nature plants

LETTERS

PUBLISHED: 1 AUGUST 2016 | ARTICLE NUMBER: 16115 | DOI: 10.1038/NPLANTS.2016.115

Whole-genome duplication as a key factor in crop domestication

Ayelet Salman-Minkov†, Niv Sabath† and Itay Mayrose*

Polyploidy is commonly thought to be associated with the domestication process because of its concurrence with agriculturally favourable traits and because it is widespread among the major plant crops[1–4]. Furthermore, the genetic consequences of polyploidy[5–7] might have increased the adaptive plasticity of those plants, enabling successful domestication[6–8]. Nevertheless, a detailed phylogenetic analysis regarding the association of polyploidy with the domestication process, and the temporal order of these distinct events, has been lacking[3]. Here, we have gathered a comprehensive data set including dozens of genera, each containing one or more major crop species and for which sufficient sequence and chromosome number data exist. Using probabilistic inference of ploidy levels conducted within a phylogenetic framework, we have examined the incidence of polyploidization events within each genus. We found that domesticated plants have gone through more polyploidy events than their wild relatives, with monocots exhibiting the most profound difference: 54% of the crops are polyploids versus 40% of the wild species. We then examined whether the preponderance of polyploidy among crop species is the result of two, non-mutually-exclusive hypotheses: (1) polyploidy followed by domestication, and (2) domestication followed by polyploidy. We found support for the first hypothesis, whereby polyploid species were more likely to be domesticated than their wild relatives, suggesting that the genetic consequences of polyploidy have conferred genetic preconditions for successful domestication on many of these plants.

During the past 13,000 years of human history, hundreds of crop plants were independently domesticated at different regions across the globe[9]. Despite their independent origin, many domesticated plants share a similar set of morphological and physiological traits, termed the domestication syndrome[10], that collectively distinguish crop plants from their wild progenitors. Polyploidy is also considered as an important trait in the domestication process[11–13] and it has been hypothesized that the genetic consequences of polyploidy, including increased allelic diversity, heterozygosity and enhanced meiotic recombination, have increased the adaptive plasticity of polyploid plants under cultivation conditions[5–7]. This has resulted in larger phenotypic breadth on which natural and artificial selection could act, enabling successful domestication. Indeed, some of our most important crop species, including wheat, potato, cotton and sugar cane, have experienced complex histories of repeated polyploidization events. However, previous surveys[1,14] did not find statistical support for the hypothesis that polyploidy is a more frequent phenomenon in cultivated plants than in wild species.

To test whether crop domestication was associated with polyploidy, we compiled a taxonomically broad data set spanning 107 angiosperm genera, each containing at least one major crop species, for a total of 297 crop and 2,836 wild species. Since we focused on relatively short evolutionary time scales, shifts in chromosome numbers along the phylogenies can be reliably used to infer polyploidy events. We reconstructed the phylogeny of each genus, using as many of its publically available sequence data as possible. Chromosome numbers for species on the phylogeny were extracted from the Chromosome Counts DataBase[15]. Ploidy shifts were mapped onto branches of the tree using a probabilistic model of chromosome number evolution that accounts for various types of chromosome number transitions[16]. This allowed us to define an extant taxon as polyploid if it has undergone a polyploidization event since divergence from its generic ancestor and as diploid otherwise. Overall, 771 (25%) species in our database were categorized as polyploids. These inferences tightly agree with ploidy levels manually inferred in the Plant DNA C-values database[17] (Supplementary Methods and Supplementary Table 1), although this figure is lower than the 35% estimate given by Wood *et al.*[18], as might be expected given that the latter is based on a larger taxonomic sample (but which may not be as representative to the specific clades analysed here) and given that it was based on a different method to infer polyploid taxa. In agreement with previous reports[19] there are major differences in polyploidy frequency depending on taxonomic classification, life cycle and growth form. Polyploids are particularly abundant in monocots (41%) and much less so across eudicots (18%). In addition, the frequency of polyploidy is higher in perennial (26%) and herbaceous (29%) species relative to annual (21%) and woody (16%) species, respectively (Table 1).

Across the whole data set, polyploids are over-represented in crop species relative to the frequency of polyploidy in their wild congeners (30% versus 24%, respectively; $P < 0.05$, Fisher's exact test, which was used unless noted otherwise). This trend holds also when considering separately genera belonging to monocots and eudicots ($P = 0.031$ and 0.026; Table 2), with monocots exhibiting the most profound difference: 54% of the crops are polyploids versus 40% of the wild species. The trend of higher polyploidy abundance in crops relative to wild taxa is also apparent when considering separately species within growth forms and life cycle categories (Table 2). These results are only marginally significant in the woody and perennial categories and non-significant in herbaceous and annual categories, most probably resulting from data partitioning.

The above analysis considered all wild congeners of a domesticated lineage as potential candidates for domestication, disregarding their phylogenetic proximity to the crop. This could have resulted in statistical artefacts since the number of wild species considered is much larger than the number of domesticated ones. Thus, we additionally conducted a sister clade contrast analysis that only considers the phylogenetically most closely related lineages to the set of crops in our data set. This analysis reinforced the association between polyploidy and domestication: out of 92 informative

Department of Molecular Biology and Ecology of Plants, Tel Aviv University, Tel Aviv, Israel. †These authors contributed equally to this work.
*e-mail: itaymay@post.tau.ac.il

Table 1 | The distribution of polyploidy (pp) and diploidy (dp) in plants within the studied categories.

Category	State	pp	dp	pp (%)	*P*-value*
All		771	2,362	25	
Domestication status	Crop	89	208	30	0.028
	Wild	682	2,154	24	
Angiosperm classification	Monocots	379	550	41	<<0.01
	Eudicots	380	1,763	18	
Life cycle	Annual	61	235	21	0.0602
	Perennial	474	1,362	26	
Growth form	Woody	166	842	16	<<0.01
	Herbaceous	398	983	29	

*P-value for the association between polyploidy frequency and the states within each pair of categories examined was computed using Fisher's exact test.

contrasts identified, 68 supported the crop–polyploid combination (with wild diploids being the sister clade) and in 24 contrasts the opposite trend was found ($P = 4.9 \times 10^{-06}$; a two-tailed exact binomial test). These results further suggest that an intricate set of attributes had played a role in the domestication of any specific lineage[1], with chance processes and polyploidy being among them. Indeed, despite the significant association between polyploidy and domestication, there are multiple diploid species that were successfully domesticated whereas their most closely related polyploid species were not.

Our results are in contrast to those reported in Hilu[14] (see also Meyer *et al.*[1]), who found no difference in the frequency of polyploidy between crops and wild species, regardless of the taxonomic classification and life history traits. In that study, however, polyploids were defined as those species whose chromosome number is above a certain cutoff ($n = 11$ or $n = 13$), following earlier definitions used at that time. This definition implicitly assumes that species with chromosome number below this threshold had not experienced a genome duplication in their evolutionary past (or at least since divergence from the angiosperm common ancestor). However, our current understanding regarding the cyclical process of genome duplication and downsizing invalidates such threshold-based measures.

We also found a significant difference in polyploidy frequencies when classifying crops into different categories of commodity use ($P < 0.0001$; Fig. 1; Supplementary Table 3). Polyploidy is particularly common in crops that are used for their root and tubers, and is also over-represented in fibres and cereals. The opposite trend is found in pulses, fruits and vegetables, where polyploidy is under-represented. Most of the species in the roots and tubers category are perennial herbs, a growth form that is characterized by high frequency of polyploidy[19]. Similarly, the under-representation of polyploidy in crops belonging to the fruit trees and nuts categories is expected from the woody growth form of these species[19]. Crops belonging to both the cereals and the pulses categories exhibit similar sets of domestication syndrome traits[20] and are characterized by an annual life cycle, yet their polyploidy frequencies are contrasting. The low frequency of polyploidy in pulses is in line with the general low abundance of polyploidy in annuals (Table 1), but many cereals are of recent polyploid origin. This could be explained by the very high frequency of polyploidy found in the Poaceae[21], of which many cereals belong to (Supplementary Table 3). Alternatively, differences in selective regimes during the early stages of the domestication process might have contributed to the observed differences in polyploidy abundance between these two major crop categories. In cereals, selection for larger seeds has occurred at the very early stages of the domestication process[20], which might have led to the enrichment of polyploids resulting from the positive association between seed size and higher ploidy levels[22]. In pulses, on the other hand, selection for larger seeds is considered to occur at a later stage of the domestication process, subsequent to the emergence of other traits important for cultivation[20,23].

Table 2 | Frequency of polyploidy in crop and wild species grouped by angiosperm classification, life cycle and growth form.

Group	Crop pp	Crop dp	Wild pp	Wild dp	Crop pp (%)	Wild pp (%)	*P*-value*
All	89	208	682	2,154	30	24	0.028
Monocots	33	28	346	522	54	40	0.031
Eudicots	52	170	328	1,593	23	17	0.026
Annual	13	50	48	185	21	21	1
Perennial	69	143	405	1,219	33	25	0.020
Woody	31	106	135	736	23	15	0.047
Herbaceous	49	96	349	887	34	28	0.175

*P-value was computed using Fisher's exact test.

The coincidence of polyploidy with the domestication process could be a result of two scenarios[12]: (1) polyploidy followed by domestication ('polyploidy first'), and (2) domestication followed by polyploidy ('domestication first'). Accordingly, artificial selection during the initial stages (under the polyploidy first hypothesis) and during the domestication process (under domestication first) has selected for polyploids because of the association of polyploidy with agriculturally favourable phenotypic traits such as larger organs (for example, fruits and seeds) or uniparental reproduction[12,24,25]. Polyploidy may further facilitate domestication by posing strong reproductive barriers between nascent crops and their nearby wild progenitors, thereby enabling selective gains to accumulate without being eroded by continuous gene flow[26]. Although this process could have selected for polyploids subsequent to initial domestication, it could also represent a pre-adaptation to domestication (in agreement with the domestication first or polyploidy first scenarios, respectively). Beyond artificial selection, secondary contacts owing to human activity that have juxtaposed multiple cultivars into sympatry could have increased the chance for hybridization and emergence of allopolyploid domesticated forms from an initial set of (pre)domesticated lineages[27] (in line with the domestication first scenario).

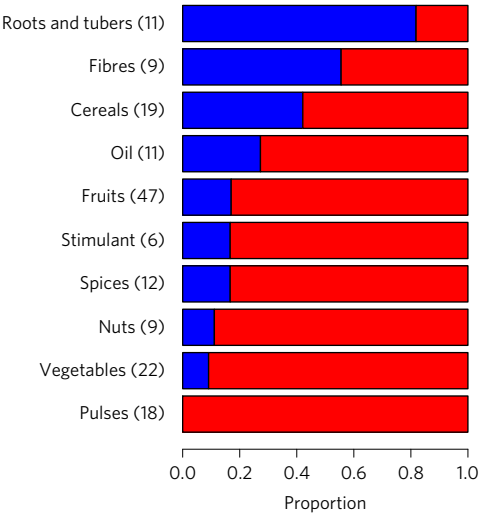

Figure 1 | Polyploidy frequency across different categories of commodity use. Numbers in parentheses correspond to the number of species in each category. Blue and red correspond to fractions of polyploids and diploids within each category, respectively.

Table 3 | The observed and simulated number of transitions on a specific background state.

Transition	Observed*		Simulated*		*P*-value
	Wild background	Crop background	Wild background	Crop background	
Diploid→polyploid	447.56	26.81	433.70	19.09	0.109
	DP background	PP background	DP background	PP background	
Wild→crop	137.55	57.19	149.39	42.30	0.006

*Observed and expected numbers were summed over all genera.

To test these hypotheses, we examined 68 genera in which polyploidy transitions had occurred (with both diploids and polyploids) for a total of 217 crop species and 2,411 wild species. Using a stochastic mapping approach[28], we inferred the location of 195 domestication and 474 polyploidy events along these phylogenies. This allowed us to estimate the number of domestication events that occurred on diploid and on polyploid backgrounds as well as the number of polyploidy events that occurred on wild and crop backgrounds. In 32 cases, both domestication and polyploidy events were inferred to occur along the same branch, thus precluding our ability to reliably identify the order of events in these cases. Of the 195 domestication events, 29% (57 events) have occurred on a polyploid background. Since a rather small fraction of the total branch lengths in the examined phylogenies is in the polyploid state (using our ancestral state reconstruction this was inferred to be ~0.18), a rough estimate for the expected number of domestication events on a polyploid background is $195 \times 0.18 = 35.1$. Accordingly, the rate of domestication event on a polyploid background is roughly twice as that on a diploid background [(57/0.18)/(138/0.82) = 1.9]. This back-of-the-envelope calculation, however, disregards the non-uniform distribution of polyploidy and domestication events across the phylogenies. Thus, to more formally assess the significance of this observation, we generated a null distribution for the number of domestication events expected on each ploidy background assuming polyploidy and domestication transitions are unlinked. To ensure realistic simulations, the number of transitions and their phylogenetic depth were kept identical to that of the observed data (see Methods). Our results demonstrated a significant excess of domestication events on a polyploid background to what can be expected by chance ($P = 0.006$; Table 3), supporting the polyploidy first hypothesis, whereby higher ploidy levels increase the probability of successful domestication.

Similarly, we examined the 'domestication first' hypothesis by inferring the location of polyploidy events on wild and crop backgrounds (Table 3). We identified 474 polyploidy events, of which 5.7% (27 events) are on a crop background. Although this is higher than the number of events expected by chance this increase is statistically non-significant (18 polyploidy events are expected on a domestication background assuming no association between the two processes, $P = 0.11$; Table 3). These results nonetheless should be interpreted with caution because of several limitations of the phylogenetic approach used to infer the relative order of polyploidy and domestication. First, the relative order cannot be accurately assessed when both polyploidy and domestication had occurred along the same (usually terminal) branch of the phylogeny. Second, intraspecific variation in both ploidy and domestication status are possible, and such instances require a higher-resolution population-level analysis. Third, the possible absence of putative progenitor species from the reconstructed phylogenies (because of missing genetic or chromosome count data) might lead to erroneous inferences. Feral crop populations and early domesticated forms that were completely lost (for example, *Iva annua*[29]) present another challenge to such phylogenetic inferences, and the extent of crop-to-wild back transitions is generally unknown. Thus, the question whether the polyploidization rate was altered in domestication lineages awaits future investigations that will rely on more precise timing (rather than phylogenetic placement) of the domestication events.

To obtain alternative evidence for the relative order of polyploidy and domestication, we mined the literature and identified the wild progenitor of 30 polyploid crops in our database (Supplementary Materials and Supplementary Table 2). In 22 of these cases, the wild progenitor(s) could be identified as a polyploid, providing additional support for the 'polyploid first' scenario. The situation is more complicated for the eight cases where the wild progenitor was identified as diploid since the polyploidy event could have occurred anytime since divergence of the two species (before or during domestication), again illustrating the difficulty in providing direct support for the domestication first scenario.

Taken together, our results indicate a strong association between domestication and polyploidy abundance, most prominently through a higher than expected tendency of domesticating an already polyploid genome. Our findings thus support earlier hypotheses[6–8] that argued for adaptive significance of polyploidy to crop domestication and improvement. This suggests that under certain circumstances, the expanded genetic degrees of freedom afforded by a polyploid genome has provided these lineages with phenotypic novelties that were important for their success in agronomic settings and enhanced their adaptability during domestication and subsequent improvement. As has been shown in yeast[30], polyploidy does not only lead to higher genetic diversity but could also foster adaptation to new environments, irrespective of initial fitness. It is perhaps this plasticity, coupled with the benign environments introduced during cultivation, that enabled wild polyploid plants to rapidly acclimatize to agricultural settings and to become successful crops.

Methods

We have constructed a database that includes crop species and their wild congeners classified according to their commodity use group (crops only), growth form, life cycle and higher level taxonomic circumscription. Database construction details are given in the Supplementary Methods. The phylogeny for each genus was reconstructed and ploidy level inference for each species was determined using chromEvol[16]. Phylogeny reconstruction, ploidy inference and sister clade contrasts procedures are detailed in the Supplementary Methods.

Inferring the temporal order of polyploidy and domestication. To better understand the relationship between domestication and polyploidy, it would be useful to know the historical order in which these events occurred. Specifically, we examined whether the probability of a domestication event is influenced by the background ploidy level of a lineage, and, similarly, whether the probability of a polyploidy event is different at either crop or wild background. We used the R platform[31] to infer the locations of state transitions (from wild to crop and from diploid to polyploid) along the phylogenies within the 68 genera that show variation in ploidy level (where polyploidy events were inferred) by applying the stochastic mapping approach[28] using the asr.stoch function from the Diversitree package[32]. The asr.stoch function uses the MK2 model, which requires two rate parameters, describing the transitions from state 0 to state 1 and back. Here, the model was constrained to only allow transitions from diploid to polyploid and from wild to crop. Transition rates were estimated independently for ploidy and domestication using maximum likelihood (find.mle function in the Diversitree package[32]). Using the reconstructed mappings along the tree branches, the location of each transition along the tree and the background state of the other trait were identified (whether a wild to crop transition occurred on a diploid or polyploid background; an illustrative example for *Fragaria* is shown in Supplementary Fig. 1). To account for phylogenetic uncertainties, for each genus the number of transition events was averaged over 100 trees sampled randomly from the posterior distribution. We then summed the number of transitions across all genera to obtain the observed number of transition events occurring in each of the possible backgrounds, that is the number of domestication events occurring on a polyploid or a diploid background,

denoted Obs($T^{pp}_{wild\rightarrow crop}$), and Obs($T^{dp}_{wild\rightarrow crop}$), respectively. Diploid to polyploid transitions on a wild/crop backgrounds were similarly defined, denoted Obs($T^{wild}_{dp\rightarrow pp}$) and Obs($T^{crop}_{dp\rightarrow pp}$). We then calculated the proportion of transition events on polyploid and crop backgrounds:

$$\mathrm{Obs}\left(T^{pp}_{wild\rightarrow crop}\right)/\left(\mathrm{Obs}\left(T^{pp}_{wild\rightarrow crop}\right)+\mathrm{Obs}\left(T^{dp}_{wild\rightarrow crop}\right)\right)$$

and

$$\mathrm{Obs}\left(T^{crop}_{dp\rightarrow pp}\right)/\left(\mathrm{Obs}\left(T^{wild}_{dp\rightarrow pp}\right)+\mathrm{Obs}\left(T^{crop}_{dp\rightarrow pp}\right)\right)$$

We used simulations to test whether the observed number of wild to crop transitions on a certain ploidy background deviates from the expected value under no association between domestication and ploidy level. A possible approach to construct the background distribution could have been to apply a parametric bootstrap approach by simulating random states using the MK2 model with the inferred transition rates. However, this approach assumes that state transitions occur with homogenous probability along the phylogeny, an assumption that is violated for both polyploidy[33,34] and domestication. Instead, for each of the 100 phylogenies used in each genus, we simulated random states of domestication status and ploidy levels by placing events along random branches of the phylogeny, whose depth is equal to the branches in which the true events were inferred to occur. One hundred simulations were performed per tree, resulting in 10,000 simulated data sets (each data set consists of simulated ploidy and domestication states for the extant taxa in each of the genera). For each data set, we repeated the same procedure as in the original data, resulting in a distribution of the expected number of transitions: Exp($T^{pp}_{wild\rightarrow crop}$), Exp($T^{dp}_{wild\rightarrow crop}$), Exp($T^{wild}_{dp\rightarrow pp}$), and Exp($T^{crop}_{dp\rightarrow pp}$). To compare between the observed and expected number of transitions, we calculated the expected proportion of transition events on polyploid and crop backgrounds as

$$\mathrm{Exp}\left(T^{pp}_{wild\rightarrow crop}\right)/\left(\mathrm{Exp}\left(T^{pp}_{wild\rightarrow crop}\right)+\mathrm{Exp}\left(T^{dp}_{wild\rightarrow crop}\right)\right)$$

and

$$\mathrm{Exp}\left(T^{crop}_{dp\rightarrow pp}\right)/\left(\mathrm{Exp}\left(T^{wild}_{dp\rightarrow pp}\right)+\mathrm{Exp}\left(T^{crop}_{dp\rightarrow pp}\right)\right).$$

We used the distribution of simulated values to calculate a *P*-value as the proportion of simulated values that are as extreme as the observed value for each trait, multiplied by two, to account for the two-tailed hypothesis. The R script 'analysis_script.R' for the temporal order of polyploidy and domestication analysis can be found within the Supplementary data files.

Received 11 February 2016; accepted 30 June 2016; published 1 August 2016

References

1. Meyer, R. S., DuVal, A. E. & Jensen, H. R. Patterns and processes in crop domestication: an historical review and quantitative analysis of 203 global food crops. *New Phytol.* **196,** 29–48 (2012).
2. Gepts, P. in *Plant Breeding Reviews: Long-term Selection: Crops, Animals, and Bacteria* Vol. 24 (ed. Janick, J.) 1–44 (John Wiley & Sons, Inc., 2004).
3. Bennett, M. D. Perspectives on polyploidy in plants–ancient and neo. *Biol. J. Linn. Soc. Lond.* **82,** 411–423 (2004).
4. Ross-Ibarra, J., Morrell, P. L. & Gaut, B. S. Plant domestication, a unique opportunity to identify the genetic basis of adaptation. *Proc. Natl Acad. Sci. USA* **104,** 8641–8648 (2007).
5. Pecinka, A., Fang, W., Rehmsmeier, M., Levy, A. A. & Scheid, O. M. Polyploidization increases meiotic recombination frequency in *Arabidopsis*. *BMC Biol.* **9,** 24 (2011).
6. Renny-Byfield, S. & Wendel, J. F. Doubling down on genomes: polyploidy and crop plants. *Am. J. Bot.* **101,** 1711–1725 (2014).
7. Paterson, A. H. Polyploidy, evolutionary opportunity, and crop adaptation. *Genetica* **123,** 191–196 (2005).
8. Udall, J. A. & Wendel, J. F. Polyploidy and crop improvement. *Crop Sci.* **46,** S-3–S-14 (2006).
9. Diamond, J. Evolution, consequences and future of plant and animal domestication. *Nature* **418,** 700–707 (2002).
10. Hammer, K. The domestication syndrome. *Die Kulturpflanze* **32,** 11–34 (1984).
11. Emshwiller, E. in *Documenting Domestication: New Genetic And Archaeological Paradigms* (eds Zeder, M. A., Bradley, D., Emshwiller, E. & Smith, B. D.) Ch. 12 (Univ. of California Press, 2006).
12. Zeven, A. C. in *Polyploidy: biological relevance* (ed. Lewis, W. H.) 385–407 (Plenum, 1980).
13. Hancock, J. F. Contributions of domesticated plant studies to our understanding of plant evolution. *Ann. Bot.* **96,** 953–963 (2005).
14. Hilu, K. Polyploidy and the evolution of domesticated plants. *Am. J. Bot.* 1494–1499 (1993).
15. Rice, A. *et al.* The chromosome counts database (CCDB)–a community resource of plant chromosome numbers. *New Phytol.* **206,** 19–26 (2015).
16. Glick, L. & Mayrose, I. ChromEvol: assessing the pattern of chromosome number evolution and the inference of polyploidy along a phylogeny. *Mol. Biol. Evol.* **31,** 1914–1922 (2014).
17. Plant DNA C-values database. http://data.kew.org/cvalues (2012).
18. Wood, T. E. *et al.* The frequency of polyploid speciation in vascular plants. *Proc. Natl Acad. Sci. USA* **106,** 13875–13879 (2009).
19. Stebbins, G. L. Cytological characteristics associated with the different growth habits in the dicotyledons. *Am. J. Bot.* **25,** 189–198 (1938).
20. Fuller, D. Q. Contrasting patterns in crop domestication and domestication rates: recent archaeobotanical insights from the Old World. *Ann. Bot.* **100,** 903–924 (2007).
21. de Wett, J. M. J. in *Grass Systematics and Evolution* (eds Soderstorm, T. R., Hilu, K. W., Campbell, C. S. & Barkworth, M. A.) 188–194 (Smithsonian Institution Press, 1987).
22. Ramsey, J. & Schemske, D. W. Neopolyploidy in flowering plants. *Annu. Rev. Ecol. Syst.* **33,** 589–639 (2002).
23. Fuller, D. Q. & Harvey, E. L. The archaeobotany of Indian pulses: identification, processing and evidence for cultivation. *Environ. Archaeol.* **11,** 219–246 (2006).
24. Wu, J. H. *et al.* Induced polyploidy dramatically increases the size and alters the shape of fruit in *Actinidia chinensis*. *Ann. Bot.* **109,** 169–179 (2012).
25. te Beest, M. *et al.* The more the better? The role of polyploidy in facilitating plant invasions. *Ann. Bot.* **109,** 19–45 (2011).
26. Dempewolf, H., Hodgins, K. A., Rummell, S. E., Ellstrand, N. C. & Rieseberg, L. H. Reproductive isolation during domestication. *Plant Cell* **24,** 2710–2717 (2012).
27. Hughes, C. E. *et al.* Serendipitous backyard hybridization and the origin of crops. *Proc. Natl Acad. Sci. USA* **104,** 14389–14394 (2007).
28. Huelsenbeck, J. P., Nielsen, R. & Bollback, J. P. Stochastic mapping of morphological characters. *Syst. Biol.* **52,** 131–158 (2003).
29. Diamond, J. *Guns, Germs, and Steel. The Fates of Human Societies* (WW Norton & Company, 1999).
30. Selmecki, A. M. *et al.* Polyploidy can drive rapid adaptation in yeast. *Nature* **519,** 349–352 (2015).
31. R Foundation for Statistical Computing. A Language and Environment for Statistical Computing (R Core Team, 2013); https://www.R-project.org/
32. FitzJohn, R. G. Diversitree: comparative phylogenetic analyses of diversification in R. *Methods Ecol. Evol.* **3,** 1084–1092 (2012).
33. Escudero, M. *et al.* Karyotypic changes through dysploidy persist longer over evolutionary time than polyploid changes. *PLoS ONE* **9,** e85266 (2014).
34. Mayrose, I. *et al.* Recently formed polyploid plants diversify at lower rates. *Science* **333,** 1257–1257 (2011).

Acknowledgements

We thank A. A. Levy and A. Rice for helpful discussions and suggestions. This study was supported by a post-doctoral fellowship to N.S. from the Edmond J. Safra postdoctoral fellowship and the Israel Science Foundation (1265/12) to I.M.

Author contributions

The authors contributed in the following ways: conceptualization, I.M.; methodology, A.S.-M., N.S. and I.M.; software, N.S.; validation, A.S.-M. and I.M.; formal analysis, A.S.-M. and N.S.; investigation, A.S.-M. and N.S.; writing, A.S.-M., N.S. and I.M.; supervision, I.M.

Additional information

Supplementary information is available online. Reprints and permissions information is available online at www.nature.com/reprints. Correspondence and requests for materials should be addressed to I.M.

Competing interests

The authors declare no competing financial interests.