The effect of singletons and interval length on interpreting diversity trends from the palaeobotanical record

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ABSTRACT

The reliability and the identification of potential biases are central aspects to providing an accurate robust palaeontological data analysis. In the last decade, older concepts of evolutionary processes and patterns have been revised in the light of new methods and hypotheses. Moreover, new mathematical algorithms have been developed to better interpret evolution and to reduce several biases inherent in the fossil record from the animal viewpoint. This new global study, based on a complete overview of the plant fossil record, uses comparisons with previously established palaeofloristic patterns and employs a set of regression, accumulative and evolutionary analyses to test the influence of two important variables in the inference methods: the role of singleton taxa and the duration of the time units. The regression analyses reveal that the duration of the time units employed does not distort our perception of the number of singletons at the family level. Likewise, the duration as single factor also does not affect the measures of taxonomic diversity, and does not influence representation of the main evolutionary patterns of vascular plants. The analysis reveals that the per-capita origination and extinction rates used provide global diversity patterns that diminish the effects of the possible taxonomic problems and preservational biases relating to the controversial nature of singleton taxa due to its restricted record, and they reveal that the main trends and plant turnover is characterized by slight abrupt changes, thus providing a more realistic vision about the dimension and magnitude of the observed evolutionary processes and diversification patterns from the plant fossil record.

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INTRODUCTION

In agreement with the Niklas' works (Niklas et al., 1980, 1983, 1985; Niklas, 1982, 1997, 2000), and the Benton's reflections on the fossil record (Benton, 1995, 1997; Benton and Hitchin, 1996, 1997; Benton et al., 2000), recent studies using the entire plant fossil record have clarified the main episodes of plant evolution on Earth by incorporating origination processes and extinction events (Cascales-Miñana et al., 2010; Cascales-Miñana and Cleal, 2012). Nevertheless, many aspects of such analyses, particularly those concerning the methodological biases, remain poorly resolved.

Over the past 15 years, many ideas on Phanerozoic animal evolution have been revised in the light of new methods and hypotheses, and Foote's works on the limitations and use of a taxon's stratigraphic range as a source of information about past life became particularly relevant, together with the application of new mathematical algorithms to better interpret evolution from the fossil record (Foote, 2000a, 2000b, 2003, 2005, 2007; Peters and Foote, 2001, 2002). In this way, from the Raup's studies about the role of the geologic record, in particular about the influence of the outcrop areas, in our perception of the life of the past (Raup, 1972, 1976; Raup and Stanley, 1978), many studies have followed these principles, and they have improved the measures of potential constraints of the fossil record employing modern computerized databases (Markwick and Lupia, 2002; Alroy, 2003; Ros and De Renzi, 2005; Uhen and Pyenson, 2007).

Nevertheless, all these methodologies have generally been tested based on the animal fossil record working on the palaeontological data analysis through time. Many of these about the ideas about real perception of the evolution using diversity metrics have never been tested from the plant fossil record into a comparative approach from a global viewpoint. On the other hand, despite that in the past 10 years crucial advances have been carried out in the field of the inference from the palaeobotanical data using compiled datasets, in general lines many of these works were focused on concrete geologic moments or restricted to particular palaeogeopgraphycal regions (Lupia et al., 1999; Lupia, 2004; Wilf and Johnson, 2004; Cleal, 2007, 2008).

In order to embrace modern methodologies on the plant record into a global perception, this paper has two specific aims: to test the role of singleton taxa and the length of the time units employed as a source of "distortion" (variability) in the pattern on plant diversification, and secondly, to re-evaluate the evolutionary patterns of vascular plants analysed in previous works using more recent methodologies to check the robustness of the palaeobotanical data.

MATERIAL AND METHODS

Palaeobotanical Data and Temporal Setting

Traditionally, in palaeobiology, the major contribution to understanding of diversity metrics through time have been consolidated from the palaeontological data analysis based on the animal record. Thus, for example, the Sepkoski's compendium about the marine invertebrates (Sepkoski, 1982, 1992) have been used as a methodological case study (Adrain and Westrop, 2000; Ausich and Peters, 2005; Ros and De Renzi, 2005) or from a classic viewpoint, as a data source (Flessa and Jablonski, 1985; Sepkoski, 1989; Gilinsky, 1994), for testing methodological procedures and biases or extracting information about the life extinction patterns through the study of evolutionary rates, respectively. These compendiums are currently in use (Nee, 2006; Markov, 2009). In contrast, in this approach we will show a methodological study from the plant viewpoint.

In order to test the role of the singleton taxa and the length of the intervals on our perception of the palaeophytodiversity, following the methodological principles present into the first general palaeobiological works based on large data compilations (Newell, 1952; Simpson, 1953; Müller, 1961; Schindewolf, 1962; Valentine, 1969), and more recently, the general ideas about the use of computerized palaeontogical data to test methodological aspect in the inference from the fossil record (Alroy et al., 2001; Alroy, 2003; Fara, 2004; Olszewski, 2004; Ros and De Renzi, 2005; Finnegan et al., 2008; Heim, 2008; Melott, 2008; Wall et al., 2009), a set of palaeobotanical data have been extracted from the descriptive/taxonomic literature and classic monographic studies. In this particular case, the data were extracted from *The Fossil Record 2* (Cleal, 1993a, 1993b; Collinson et al., 1993) following the information recovered by Cleal and Thomas (1999). Nevertheless, computerized databases can still be considered as essential tool for investigating large-scale palaeontological problems, as it was well thought out by Markwick and Lupia (2002), the highly heterogeneous nature of the fossil record data and the dynamism of the taxonomic processes, confers to the any database a marked temporal character.

TABLE 1. Temporal data and taxonomic parameters of the study. Time units and absolute ages extracted from Gradstein and Ogg (2004). The limits and the duration (Δt) of each interval are shown in million years. N_0, number of initial taxa; N_t, number of taxa with record in the subsequent interval; O, number of originated taxa; E, number of extinguished taxa; T, number of total taxa; S_t, number of singleton taxa; N_r, number of range-through taxa; N_e, number of extinguished taxa by discounting the singletons; N_f, number of originated taxa by discounting the singletons.

Temporal setting					Taxonomic counts								
Time unit	Abbreviation	Lower limit	Upper limit	Δt	N_0	N_t	O	E	T	S_t	N_r	N_e	N_f
Late Silurian	US	428.2	416.0	12.2	1	2	2	0	3	0	/	0	2
Early Devonian	LD	416.0	397.5	18.5	2	4	4	2	6	1	1	1	3
Middle Devonian	MD	397.5	385.3	12.2	4	11	8	1	12	0	3	1	8
Late Devonian	UD	385.3	359.2	26.1	11	10	7	8	18	4	7	4	3
Mississippian	LCa	359.2	318.1	41.1	10	21	21	10	31	6	6	4	15
Pennsylvnian	UCa	318.1	299.0	19.1	21	27	25	19	46	10	12	9	15
Early Permian	LPe	299.0	270.6	28.4	27	20	7	14	34	2	15	12	5
Late Permian	UPe	270.6	251.0	19.6	20	10	7	17	27	3	6	14	4
Early Triassic	LT	251.0	245.0	6.0	10	13	5	2	15	2	10	0	3
Middle Triassic	MT	245.0	228.0	17.0	13	13	0	0	13	0	13	0	0
Late Triassic	UT	228.0	199.6	28.4	13	25	15	3	28	1	11	2	14
Early Jurassic	LJ	199.6	175.6	24.0	25	28	3	0	28	0	25	0	3
Middle Jurassic	MJ	175.6	161.2	14.4	28	31	4	1	32	0	27	1	4
Late Jurassic	UJ	161.2	145.5	15.7	31	31	2	2	33	0	29	2	2
Early Cretaceous	LCr	145.5	99.6	45.9	31	33	6	4	37	0	27	4	6
Late Cretaceous	UCr	99.6	65.5	34.1	33	58	32	7	65	1	27	6	31
Early Palaeogene	LPa	65.5	55.8	9.7	58	77	19	0	77	0	58	0	19
Middle Palaeogene	MPa	55.8	33.9	21.9	77	140	63	0	140	0	77	0	63
Late Palaeogene	UPa	33.9	23.0	10.9	140	158	18	0	158	0	140	0	18
Early Neogene	LN	23.0	5.3	17.7	158	183	25	0	183	0	158	0	25
Late Neogene	UN	5.3	0.0	5.3	183	183	3	0	186	0	/	0	3

This temporal aspect is due to the palaeontogical datasets are always undergoing continuous revision because, among other considerations, new findings and/or new phylogenetic models modify the stratigraphic information and the hierarchy of the taxonomic systems, respectively. For these reasons, and attending this background, the dataset used herein have been taken uniquely as a methodological case study to test the per-capita rates and inference methods commented below.

Following the taxonomic ideas expressed by Cascales-Miñana et al. (2010) and Cascales-Miñana and Cleal (2012), this study has been performed at the family level. This taxonomic level was chosen since it provided very thorough and consistent information. Using the same line of rea-

soning, this approach uses 21 time units extracted from Gradstein and Ogg (2004) embracing the complete history of the vascular plants from the Silurian to the present-day, see Table 1 for details. To perform the algorithms explained below, the families were put into a binary matrix placing the taxa in rows and the time units in columns; complete list of family taxa and binary matrix available from supporting on-line information (see Appendix for details).

Data Analysis

Singleton taxa (taxa to appear first and last in the same time unit) were analysed using accumulative abundance analyses (S_t) according to the expression $S_t = (\Sigma^{i,k} S_{tk} / S_c) * 100$, where i corre-

sponds to the first interval analysed, S_{tk} corresponds to the number of singletons in time unit k, and S_c is the total of number of singleton taxa in the dataset from the Silurian to the present-day to illustrate the general distribution pattern across the geologic time of this type of taxa in the dataset. Together with this approach, the taxonomic model present in the original sources was firstly studied from an abundance analysis of the higher taxonomic categories of the singleton taxa to evaluate possible simple taxonomic bias. These complementary analyses have contemplated the higher levels of orders and divisions.

The effect of the length of the time units between the duration in millions of years for each time unit and the number of taxa registered in these intervals has been tested using analysis of simple regression under a liner generalized model representing the results with a correlation diagram in agreement with the general statistical procedure presents in the literature (Mitchell-Olds and Shaw, 1987; Payne, 2003; Freund et al., 2006). With this methodology, the originated, extinguished, total and singleton taxa have been independently tested. In order to avoid the subjective component in the interpretation of the results, the regression value has been calculated for each analysis performed. These analyses have been performed using the PAST software (Hammer et al., 2001).

The study of the evolutionary rates and the re-evaluation of the previous evolutionary patterns have been conducted using the methodological principles indicated by Foote (2000a, 2000b). The use of these per-capita rates rates has increased in recent years (Peters, 2006; Kiessling et al., 2007; Fröbisch, 2008; Liow et al., 2008; Sengor et al., 2008; Simpson and Harnik, 2009), and today these algorithms, which do not consider singleton taxa, are reference rates in modern palaeobiology. These type of rates based on boundary crossed taxa, as it was commented by Foote (2000a, 2000b), present a relative insensitivity to the preservation problems and, therefore, they can potentially diminish the biases related to the incompleteness of the record in comparison with the classic diversity measures. To simplify the explanation of the expressions, we have used the same nomenclature presented in Cascales-Miñana et al. (2010). The origination rate (T_O) has been calculated according to the following expression $T_O = ln(N_t / N_r) / \Delta t$, where for a given time unit k, N_t corresponds to the number of taxa present in this time unit which cross its upper limit and have

record in the subsequent interval ($k + 1$), N_t can be calculated for each time unit from the expression $N_{tk} = T_{k+1} - O_{k+1}$, where T_{k+1} and O_{k+1} are the number of total and originated taxa of the subsequent interval, respectively. N_r is the number of taxa that cross both the earlier and later boundary of a time unit, also known as range-through taxa; that is, the taxa known before and after the interval (Casanovas-Vilar et al., 2010). Likewise, the extinction rate (T_E) has been calculated from the expression $T_E = ln(N_0 / N_r) / \Delta t$, where N_0 is the number of taxa originating from the previous time units or also defined as the initial number of plant families. This parameter as in the previous case can be calculated for a time unit k according to the expression $N_{0k} = T_k - O_k$. Finally, the diversification rate (T_D) was obtained from the difference of the origination and extinction rates according to the expression $T_D = T_O - T_E$.

Finally, in order to evaluate the diversity changes associated with the origination and extinction levels described by the rates of evolution, Van Valen's mean standing diversity (Van Valen, 1984) has been calculated in terms of this parameter according to the expression $N_{st} = (N_0 + N_t) / 2$. Alternatively, standing diversity can also be calculated with the expression $N_{st} = [(N_r + N_e) + (N_r + N_f)] / 2$, where N_e are the taxa that cross the lower boundary and become extinct during this time unit, this parameter correspond to the number of extinguished taxa by discounting the singleton taxa, and N_f are the originated taxa that cross the upper boundary, or in other words, the number of originated taxa less the singleton appearances.

RESULTS AND DISCUSSION

The characteristics of the singleton taxa make of them a special case because they may be influenced by influenced by preservational biases rather than evolutionary processes (Fitzgerald and Carlson, 2006). From a temporal perspective, singleton taxa have a very restricted distribution, but this is a subjective aspect depending on the length of the time units employed (Casanovas-Vilar et al., 2010).

Foote (2000a, 200b) noted that, this temporal aspect of singleton taxa together with the preservational biases inherent in the fossil record (Foote and Raup, 1996; Foote, 1997), produce many undesirable distortions of diversity trends through Earth's history. The vascular plant fossil record is no exception to this problem. In order to elucidate
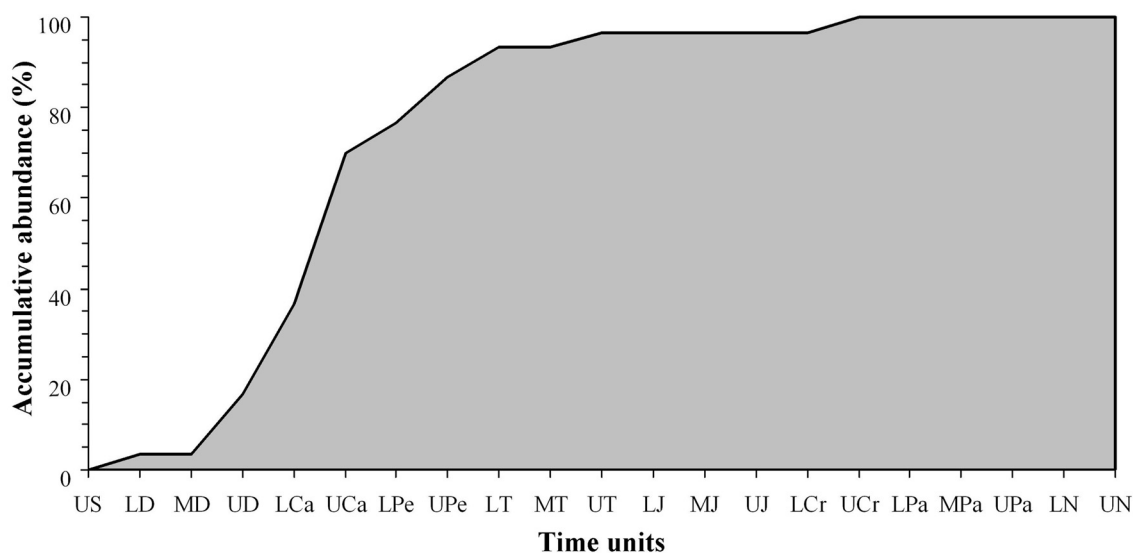
FIGURE 1. Accumulative analysis of the singleton taxa registered. Absolute ages in million years according to Gradstein and Ogg (2004). For temporal abbreviations see Table 1.

the role of such taxa in the trends of palaeofloristic diversity, we have used a dataset in which approximately 10% of the sample are singleton taxa. The temporal distribution of these taxa was plotted using an accumulative analysis (Figure 1). The results reveal that around 90% of these taxa appear to be registered before the Palaeozoic-Mesozoic transition. The results also reveal that the maximum increases of singleton taxa were registered between the Middle Devonian and the Pennsylvanian, and between the end of the Carboniferous and the Middle Triassic (Figure 1). Finally, the accumulative analysis shows that all the singleton taxa had been registered in plant life history at the family level by the end of the Cretaceous. In light of these results, a question is raised: are singleton taxa the key element to explain the profound differences in the evolutionary patterns between the Palaeozoic and the Mesozoic?

To answer this question, in the first place, the potential taxonomic biases have been evaluated from abundance analyses. Subsequently, a set of correlation analyses has been performed by focusing on the time-dependent aspects of singleton taxa. This second analysis has been performed considering the large differences among the durations of the time units employed.

Originally, a raw comparative approach between the Palaeozoic and Mesozoic taxa was performed to test the taxonomic bias in the cumulative abundance of the singleton taxa. Nevertheless, in agreement with the cumulative analysis, where it is apparent that the majority of singletons are

Palaeozoic taxa, preliminary results showed that the important difference in the sample size between the two periods does not allow extract valuate information from the Mesozoic singleton taxa. In contrast, the Palaeozoic data revealed important taxonomic patterns. In our opinion, this fact has important connotations in terms of quality of the record because it could be showing unequal equivalence robustness through time bearing in mind the global scale of the study, but how could we evaluate the quality of the information based on a dataset between the different periods from an objective viewpoint? Wing and DiMichele (1995) postulated an objective form for resolving this question using the information contained in the singleton taxa of their dataset. The reasoning was the following; the number of singletons may be the most robust point of comparison between the two data sets (Wing and DiMichele, 1995). In agreement with this idea, if we separate the global database into three datasets (one of each period), we observe that the robustness decreases towards the Palaeozoic where the maximum number of singleton taxa are registered (Figure 2). It would be in concordance with Raup's ideas about the direct effect of the age of the rocks to interpret the fossil record (Raup, 1972; Raup and Stanley, 1978).

In short, we think that these unequal quality relationships in the reading of the record through time can be strongly affecting the taxonomy. From Figure 3, where the higher taxonomic categories of the Palaeozoic singleton taxa have been analyzed, we observe that the number of singletons is not
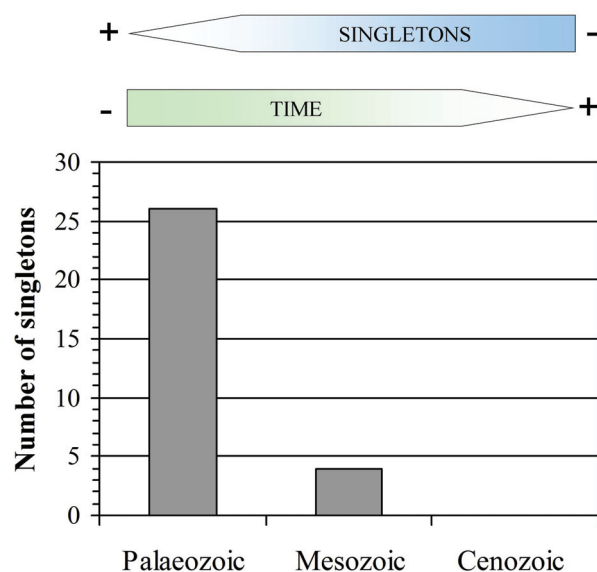
FIGURE 2. Comparative analysis of the number of singleton taxa considering the Palaeozoic, Mesozoic and Cenozoic as independent datasets.

homogeneously distributed. There are important biases towards the concrete type of plant fossils, as is the case of the order Lepidocarpales, which contain approximately a quarter part of the Palaeozoic singleton taxa or the order Pinales with a value proximal to the 15% (Figure 3.1). In this sense, for example, from the raw literature most of the singleton families of the order Pinales are based in a unique plant organ, in a unique genera, or present taxonomic unclear relations from the original consulted material (Cleal, 1993b, 1993a; Cleal and Thomas, 1999). Obviously, these aspects are transmitted into the taxonomic hierarchy, and it produces an asymmetric effect in function on what is the considered group (Figure 3.2), emphasizing the need to unify criteria in the use of the singletons when all vascular plant groups are considered together. In summary, rare forms, poor preserved remains, or material accurately undetermined can all be real explanations for more of these singletons.

Regarding changes to the taxonomic hierarchy, we provide an example extracted from the primary literature of angiosperm family that demonstrates, how taxonomic changes influence about the apparition of taxa with first and last appearances in the same interval. As remarked by Crepet et al. (2004), the angiosperm family Priscaceae was placed as a new family taking into account fructifications determined as *Prisca reynoldsii* by Retallack and Dilcher (1981). Neverthe-

less, later, Drinnan et al. (1991) tentatively referred *Prisca* to Lauraceae. In the latter case, the family does would not be a singleton. This scenario is a potential reason why the angiosperms presumably do not have this type of taxa. All these views demonstrate that the singletons can be used to measure the robustness in concordance with the idea expressed by Wing and DiMichele (1995), but that their controversial taxonomy can produce unreal or distorted patterns from the direct reading of the plant record due to their controversial taxonomy.

On the other hand, Foote (2000a, 2000b) emphasized that time intervals can also distort diversity counts significantly if the time units vary greatly in length, which is the case employed herein. Accordingly, the apparent temporal variation in evolutionary rates shown in previous studies might be an artefact of variation in interval lengths. Casanovas-Vilar et al. (2010) recently emphasized the idea that the number of singletons will increase with the duration of the time units, which is logically due to the probability of the first and last appearances of a taxon occurring within a specific time unit being directly proportional to the duration of that time unit. Following this reasoning, the number of evolutionary events in an ideal system should also bear a direct relation with the length of the time interval.

The results of the correlation analysis (summarised in Figure 4) clearly show that there is no relation between the length of the time units and the number of singletons and in the same form, between the duration and the origination, extinctions and diversification events. Consequently, duration do not seem to be a key factor in the configuration of our perception of the phytodiversity trends from a simple regression model viewpoint based on the dataset employed. All the regression values are less than 0.1 (Figure 4), thus confirming this observation. Therefore, in illustrating the main stages of plant life history, the time units employed probably produce only a minor distortion at the suprageneric level.

In the light of these assessments, a re-evaluation of the classic palaeofloristic patterns has been performed. As Foote (2000a, 200b) recommended, this re-evaluation is based on the per-capita evolutionary rates that use taxa, which are boundary-crossers for counts of diversity rather than those that are confined to the time interval alone in diversity analyses to avoid possible problems associated with interval length and the presence of singleton taxa (Figure 5.1).
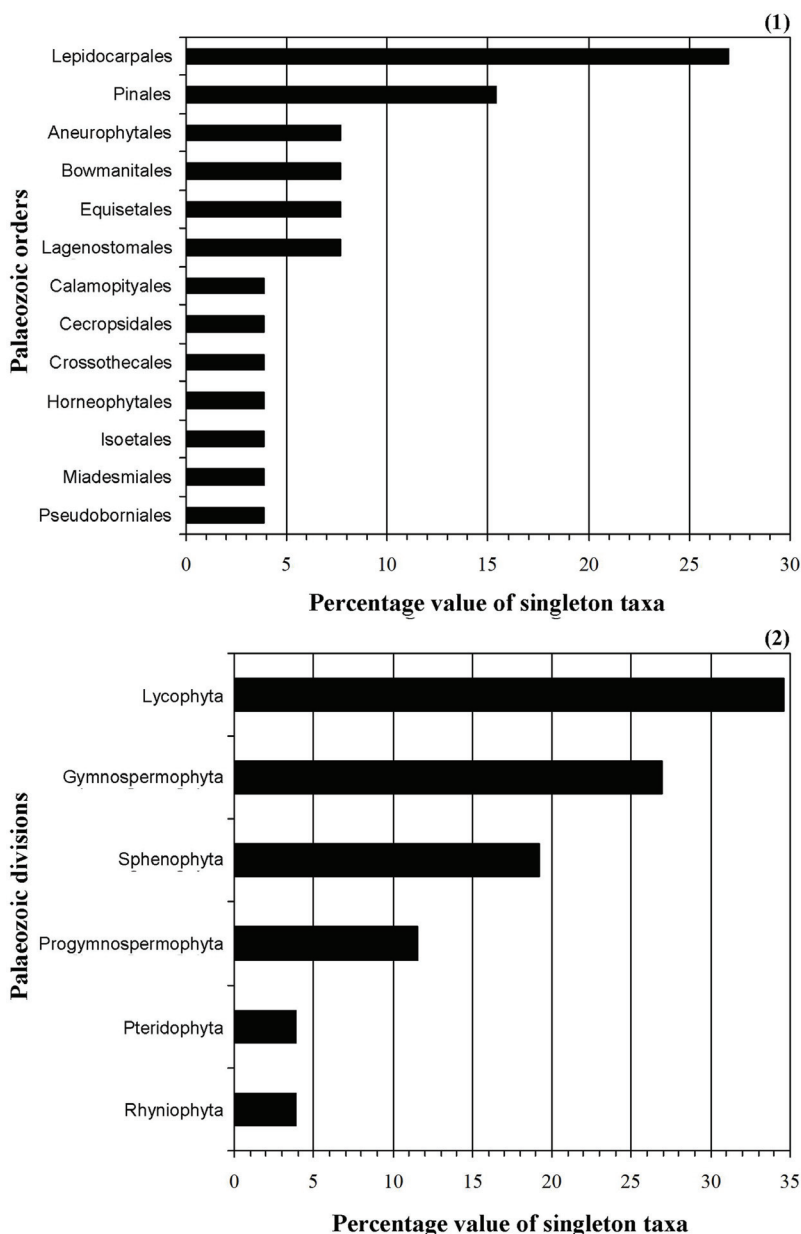
FIGURE 3. Taxonomic abundance analysis of the Palaeozoic singleton taxa. (1) Analysis performed considering the order level. (2) Analysis performed considering the division level.

Palaeozoic patterns reveal higher origination levels during the early stages of the Devonian, during the Carboniferous period, and particularly towards the end of the Pennsylvanian. In contrast, the main Palaeozoic extinction levels are observed in the Early Devonian, in the Carboniferous-Permian transition and especially towards the end of the Permian. Consequently, standing diversity levels are not synchronous with the origination levels; e.g., while the Pennsylvanian registers a peak in the origination rate, the diversity curve picks during the Mississippian. In contrast, the origination and diversification rates during the Mesozoic exhibit a highly parallel behaviour with the maximum values during the Early and Late Triassic, together with a slight increase during the Middle Triassic, which strongly augments during the Cretaceous. The Mesozoic extinction levels are basically residuals in comparison to the Palaeozoic extinction levels. The Cenozoic shows a continuous diversification process according to the origination levels during the Early and Middle Palaeogene. Subsequently in the last stages considered, the evolutionary levels are practically inexistent. In the most recent time
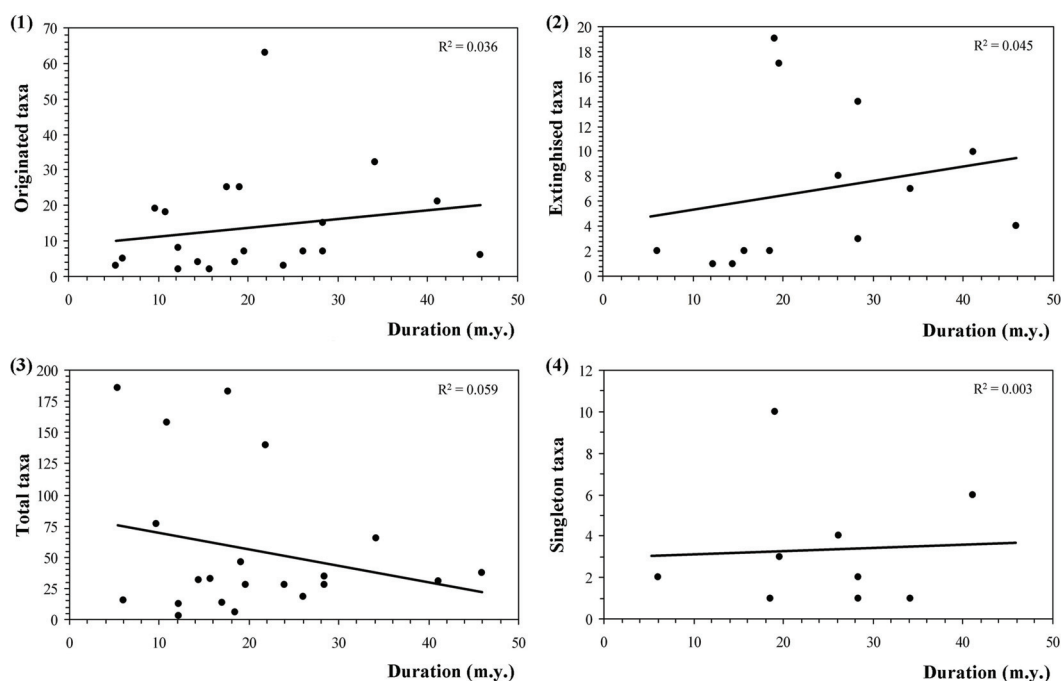
FIGURE 4. Correlation and regression analyses between the duration of the time units in millions of years and (1) the number of originated taxa, (2) extinguished taxa, (3) total taxa and, (4) singleton taxa.

intervals, origination and extinction rates approach zero.

With respect to the study of the Van Valen's mean standard diversity (Figure 5.2), the standing diversity reveals that a direct relation does not exist between the magnitude of the diversification rate and the standing diversity. Indeed, only the Permian extinction produces a sharp drop in standing diversity. During the Palaeozoic, standing diversity shows a pick at the end of the Carboniferous, and this level of diversity only recovers by the Triassic-Jurassic boundary then increases slightly towards the end of the Mesozoic. From the Late Cretaceous to the Palaeogene-Neogene transition, the mean diversity increases dramatically. Finally, this trend slows through the Neogene.

These results confirm the mean stages, in origination and extinctions terms, previously described by Niklas et al. (1980, 1983, 1985), and more recently evaluated by Cascales-Miñana et al. (2010) and Cascales-Miñana and Cleal (2012), with the peculiarity that the general evolutionary patterns are more smoothed. This study confirms two previous observations: firstly, the rates of evolution employed are not strongly influenced by singleton taxa; and secondly, that practically all such singletons are present during the Palaeozoic. Consequently, this fact allows us to describe plant history with fewer potential distortion elements because singletons do not have the possibility to exaggerate or magnify the differences between the time units.

SUMMARY AND CONCLUSIONS

This paper presents a set of inference methods to test the role of singleton taxa and the length of the time units in the study of plant life by re-evaluating previously derived evolutionary patterns observed in the literature. The analyses reveal that the temporal component of singleton taxa does not distort our understanding of phytodiversification trends at the family level in this global approach. In contrast, the taxonomy and temporal assignation of the singletons seems to be a source of potential biases for providing consistent patterns through global temporal approach. In addition, the length of the time units employed in this approach does not affect the number of singleton taxa registered. Similarly, the results obtained do not allow us to infer a direct relation between the number of evolutionary events (originations or extinctions) and the duration of the time units. Finally, the results based on the evolutionary analysis seem to show that the singleton taxa provide some genuine information at the family level. The decline in singleton taxa agrees with the decline in rates of origination and extinction. At the same time, it seems that the decline in origination and extinction rates is the primary evo-
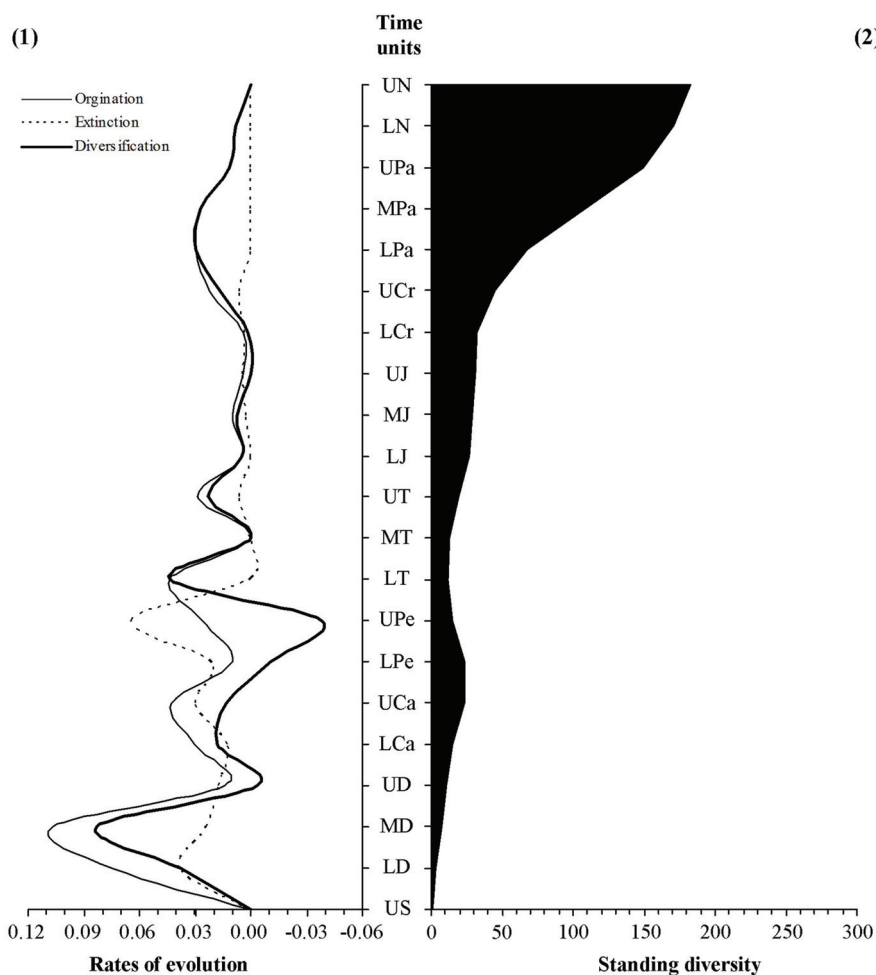
FIGURE 5. Rates of evolution and diversity analyses. (1) Comparative analysis of the evolution rates (origination, extinction and diversification). (2) Mean standing diversity values based on the number of family taxa. For temporal abbreviations see Table 1.

lutionary signal; the pattern of singletons being just a consequence or symptom of this decline.

The evolutionary patterns derived from these algorithms confirm that the number of the singleton taxa in the original dataset does not strongly change the general observed patterns. Nevertheless, the rates of evolution derived from this analysis yield new global patterns that diminish the effects of the possible taxonomic problems and preservational biases relating to the nature of singleton taxa, and they reveal the main palaeophytodiversity patterns with slight yet abrupt changes. These facts provide us more realistic patterns regarding the intensities of evolutionary events emphasizing that the role of singleton taxa should be evaluated if robust conclusions want to be extracted from the plant fossil record. Future

researches will be necessary for elucidating if these observations are extrapolated to concrete plant groups.

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APPENDIX

Original binary matrix. Classic palaeobotanical data used for testing the algorithms presented in this methodological case study. Complete list of taxa appear in rows. Taxonomic data are scored in terms of the presence (1) or absence (0) for each time unit (columns). The taxa have been ordered about their origination moment. For temporal abbreviations see Table 1.

TAXA   **TEMPORAL RANGE**

FAMILY LEVEL	PALAEOZOIC									MESOZOIC							CENOZOIC				
	US	LD	MD	UD	LCa	UCa	LPe	UPe	LT	MT	UT	LJ	MJ	UJ	LCr	UCr	LPa	MPa	UPa	LN	UN
Rhyniaceae	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Drepanophycaceae	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Zosterophyllaceae	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Horneophytaceae	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trimerophytaceae	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Protolepidodendraceae	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lycopodiaceae	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Cladoxylaceae	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ibykaceae	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Rhacophytaceae	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Zygopteridaceae	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Stauropteridaceae	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Aneurophytaceae	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Archaeopteridaceae	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Selaginellaceae	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Cyclostigmaceae	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pseudoborniaceae	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Bowmanitaceae	0	0	0	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Eviostachyaceae	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Protokalonaceae	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Elkinsiaceae	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eleutherophyllaceae	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Flemingitaceae	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sigillariostrobaceae	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lepidocarpaceae	0	0	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Cheirostrobaceae	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Archaeocalamitaceae	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Calamostachyaceae	0	0	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Corynepteridaceae	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Psalixochlaenaceae	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

TAXA   **TEMPORAL RANGE**

FAMILY LEVEL	US	LD	MD	UD	LCa	UCa	LPe	UPe	LT	MT	UT	LJ	MJ	UJ	LCr	UCr	LPa	MPa	UPa	LN	UN
				PALAEOZOIC								**MESOZOIC**						**CENOZOIC**			
Tedeleaceae	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Botryopteridaceae	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Asterothecaceae	0	0	0	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Protopityaceae	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Genomospermaceae	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Eospermaceae	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lagenostomaceae	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Physostomaceae	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Calamopityaceae	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trigonocarpaceae	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Potonieaceae	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cordaitanthaceae	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Diaphorodendraceae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Spenceritaceae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Caudatocarpaceae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pinakodendraceae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sporangiostrobaceae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Miadesmiaceae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Isoetaceae	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Chaloneriaceae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tchernoviaceae	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Biscalithecaceae	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Sermeyaceae	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Urnatopteridaceae	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Crossothecaceae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Marattiaceae	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Noeggerathiaceae	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tingiostachyaceae	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Cecropsidaceae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Callistophytaceae	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Peltaspermaceae	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
Arberiaceae	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Rufloriaceae	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Dicranophyllaceae	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Trichopityaceae	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Emporiaceae	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

TAXA **TEMPORAL RANGE**

FAMILY LEVEL	US	LD	MD	UD	LCa	UCa	LPe	UPe	LT	MT	UT	LJ	MJ	UJ	LCr	UCr	LPa	MPa	UPa	LN	UN
				PALAEOZOIC								MESOZOIC						CENOZOIC			
Buriadiaceae	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cardiolepidiaceae	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Emplectopteridaceae	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Cycadaceae	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Vojnovskyaceae	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Utrechtiaceae	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Cyclodendraceae	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Ferugliocladaceae	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Gondwanostachyaceae	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Equisetaceae	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Osmundaceae	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Gleicheniaceae	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Umkomasiaceae	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	0	0	0
Majonicaceae	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Ullmanniaceae	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Pleuromeiaceae	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0
Takhtajanodoxaceae	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Echinostachyaceae	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Voltziaceae	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	0	0	0	0	0	0
Podocarpaceae	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1
Cynepteridaceae	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Matoniaceae	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1
Dipteridaceae	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1
Polypodiaceae	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1
Dicksoniaceae	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1
Leptostrobaceae	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	0	0	0	0	0	0
Caytoniaceae	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0
Bennettitaceae	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0
Williamsoniaceae	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0
Gnetaceae	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1
Palissyaceae	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0
Araucariaceae	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1
Pinaceae	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1
Cheirolepidiaceae	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0
Ginkgoaceae	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1
Nilsoniaceae	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0

TAXA	TEMPORAL RANGE																				
	PALAEOZOIC								MESOZOIC								CENOZOIC				
FAMILY LEVEL	US	LD	MD	UD	LCa	UCa	LPe	UPe	LT	MT	UT	LJ	MJ	UJ	LCr	UCr	LPa	MPa	UPa	LN	UN
Pentoxylaceae	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0	0	0	0
Taxaceae	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1
Schizaeaceae	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1
Pararaucariaceae	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
Taxodiaceae	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1
Cephalotaxaceae	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1
Arctopityaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
Sciadopityaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1
Cyatheaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1
Tempskyaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
Loxsomaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1
Platanaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1
Chloranthaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1
Ranunculaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1
Lophosoriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1
Marsileaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1
Salviniaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1
Azollaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1
Cercidiphyllaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Fagaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Hamamelidaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Ulmaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Priscaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Magnoliaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Lauraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Nymphaeaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Berberidaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Menispermaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Sabiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Amaranthaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Cyrillaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Theaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Actinidiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Lecythidaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Pentaphylacaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Aceraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1

TAXA   TEMPORAL RANGE

FAMILY LEVEL	US	LD	MD	UD	LCa	UCa	LPe	UPe	LT	MT	UT	LJ	MJ	UJ	LCr	UCr	LPa	MPa	UPa	LN	UN
			PALAEOZOIC								MESOZOIC							CENOZOIC			
Araliaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1
Cornaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1
Icacinaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1
Rhamnaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1
Rutaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1
Sapindaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1
Araceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1
Arecaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1
Typhaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1
Zingiberaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1
Ophioglossaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Cupressaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Casuarinaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Juglandaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Trochodendraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Ceratophyllaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Ericaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Salicaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Fabaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Mimosaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Myrtaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Rosaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Staphyleaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Thymelaeaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Vitaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Oleaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Cyperaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Poaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Hydrocharitaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Moaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Myricaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Urticaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Annonaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Aristolochiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Myristicaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Saururaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1

TAXA   **TEMPORAL RANGE**

FAMILY LEVEL	US	LD	MD	UD	LCa	UCa	LPe	UPe	LT	MT	UT	LJ	MJ	UJ	LCr	UCr	LPa	MPa	UPa	LN	UN
			PALAEOZOIC							MESOZOIC							CENOZOIC				
Schisandraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Caryophyllaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Bombacaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Brassicaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Capparaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Cistaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Cucurbitaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Dipterocarpaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Droseraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Ebenaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Flacourtiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Malvaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Myrsinaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Sapotaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Sterculiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Styracaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Symplocaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Elaeocarpaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Tiliaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Anacardiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Alangiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Apiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Burseraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Buxaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Celastraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Euphorbiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Grossulariaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Hydrangaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Linaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Loranthaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Lythraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Malpighiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Melastomataceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Proteaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Meliaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Nyssaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1

TAXA TEMPORAL RANGE

FAMILY LEVEL	PALAEOZOIC											MESOZOIC					CENOZOIC				
	US	LD	MD	UD	LCa	UCa	LPe	UPe	LT	MT	UT	LJ	MJ	UJ	LCr	UCr	LPa	MPa	UPa	LN	UN
Olacaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Onagraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Rhizophoraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Santalaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Simaroubaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Apocynaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Asclepiadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Asteraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Bignoniaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Boraginaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Caprifoliaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Rubiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Scrophulariaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Solanaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Juncaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Musaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Sparganiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Alismataceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Potamogetonaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Pontederiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Betulaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
Illiciaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
Lardizabalaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Sargentodoxaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Clusiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Primulaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Violaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Aquifoliaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Cunoniaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Haloragaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Hippuridaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Trapaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Lamiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Menyathaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Lemnaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Butomaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1

TAXA   **TEMPORAL RANGE**

FAMILY LEVEL		PALAEOZOIC								MESOZOIC							CENOZOIC				
	US	LD	MD	UD	LCa	UCa	LPe	UPe	LT	MT	UT	LJ	MJ	UJ	LCr	UCr	LPa	MPa	UPa	LN	UN
Najadaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
Taccaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1
Zannichelliaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Leitneriaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Calycanthaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Coriariaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Fumariaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Piperaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Chenopodiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Polygonaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Clethraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Elatinaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Empetraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Passifloraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Stachyuraceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Combretaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Elaeagnaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Garyaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Hippocastinaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Podostemaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Viscaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Campanulaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Loganiaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Pedaliaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Valerianaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Commelinaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Xyridaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
Oxalidaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Callitrichaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Plantaginaceae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1