

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

- n/a
- Confirmed
- ☐

☒

The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
- ☐

☒

A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☐

☒

The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- ☒

☐

A description of all covariates tested
- ☒

☐

A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- ☐

☒

A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- ☐

☒

For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted
Give P values as exact values whenever suitable.
- ☒

☐

For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- ☒

☐

For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- ☒

☐

Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection	Whole genome sequencing was achieved by combining paired-end Illumina® sequencing (PE250 bp) on a NovaSeq 6000 and the Oxford Genome sequencing: Nanopore technology (5 MinION and 3 PromethION flow cells). Optical map was obtained using the Bionano Saphyr instrument.
Data analysis	Genome assembly and annotations: Genomescope (v2.0), SMARTdenovo, Redbean wtdbg2 (v2.5), Flye (v2.7), Racon (v1.4.10), Pilon (v1.24), Bionano Genomics (BNG), Bionano solve and tools (v1.3), BisCoT (v2.0), Hapo-G (v1.0), BUSCO (v5.2.2), minimap2 (v2.19), Circos (v0.69.8), GeneMark (v2.5), TransDecoder (v2.0), Stringtie (v1.3.3), exonerate (v2.2.0), EVidenceModeler (v1.1.1), RepeatMasker (v1.0.6), LTR_retriever (v2.9). Homology and synteny searches within and among genomes: BLASTn, BLASTP (BLAST, v2.9.0), MCScanX (v.1), MCScan (Python version), JCVI utility library. RBH/Ks/Synteny and graphical representation pipelines are available at https://github.com/MorganeMilin/WGD_Tracker GO term enrichment analysis: R package clusterProfiler (v.4.6.0) - pipeline available at https://github.com/tytrhr/GO_enrichment.git Divergence between duplicated subgenomes: MACSE (v2.06), PAML (v.4.10.5), R package mixtools (v2.0.0).

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

Sporobolus maritimus: The Illumina, Oxford Nanopore and Bionano Genomics data, as well as the assembly of *S. maritimus* are available in the European Nucleotide Archive under the project PRJEB73506 and at https://figshare.com/projects/Sporobolus_maritimus_genome_annotation/235733.

Sporobolus alterniflorus: Raw sequence data and genome assemblies have been deposited at the National Genomics Data Center under project no. PRJCA016449.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☐ Behavioural & social sciences ☒ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	We reports a complex history of successive genome duplications and chromosome restructuring leading to cytological diploidization in two mesopolyploid <i>Sporobolus</i> sect. <i>Spartina</i> species (Chloridoideae, Poaceae). We compare the genome of the intercontinental invader <i>Sporobolus alterniflorus</i> with the newly assembled <i>S. maritimus</i> genome. These two species are involved in the formation of the invasive neo-allopolyploid <i>S. anglicus</i> , a textbook example of neopolyploid speciation. We discover unexpected basic chromosome numbers and ploidy levels. We also show how recent chromosome repatterning led to an additional chromosome pair in <i>S. alterniflorus</i> during the speciation process. This study offers new perspectives to explore the genomic processes involved in the ecological success during the allopolyploid speciation process.
Research sample	The specimens of <i>Sporobolus maritimus</i> and <i>Sporobolus alterniflorus</i> were sampled from their native habitat, in Sapelo Island (Georgia, USA) and in the Presqu'île du Verdon (Morbihan, France) saltmarshes, respectively and maintained in the greenhouse.
Sampling strategy	After greenhouse transplantation and fresh leaves sampled for HMW DNA purifications from single individuals for both species.
Data collection	Samples of <i>S. maritimus</i> were collected by A.S, M.A. and O.L. at the Presqu'île du Verdon (Morbihan, France).
Timing and spatial scale	The <i>S. maritimus</i> specimen was collected in 2019 at the Presqu'île du Verdon (Morbihan, France); 47° 43 '11.0"N 3° 09' 19.3"W.
Data exclusions	No data were excluded.
Reproducibility	Reproducibility is not applicable in this study as de novo genome sequencing and assemblies involve single individuals for both investigated species.
Randomization	The mature plant samples for whole genome sequencing were randomly sampled.

Blinding

Blinding is not applicable in this study as it does not involve subjects receiving different treatments.

Did the study involve field work?

☐ Yes☒ No

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☐	☒ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Plants

Seed stocks

Seed stock not applicable. The analyzed mature individual of *S. maritimus* was collected in 2019 at the Presqu'île du Verdon (Morbihan, France); 47° 43 '11.0"N 3° 09' 19.3"W, and subsequently maintained in the greenhouse

Novel plant genotypes

Not applicable

Authentication

Not applicable