated SDR region, and allele specific gene expression
391 is indicated (a dash indicates that no data could be obtained).

Gene ID	Homologous protein	Description	SDR	Allele
<i>Gb_15883</i>	<i>RR12</i>	Response regulator 12	S1	X/Y
<i>Gb_15884</i>	<i>RR2</i>	Response regulator 2	S1	Y
<i>Gb_15885</i>	<i>ELF6</i>	ARLY FLOWERING 6	S1	Y
<i>Gb_15886</i>	<i>AT4G31910</i>	BR-related AcylTransferase1	S1	-
<i>Gb_28584</i>	<i>AT4G22030</i>	Putative F-box protein	S3	X/Y
<i>Gb_28585</i>	- -		S2	X/Y
<i>Gb_28586</i>	<i>SLO2</i>	SLOW GROWTH 2	S2	X/Y
<i>Gb_28587</i>	<i>AGL6</i>	AGAMOUS-like 6	S2	X
<i>Gb_28588</i>	<i>AT3G01930</i>	Major facilitator protein	S2	X
<i>Gb_28589</i>	<i>AT4G31020</i>	Esterase/lipase domain-containing protein	S2	X
<i>Gb_30340</i>	- -		S3	-
<i>Gb_30341</i>	<i>AT3G17450</i>	hAT dimerisation domain-containing protein	S3	-
<i>Gb_30342</i>	<i>AT3G17450</i>	hAT dimerisation domain-containing protein	S3	X
<i>Gb_30343</i>	<i>BIO1</i>	Biotin auxotroph 1	S3	-
<i>Gb_30344</i>	<i>AT4G30310</i>	FGGY family of carbohydrate kinase	S3	X
<i>Gb_30345</i>	<i>AT3G17450</i>	hAT dimerisation domain-containing protein	S3	-

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