

**When your favorite trait is not enough to explain diversification: An example of diversification
linked to polyploidy and breeding system in Solanaceae**

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Abstract

The effect of polyploidy in diversification remains a contentious issue. On the one hand, recent studies that found that polyploids have slower speciation rates and higher extinction rates than diploids left scientist wondering if polyploidy is truly an evolutionary dead-end. On the other hand, botanist have found strong
5 molecular support of multiple polyploidy events at the root of highly diverse clades which challenges the evolutionary dead-end conclusions reached by modeling approaches. We re-investigate the role of polyploidy in speciation and extinction from a new modeling perspective considering that patterns found in diversification models can be misleading and incorrectly attributed to polyploidy when other observed and unobserved plant traits are responsible of shaping diversification. Using statistically robust comparative
10 phylogenetic approaches, we show that it is possible to detect whether the contribution of polyploidy to speciation and extinction is significant under the presence of other potential traits also affect diversification. We use the phylogeny, polyploidy, and breeding system data of 595 Solanaceae species to understand the contribution of polyploidy to diversification. We ask if Solanaceae polyploids are evolutionary dead-ends, and whether breeding system or some other unobserved traits are responsible of the patterns of diversification
15 observed in the phylogeny.

Introduction

-Studying diversification linked to trait evolution

Here I need help (perhaps will be the last line I write)

In these context, botanist have been asking how polyploidy shapes patterns of diversification. The prevalence of polyploidy and its detection across multiple and highly diverse clades of angiosperms inevitably lead to the hypothesis of the importance of polyploidy in the speciation and extinction patterns observed across the flowering plant phylogeny. At the same time, a similar question has been asked in the breeding system world, where self-compatibility has evolved multiple times in flowering plants. However, the influence in diversification using both polyploidy and self-compatibility information has not been studied simultaneously.

- Why polyploidy and self-compatibility in particular makes for an interesting study in the context of diversification

In the polyploidy world, an important debate regarding the diversification of angiosperms has been ongoing since the publication of Mayrose et al. (2011). The authors discovered that using the latest diversification model linked to two states diploid and polyploid, the net diversification of polyploids was much slower than the net diversification rate than polyploids. This result was surprising and an sparked a discussion about the long-term evolutionary consequences of polyploidy. Soltis et al. (2014) questioned if polyploidy should be regarded as an evolutionary dead-end since the net diversification of polyploids was negative, despite overwhelming evidence about the incidence of polyploidy especially at the root of highly diverse angiosperm claims (ref here). A year later, diversification models were re-tested and corrected, and still found the same pattern (Mayrose et al. 2015), to the disappointment of plenty of botanists there was no denying of the weak trend of diversification that polyploids left behind. The most recent study by Landis et al. (2018) that used not only the presence of polyploidy in the tips but also the number of whole genome duplications in a taxon lineage found that....

Meanwhile, studies focusing on diversification patterns and breeding system have consistently found that self-incompatible plants often have higher net diversification rates compare to their self-compatible counterparts (Emma and Boris' papers here, what about papers that are not solanaceae?)

- Why other traits need to be considered as well

- What other models and studies have done in the past

- What is lacking from past approaches?

There are two key questions that at the time of the polyploidy debate were difficult to ask. The first is if the models used to measure the diversification of polyploids were correct, and the second question is if the models have potentially included more evidence and potential traits that are not polyploidy or other lines of evidence that could be driving the patterns. At the time, in a different context Beaulieu and O'Meara (2016) were finding an alternative solution to the first question, coming up with a new model that could represent the broad heterogeneity of the diversification process and parse out the signal between the trait of interest and the noise in diversification. Their model, the hidden state speciation and extinction model is a key component to detect whether polyploidy or something else unknown but related to it is driving the speciation and extinction patterns that we see in angiosperms.

-What is our proposal to tackle this problem?

- How this paper is structured

The second question (talk here about breeding system and polyploidy, and how this could be different across clades and this is one of the reasons why we focused on Solanaceae). -Diversification and breeding systems
Goldberg and Igic 2012, different perspectives

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Methods

Data

Chromosome number data were obtained for all Solanaceae taxa in the the Chromosome Counts Database (CCDB; Rice et al. 2015), and the ca. 14,000 records were cleaned semi-automatically using the CCDBcurator R package (Rivero et al. 2019). This large dataset includes the compilation of Solanaceae ploidy states from (Robertson et al. 2011). Species were coded as either diploid (D) or polyploid (P). For the majority of species, ploidy was assigned according to information from the original publications and the Kew Royal Botanic Gardens C-value DNA resource (Bennett and Leitch 2005). For taxa without ploidy information but with information about chromosome number, we assigned ploidy based on the multiplicity of chromosomes within the genus. For example, *Solanum betaceum* did not include information about ploidy level but it has

24 chromosomes, so because $x = 12$ is the base chromosome number of the *Solanum* genus (Olmstead and Bohs 2007), we assigned *S. betaceum* as diploid. Species with more than one ploidy level were assigned the smallest and most frequent ploidy level recorded. We also cross-verified using the breeding system information and found that there were no self-incompatible species possibly listed as polyploid, or listed as polyploid and diploid which increase our confidence in the assignments. Breeding system was scored as self-incompatible (I) or self-compatible (C) based on results hand-curated from the literature (as in Igić et al. 2006; Goldberg et al. 2010; Robertson et al. 2011; Goldberg and Igić 2012). Most species could unambiguously be coded as either SI or SC (Raduski et al. 2012). Following previous work, we coded as I any species with functional I systems, even if C or dioecy was also reported. Dioecious species without functional I were coded as C.

To those existing data sets, we added some additional records for chromosome number and breeding system. The Supplementary Information contains citations for the numerous original sources for all of the data. Synonymy followed Solanaceae Source (PBI *Solanum* Project 2012). Hybrids and cultivars were excluded because ploidy and breeding system are likely to be altered by domestication. As in Robertson et al. (2011), we examined closely the few species for which the merged ploidy and breeding system data indicated the presence of I polyploids. Although SI populations frequently contain some C individuals and diploid populations frequently contain some polyploid individuals, in no case did we find individuals that were both SI and polyploid. Because of this empirical observation and the functional explanation for whole genome duplication disabling gametophytic self-incompatibility (reviewed in Ramsey and Schemske 1998; Stone 2002), we consider only three observed character states: self-incompatible diploid (ID), self-compatible diploid (CD), and polyploid (P) which are always self-compatible.

Matching our character state data to the largest time-calibrated phylogeny of Solanaceae (Särkinen et al. 2013) yielded 595 species with ploidy and/or breeding system information on the tree. Binary or three-state classification of ploidy and breeding system for the 595 taxa is summarized in Table 1. We retained all of these species in each of the analyses below, because pruning away tips lacking breeding system in the ploidy-only analyses (and vice versa) would discard data that could inform the diversification models. A total of 405 taxa without any information about breeding system nor polyploidy were pruned. Tips without trait data are non informative for diversification parameters linked to trait change and can significantly slow down the convergence of inferences in trees with already hundreds of tips.

Models for Diversification and Polyploidy

We first defined a binary state speciation and extinction model (BiSSE, Maddison et al. (2007)) for polyploidy evolution where taxa was classified as diploid (D=0) and polyploid (P=1) Table 1. We refer to this model as the D/P polyploidy model. In a Bayesian framework, we obtained posterior probability distributions of speciation rates (λ_D, λ_P), extinction rates (μ_D, μ_P), net diversification rates ($r_D = \lambda_D - \mu_D, r_P = \lambda_P - \mu_P$), and relative extinction rates ($v_D = \frac{\mu_D}{\lambda_D}, v_P = \frac{\mu_P}{\lambda_P}$) just as previously explored in Mayrose et al. (2011) and Mayrose et al. (2015). However, our analyses differ from previous models since we consider not only a polyploidization rate ρ and but also a diploidization parameter rate δ .

As a second step, we fitted a hidden state speciation and extinction model (HiSSE, Beaulieu and O'Meara (2016)) to evaluate whether the differences in diversification rates were found due to a hidden trait associated to polyploidy. This model is referred to as the D/P-A/B polyploidy and hidden state model. As discussed by Beaulieu and O'Meara (2016) BiSSE-like models suffer from a large type I error since they fail to account as part of the null hypothesis heterogeneous diversification rate changes that do not directly depend on the trait of interest. By expanding the D/P model by using a hidden trait with states A and B, the polyploidy and hidden state model addressed the signal of diversification due to polyploidy while parsing out the heterogeneity of diversification rates due to unobserved traits. The D/P-A/B polyploidy and hidden trait is composed by four states: diploid and polyploid subdivided by a binary hidden trait with states A and B for which we estimated the posterior probability distributions of speciation rates ($\lambda_{DA}, \lambda_{DB}, \lambda_{PA}, \lambda_{PB}$), extinction rates ($\mu_{DA}, \mu_{DB}, \mu_{PA}, \mu_{PB}$), net diversification rates ($r_{DA}, r_{DB}, r_{PA}, r_{PB}$), and relative extinction rates ($v_{DA}, v_{DB}, v_{PA}, v_{PB}$). In this model polyploidization rate ρ , diploidization rate δ are also considered, while changes between every hidden state are symmetrical with the same rate α .

Models for Diversification and Breeding System

In order to analyze the effects of breeding system in the diversification process, two models the I/C (I= self-incompatible, C= self-compatible) and the I/C-A/B were performed. The I/C breeding system model (BiSSE) was done with the goal of investigating if the effect of self-incompatibility in diversification similar to the analysis performed by Goldberg and Igić (2012). The I/C-A/B breeding system with hidden trait model parses out the effect of breeding system in diversification by incorporating the possibility of heterogeneous changes in the diversification rates that can be attributed to a hidden state. A hidden state model has not previously been fitted to Solanaceae data. For these two models, we assumed that self-compatibility is irreversible as discussed by Igić and Busch (2013), so we defined the transition rate q_{IC} as the parameter for changes from self-incompatible to self-compatible state. This is an important assumption because ancestral

state reconstruction in the models might differ when polyploidy and breeding system are analyzed as independent in the Solanaceae tree. This irreversibility assumption prevents self-compatible state from evolving into self-incompatible state and as a result, the ancestral state of all taxa in this model has probability one of being self-incompatible.

Models for Polyploidy, Breeding System, and Diversification

As a third approach, we analyzed the roles of both polyploidy and breeding system in the process of diversification using a multivariate speciation and extinction model (MuSSE, FitzJohn (2012)). We named our MuSSE the ID/P/CD breeding system and polyploidy model, where the three states are self-incompatible diploids (ID), polyploids (always self-compatible, $P=1$), and self-compatible diploids (CD). The model is defined via ten parameters; six defining diversification ($\lambda_{CD}, \mu_{CD}, \lambda_P, \mu_P, \lambda_{ID}, \mu_{ID}$) and four parameters defining key trait changes: polyploidization of self-compatible diploids ρ_C , diploidization δ , polyploidization of self-incompatible diploids ρ_I , and self-incompatible to self-compatible rate q_{IC} .

Since the null hypothesis of the MuSSE model is that the diversification is equal and constant for all three states defined, it is possible that MuSSE can also suffer from large type I errors as their BiSSE equivalents. Therefore, we extended MuSSE model to account for a hidden state like the methodology recently proposed by Caetano et al. (2018) and Herrera-Alsina et al. (2018). A full fitted MuHiSSE model would have 26 parameters total (Herrera-Alsina et al. 2018). Since our goal was to look for diversification rate differences polyploidy and breeding system rather than differences occurring at hidden state, we fitted a simplified version, the ID/P/CD-A/B model, that is defined via 16 parameters. The reduction in parameter space is achieved by fixing the rates amongst hidden states to be equal with parameter α and fixing the transition rates amongst breeding system to be the same as the ones defined in the MuSSE model ($\rho_{ID}, \delta, \rho_{CD}, q_{IC}$) independently from the hidden state. Therefore, the ID/P/CD-A/B model was used to estimate twelve speciation and extinction rates ($\lambda_{IDA}, \mu_{IDA}, \lambda_{PA}, \mu_{PA}, \lambda_{CDA}, \mu_{CDB}, \lambda_{IDB}, \mu_{IDB}, \lambda_{P_B}, \mu_{P_B}, \lambda_{CDB}, \mu_{CDB}$), and the net diversification and relative extinction rates associated with them.

Diploidization as an exploratory hypothesis

For all the four models that consider ploidy changes we assumed that diploidization could happen. Previous modeling approaches (Mayrose et al. 2011) have argued against inferring diploidization rates when using ploidy data that comes from classifications based on chromosome number multiplicity or chromosome number change models like ChromEvol (?). These types of classifications do not allow for a ploidy reversion. Where indicated, the classification of ploidy for the data used in our models was based on chromosome

multiplicity at the genus level. However, the majority of the ploidy classifications were adopted from original studies with alternative sources of information (i.e. geographic distribution, genus ploidy distribution) where ploidy was defined by authors that found evidence for it. Since it is not clear whether diploidization can be detected under alternative ploidy classifications or even classifications based on chromosome number multiplicity at the genus level, we also fitted the models without diploidization in order to test whether including an assumption of diploidization is sensitive. As discussed by Servedio et al. (2014) the presence or absence of a hypothesis can have an exploratory goal. In our case the diploidization parameter (or the lack of denoted by no δ) in our models is an opportunity to explore an assumption that might be important but it is not the single definitive process to understand the interactions among polyploidy, breeding system, and diversification.

Statistical Inference under the models

Parameters for each of the ten diversification models described previously were performed using custom code in RevBayes (Höhna et al. 2016) environment. Code and results for all analyses is freely available at <https://github.com/roszenil/solploidy>. For all analyses, a correction for sampling bias is included assuming that Solanaceae family has approximately 3,000 species ($s = 595/3000$) as estimated by the Solanaceae Source project (PBI *Solanum* Project 2012). For all ten models, we assumed that speciation and extinction parameters for all models had log-normal prior distributions with means equal the expected net diversification rate ($\frac{(\text{number of taxa})/2}{\text{root age}}$) and standard deviation 0.5. Prior distributions for parameters defining trait changes were assumed to be gamma distributed with parameters $k = 0.5$ and $\theta = 1$. For each model, an MCMC was performed for 96 hours in the high-performance computational cluster at Minnesota Supercomputing Institute which allowed for 5,000 generation of burn-in and a minimum of 200,000 generations of MCMC for each of the 6 models. For each model, convergence and mixing of the MCMC was tested using R package coda and software Tracer (see supplementary information for convergence plots).

Model selection

We calculated the marginal likelihoods for each of the ten models using custom code in RevBayes Höhna et al. (2016). Marginal likelihoods were calculated using 50 stepping stone steps using the methodology of Xie et al. (2010). Each stepping stone step was found by calculating 500 generations of burn-in followed by a total of 1000 MCMC steps Table 2. The calculation of each marginal likelihood ran for 24 hours in the high-performance computational cluster at Minnesota Supercomputing Institute.

Using the marginal likelihood values we calculated fourteen different Bayes factors in log-scale.

The first six Bayes factors compared the four models of polyploidy against each other, followed by one single comparison between the breeding system models, and finalizing with four comparisons between each polyploidy and breeding system models (see Table 3 for all comparisons). Comparison between polyploidy models vs. polyploidy and breeding system models are not valid for two reasons: first, the input data in each model is numerically different (see Table 1 for data classifications) ; second, even when it is possible to re-write the polyploidy and diversification models to include a hidden state that would account for breeding system allowing to use the same input data, the re-written model would still not be comparable to the multivariate SSE models proposed for polyploidy and breeding system due to the hierarchical structure imposed by the interaction between breeding system and polyploidy. This second point has been recently denoted by Tarasov (2018) as the lack of lumpability in Markov models for discrete traits. In our particular case, polyploids cannot be self compatible, and the irreversibility of self-compatible to self-incompatible state makes the three-state Markov models non-lumpable into two-state models ultimately making multivariate and the bivariate models incomparable.

Results

Polyploidy and Diversification Models

Similarly to the results obtained by Mayrose et al. (2011) and Mayrose et al. (2015), the D/P polyploidy model we found that net diversification of diploids is significantly higher than the the net diversification of polyploids. This result holds true whether or not the diploidization parameter is present. However, when diploidization is present the net diversification of polyploids is nonnegative with probability 1, whereas in the absence of diploidization the net diversification of polyploids is negative with probability 0.75(HERE VERIFY QUANTILE). In terms of the relative extinction, when the diploidization parameter is present both polyploids and diploids have posterior distributions that overlap, but that pattern changes in the absence of the diploidization parameter leading to a significant difference between relative extinction where polyploids have a significant higher relative extinction rate. Polyploidization rate ρ has a credible interval between (a,b) and diploidization rate has a credible interval between (c,d).

For the D/P- A/B model with diploidization the diploid and polyploid net diversification rates are overlapping for both state A and B of the hidden trait. In this model, the differences in net diversification are due to the presence of a hidden trait and not to the differences in ploidy. When diploidization parameter is absent the pattern holds. Rates of polyploidization have a 95% credible interval of (a,b) and diploidization rate has a 95% credible interval () for the model with diploidization, and polyploidy rate has a 95% credible interval (c,d) for the model without diploidization.

Breeding System and Diversification models

Bre

Discussion

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Type	Total of	Models		
		D/P and D/P-A/B	I/C and I/C-A/B	ID/P/CD and CD/P/ID-A/B
Diploid Self Compatible	152	0	0	0
Diploid Self Incompatible	97	0	1	2
Diploid with unknown breeding system	219	0	(0,1)	(0,2)
Polyploid	81	1	0	1
Unknow ploidy and self compatible	34	(0,1)	0	(0,1)
Unknown ploidy and self incompatible	12	0	1	2

Table 1: Binary and three state classifications for 595 taxa with ploidy and/or breeding system data. The number of taxa in the t he sample was maximize by including tips with only ploidy or only breeding system and assigned them as uncertain in the unknown character.

Model	Model Type	Ploidy	Diploidization	Breeding System	Hidden State	Parameters	Marginal Log- Likelihood
1. D/P	BiSSE	Yes	Yes	No	No	6	-1182.93
2. D/P no δ	BiSSE	Yes	No	No	No	5	-1193.66
3. D/P- A/B	HiSSE	Yes	Yes	No	Yes	11	-1145.69
4. D/P no δ -A/B	HiSSE	Yes	No	No	Yes	10	-1150.99
5. I/C	BiSSE	No	No	Yes	No	5	-1194.80
6. I/C-A/B	HiSSE	No	No	Yes	Yes	10	-1155.37
7. ID/P/CD	MuSSE	Yes	Yes	Yes	No	10	-1344.50
8. ID/P/CD no δ	MuSSE	Yes	No	Yes	No	9	-1345.87
9. ID/P/CD-A/B	MuHiSSE	Yes	Yes	Yes	Yes	16	-1300.35
10.ID/P/CD no δ -A/B	MuHiSSE	Yes	No	Yes	Yes	15	-1303.55

Table 2: Marginal likelihoods for the ten diversification models proposed.

Polyploidy Models				Breeding System Models	Polyploidy and Breeding System Models							
1	2	3	4	5	6	7	8	9	10			
1. D/P	·	10.72	-37.24	-31.94	5. I/C	·	-39.43	7. CD/P/ID	·	1.36	-44.15	-40.95
2. D/P no δ	·	·	-47.97	-42.66	6. I/C-A/B	·	·	8. CD/P/ID no δ	·	·	-45.51	-42.31
3. D/P- A/B	·	·	·	5.30				9. CD/P/ID-A/B	·	·	·	3.2
4. D/P no δ -A/B	·	·	·	·				10. ID/P/CD no δ -A/B	·	·	·	·

Table 3: Bayes factors in log scale. We compare every possible pair. Number models as indicated in Table 2.