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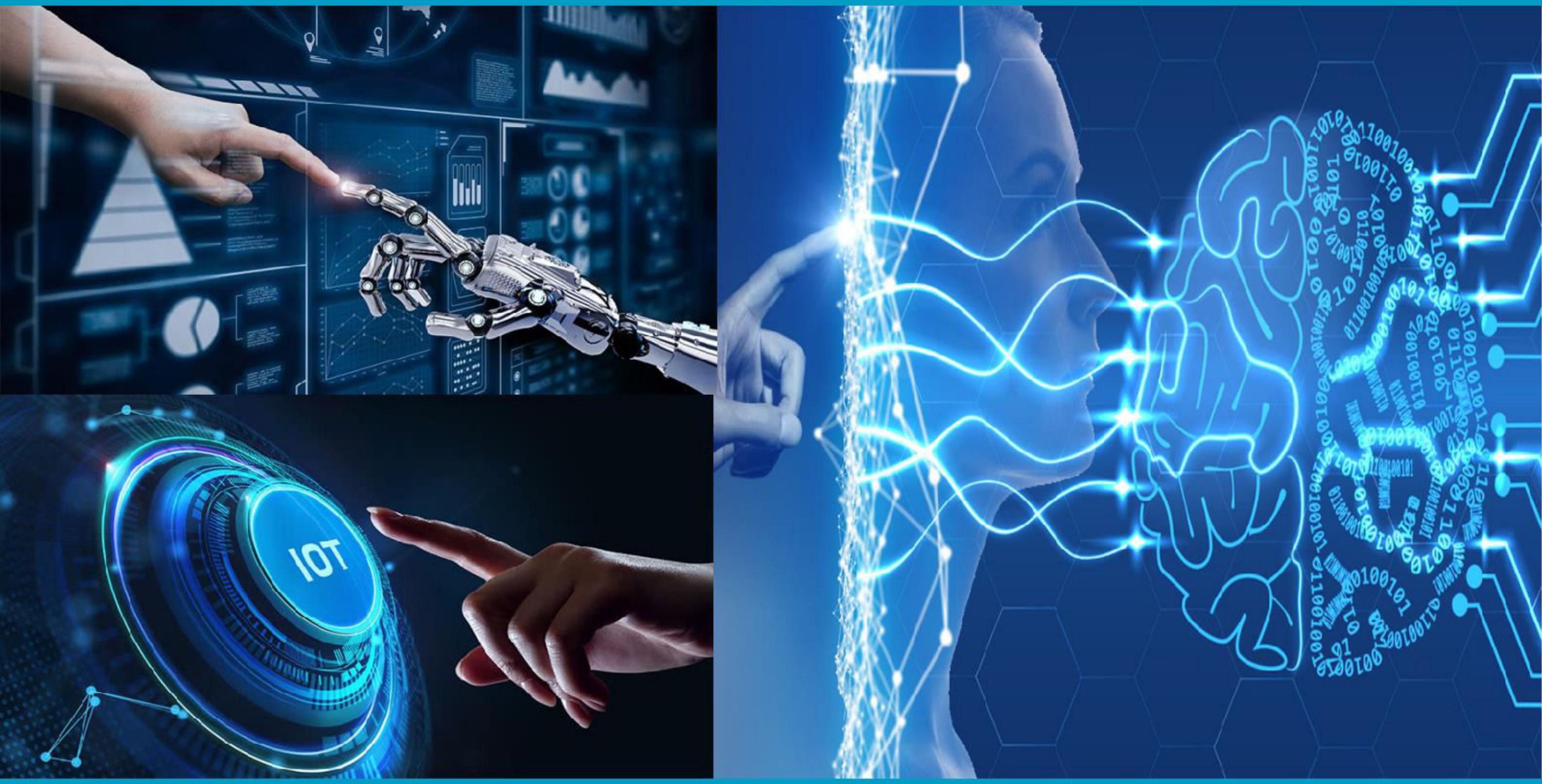

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STUDY OF FOSSIL FLORA OF SALKHAN SONBHADRA INDIA IN LIGHT OF EXPLORATION AND COMPARISON WITH THEIR NEAREST LIVING RELATIVE

[1]Ramashray Singh & [2]Prof. Anil K Dwivedi

[1,2]Dept. of Botany, DDU Gorakhpur University, Gorakhpur, Uttar Pradesh, India

ABSTRACT: Salkhan Fossils Park, officially known as Sonbhadra Fossils Park, is a fossil park in Uttar Pradesh, India. It is located 12 km from Robertsganj, near Salkhan village on state highway SH5A in Sonbhadra district. The fossils in the park are estimated to be nearly 1.4 billion years old. The fossils appear as rings on the boulders and are scattered in Fossil rings on boulders in the park which is spread over an area of about 25 hectares in the Kaimoor Wildlife range.[1] The fossils found in the Sonbhadra Fossils Park are algae and stromatolites types of fossils. The park is spread over an area of about 25 hectares in Kaimur Range, adjacent to Kaimoor Wildlife Sanctuary. It comes under jurisdiction of the State forest department.[1] Geologists have been aware of the fossils found in the present-day park area since the 1930s. People who have carried out research in the area include Mr. Auden (1933), Mr. Mathur (1958 and 1965), and Professor S. Kumar (1980–81). On 23 August 2001, the area was featured in an article written by journalist Vijay Shankar Chaturvedi for the Hindi newspaper Hindustan. Subsequently, it was formally inaugurated as a fossil park by District Magistrate Bhagawan Shankar on 8 August 2002.[1]

An international workshop was organised in December 2002, attracting participation from 42 delegates from India and abroad. Canadian geologist H.J. Hoffman was impressed by the fossils, and remarked that he had not seen such "beautiful and clear fossils" anywhere else in the world.[2] In 2004, researcher Mukund Sharma further explored the area.[1]

In 2013, the state government sanctioned ₹12.5 million for the development of the Salkhan Fossils Park.[3]

KEYWORDS: Salkhan fossils park, Sonbhadra, Uttar Pradesh, wildlife sanctuary, forest dept., fossils world

I.INTRODUCTION

Cyanobacteria played an important role in the evolution of Early Earth and the biosphere. They are responsible for the oxygenation of the atmosphere and oceans since the Great Oxidation Event around 2.4 Ga, debatably earlier. They are also major primary producers in past and present oceans, and the ancestors of the chloroplast. Nevertheless, the identification of cyanobacteria in the early fossil record remains ambiguous because the morphological criteria commonly used are not always reliable for microfossil interpretation. Recently, new biosignatures specific to cyanobacteria were proposed. Here, we review the classic and new cyanobacterial biosignatures. We also assess the reliability of the previously described cyanobacteria fossil record and the challenges of molecular approaches on modern cyanobacteria. Finally, we suggest possible new calibration points for molecular clocks, and strategies to improve our understanding of the timing and pattern of the evolution of cyanobacteria and oxygenic photosynthesis.

The nearest-living-relative (NLR) method represents a standard and powerful tool in paleoclimatology and paleoecology. It uses the climatic or ecologic characteristics of the NLRs of fossil taxa or assemblages to estimate the paleoclimatic or paleoecologic conditions under which the fossil taxa or assemblages lived.

The “Coexistence Approach” is a mutual climate range (MCR) technique combined with the nearest-living relative (NLR) concept. It has been widely used for palaeoclimate reconstructions based on Eurasian plant fossil assemblages, most of them palynofloras (studied using light microscopy). The results have been surprisingly uniform, typically converging to subtropical, per-humid or monsoonal conditions. Studies based on the coexistence approach have had a marked impact in literature, generating over 10,000 citations thus far. However, recent studies have pointed out inherent theoretical and practical problems entangled in the application of this widely used method. But so far little is known how results generated by the coexistence approach are affected by subjective errors, data errors, and violations of the basic assumptions. The majority of Coexistence Approach studies make use of the Palaeoflora database (the combination of which will be abbreviated to CA+PF). Testing results produced by CA+PF studies has been hindered by the general unavailability of the contents in the underlying Palaeoflora database; two exceptions are the mean-annual temperature tolerances and lists of assigned associations between fossils and nearest-living relatives. Using a recently published study on the Eocene of China, which provides the first usable insight into the data structure of the Palaeoflora database, we compare the theory and practice of Coexistence Approach using the Palaeoflora database (CA+PF). We show that CA+PF is riddled by association and climate data error. We reveal the flaws in the application of CA, which is often in stark contrast to the theory of the method. We show that CA+PF is highly vulnerable against numerous sources of errors, mainly because it lacks safeguards that could identify unreliable data. We demonstrate that the CA+PF produces coherent, pseudo-precise results even for artificially generated, random plant assemblages. Alternative MCR-NLR methods can surpass the most imminent deficits of CA, and may be used as a stop-gap until more accurate bioclimatic and distribution data on potential Eurasian NLRs, and theoretically- and statistically-robust methods will become available. Finally, general guidelines are provided for the future application of methods using the mutual climatic range with nearest living relatives approach when reconstructing climate from plant fossil assemblages.

II.DISCUSSION

Reconstructing past climates is an extensive field of research where a range of proxies are used to determine this aspect of the earth's history. There are many proxies used to determine past climates, ranging from stable isotopes from ocean floor sediments (e.g. Zachos et al., 2001) to biological proxies such as pollen (e.g. Zagwijn, 1994). The approaches used to reconstruct past climates need to be theoretically and methodologically sound else results may be erroneous and misleading. The “Coexistence Approach” has been widely used by to reconstruct Cenozoic climates from Eurasian plant fossils (Utescher et al., 2014), generating in total over 10,000 citations. Here we examine whether the Coexistence Approach is scientifically sound in terms of its methodological approach; in a separate study we consider the theoretical underpinnings of the Coexistence Approach and other methods based on the mutual climate range coupled with nearest living relative associations. In order to provide this assessment we will focus on two recent Coexistence Approach publications: the first is a review of the method by Utescher et al. (2014), which also provides new guidelines for best practise, and the second is a study that reconstructs the Eocene climate of China (Quan et al., 2012) using the Palaeoflora database (Coexistence Approach studies that use the Palaeoflora database are henceforth abbreviated to CA+PF); the authors consider the latter to be the most extensively documented CA+PF study to date. The data (climatic ranges and assignments of nearest living relatives) for previous studies using this method have, by and large, been unavailable for scrutiny (Grimm and Denk, 2012). We argue that if we find that the method and application of the Coexistence Approach is severely flawed based on an assessment of these two publications, then climate reconstructions generated by all other such studies over the last 15 years should be considered spurious. We also provide a brief summary of alternative approaches and suggestions for the future of this field.

The Coexistence Approach is a mutual climate range technique in the family of “nearest-living relative” approaches. Using nearest-living relatives is usually obligatory as most of the species present during the Cenozoic are now extinct. The foundational principle behind methods that use the mutual climate range and nearest-living relative approaches (henceforth referred to as MCR-NLR) is that of physiological uniformitarianism (Tiffney, 2008): this is the assumption that form does not change as long as a lineage thrives in the same ecological or climatic niche. Mutual climate range techniques share the basic idea of species distribution modelling: the climatic niche or tolerance of a species (sensu Hutchinson, 1957) can be extracted from its current distribution and is stable over time. Species distribution modelling estimates an n-dimensional niche for a single species, whereas mutual climate range techniques estimate the mutually shared climatic range of a community, however the niche dimensions are usually analysed in isolation or with limited interactions. Pure mutual climate range techniques are restricted to the relative recent past, where an assemblage consists of extant taxa (e.g. Böcher, 1995; Elias, 2001; Thompson et al., 2012a). The nearest-living relative principle extends such approaches to fossil taxa; this principle has been used since the dawn of palaeobotanical research (Taylor et al., 2009, p. 6). It involves replacing each fossil species by a modern analogue representing the same phylogenetic lineage. The basic assumption of MCR-NLR is that the climatic niche has not substantially changed for a phylogenetic lineage, including the fossil and its nearest-living relative.

In case of the Coexistence Approach, the MCR-NLR estimates are based on minimum-maximum tolerances recorded for modern taxa, the nearest-living relatives, which then are used to reconstruct the putative mutual climate ranges for the fossil (usually plant) assemblage (Mosbrugger and Utescher, 1997; Utescher et al., 2014). Each individual climate parameter is estimated independently. Aside from theoretical issues, which will be addressed elsewhere, this has many potential sources of subjective and data errors (Mosbrugger and Utescher, 1997; Grimm and Denk, 2012; Utescher et al., 2014). The most apparent are misidentification of fossil specimens, poor choice of nearest-living relatives and difficulties in obtaining accurate tolerance data for these taxa. The applicability of the method and the validity of the Palaeoflora database (Utescher and Mosbrugger, 2009), which has been used in nearly all Coexistence Approach studies, has rarely been questioned (but see Klotz, 1999; Grimm and Denk, 2012). However, Utescher et al. (2014) have recently reassessed the Coexistence Approach and provided extensive details on potential errors. The majority of these have thus far been largely ignored in the Coexistence Approach literature (but see Eldrett et al., 2014; Kotthoff et al., 2014). Earlier, Grimm and Denk (2012) pointed out similar inconsistencies and shortcomings of this method for the reconstruction of mean-annual temperature using the Palaeoflora database and provided a number of suggestions on how to correct for these. The conclusions and suggestions put forward by Utescher et al. (2014) largely overlap with this earlier study , suggesting that these authors independently followed the same lines of reasoning after 15 years of uncritically using this method on Eurasian plant fossil assemblages.

III.RESULTS

The lack of documentation for climate tolerances of the nearest-living relatives is particularly problematic as Utescher et al. (2014) state that the Palaeoflora database undergoes permanent updates; thus comparing published results is impossible. Utescher et al. (2014) now recommend that in the future – after 15 years of "successfully" applying this method – all used data (lists of fossils and nearest-living relative associations, tolerance data of nearest-living relatives) shall be documented. The only pre-2014 publications that are in-line with the new guidelines are those that used (to some degree) independent climate tolerance data (i.e. not extracted from the Palaeoflora database; Xu et al., 2008; Jacques et al., 2011).

Mosbrugger and Utescher (1997) list four basic assumptions that need to be fulfilled to apply the Coexistence Approach (Table 2; cf. Utescher et al., 2014, section 3): 1) a nearest-living relative can be identified, 2) the minimum and maximum climate tolerances of the fossil taxon are similar to that of its nearest-living relative, 3) these tolerances of the nearest-living relative can be deduced from its area of distribution, and 4) the modern climate [and distribution] data are of good quality. Because of poor documentation, it has been impossible to assess whether any violations of these basic assumptions bias the outcome of CA+PF results. The only parameter that has been evaluated is the mean annual temperature, which showed little reliability of palaeoclimate reconstructions based on the Coexistence Approach (Grimm and Denk, 2012). In 2012, a CA+PF study was published that complies (almost entirely) with the new policy (Quan et al., 2012). Using literature data, Quan et al. compiled taxon lists for the Eocene of China, the distribution of these assemblages span the entire country. Please note that we use the climate parameter abbreviations common to Coexistence Approach studies and these are listed in Section 1.1. Based on the substantial drop observed in CMT (average temperature of the coldest month), slight potential increase in WMT (average temperature of the warmest month) and generally low LMP (monthly precipitation of the driest month) observed in southern China, they concluded that the Himalayan uplift must have already occurred by the late Eocene inflicting monsoonal climate in southern China. Appendix A of Quan et al. (2012) lists the floral assemblages, their constituent fossil taxa and the nearest-living relatives used to represent those taxa. Appendix B of Quan et al. (2012) lists the climatic min-max tolerances of all nearest-living relatives (including unused taxa) extracted from Palaeoflora database. The number of nearest-living relatives per assemblage is high (usually more than 20 up, with one instance over 100). Therefore, one would expect that the reconstructed intervals are highly reliable (Utescher et al., 2014, p. 61). The study of Quan et al. (2012) provides the first opportunity to compare theory (Mosbrugger and Utescher, 1997; Utescher et al., 2014) and practise of Coexistence Approach studies relying on the Palaeoflora database. Utescher et al. (2014, p. 60) state that the "general agreement" of the results from this method with alternative palaeoclimate reconstructions (using floristic assemblages or isotope data) and palaeoclimate model predictions demonstrates that (inevitable or correctable) errors ("uncertainties", Utescher et al., 2014) in the database are not of general concern. Here we will examine this claim using the data of Quan et al. (2012).

Ideally, only one or several modern species would be considered the closest (nearest-living) relative\s of one fossil taxon. However, many species-level associations are problematic (Grimm and Denk, 2012) and studies that clarify systematic affinities of fossil taxa are either not available or generally overlooked by researchers using the Coexistence Approach and/or the curators of the Palaeoflora database (Grimm and Denk, 2012). Examples of overlooked updated taxa critical to palaeoclimate reconstructions include Engelhardioideae (Manchester, 1987; Manos et al., 2007) and the Fagaceae genera Fagus and Quercus (Denk et al., 2002, 2005; Grimm et al., 2007; Denk and Grimm, 2009a, b, 2010). According to Utescher et al. (2014), the Palaeoflora database includes association information of c. 5800 macrofossil taxa and c. 2500 microfossil taxa (ranging across species, genera and families), but this information cannot be tested based on available documentation. The homepage lists numerous palaeobotanical works which have been harvested for potential associations between fossil taxa and nearest-living relatives, but this information is not linked to the association list. This linkage is essential as Grimm and Denk (2012) and Utescher et al. (2014, p. 64) warn against the blind usage of such association lists, in particular when using macrofossil assemblages. Indeed, Grimm and Denk (2012) highlighted erroneous associations that severely biased Coexistence Approach reconstructions. Utescher et al. (2014) stated that good taxonomy is critical for CA+PF studies, and that efforts were underway to incorporate new phylogenetic and systematic-taxonomic evidence into the Palaeoflora database. Often it is even difficult to determine in CA+PF studies to what degree the fossil taxon–nearest-living relative association follows the Palaeoflora database or is based on other work, which adds additional uncertainty.

IV.CONCLUSIONS

In most cases, Quan et al. (2012) selected a genus-level nearest-living relative based on the (assumed) generic affinity of the fossil taxon (macrofossil or microfossil). If the generic affinity of a fossil taxon was ambiguous, Quan et al. (2012) used the subfamily or family. If the fossil taxon resembled more than one (related or unrelated) modern genera or families then an artificially fused taxon was created by merging the tolerances of the modern taxa. This violates assumption 1 of the Coexistence Approach (Table 2): a nearest living relative can be identified (outlined below; see also Grimm and Denk, 2012).

Poor taxonomic control can be a source of error, particular in studies that use macrofossil assemblages to reconstruct past climates. Utescher et al. (2014, p. 64) mystically claim that the “type status” of pollen “accommodates [taxonomic] uncertainties”. Most of the assemblages used by Quan et al. (2012) are palynofloras studied using light microscopy – not scanning-electron microscopy that could provide better taxonomic resolution – translated into lists of genus- to family-level nearest-living relatives. Unfortunately, the translation of fossil pollen taxa does not include the original ‘species’ names. This is crucial for the choice of a particular nearest-living relative as palynological taxonomy focuses on form and not systematic affinity. Thus, ‘species’ of the same pollen ‘genus’ may represent different families or higher-level taxa. For example, Quan et al. (2012) link Inaperturopollenites with “taxodioid Cupressaceae” (former Taxodiaceae). However Inaperturopollenites ‘species’ can represent a far wider range of biological taxa (Table 3). We observe that, except for very few examples, pollen genera were linked with a specific nearest-living relative by Quan et al. (2012). Consequently, we are forced to assume that the omitted species names are irrelevant in case of the Chinese Eocene floras. Under this assumption and using available compendia on palynological taxa (Martin and Drew, 1969; Huang, 1972; Solomon et al., 1973; Stuchlik et al., 2001; Stuchlik et al., 2002; Beug, 2004; Stuchlik et al., 2009; Li, 2011; Miyoshi et al., 2011; Stuchlik et al., 2014) we crosschecked the validity of the associations used to link fossil taxa with a nearest-living relative.

REFERENCES

1. ↵
Beug HJ. 2004. Leitfaden der Pollenbestimmung für Mitteleuropa und angrenzende Gebiete. München: Verlag Dr. Friedrich Pfeil.
Google Scholar
2. ↵
Böcher J. 1995. Palaeoentomology of the Kap København Formation, a Plio-Pleistocene sequence in Peary Land, North Greenland. Meddelelser om Grønland Geoscience, 33: 1–89.
Google Scholar
3. ↵
Bouchal J, Zetter R, Grímsson F, Denk T. 2014. Evolutionary trends and ecological differentiation in early Cenozoic Fagaceae of western North America. American Journal of Botany, 101: 1–18.
FREE Full TextGoogle Scholar
4. ↵
Denk T, Grimm G, Stögerer K, Langer M, Hemleben V. 2002. The evolutionary history of Fagus in western Eurasia: Evidence from genes, morphology and the fossil record. Plant Systematics and Evolution, 232: 213–236.
CrossRefWeb of ScienceGoogle Scholar
5. ↵
Denk T, Grimm GW. 2009a. The biogeographic history of beech trees. Review of Palaeobotany and Palynology, 158: 83–100.
CrossRefGeoRefWeb of ScienceGoogle Scholar
6. ↵
Denk T, Grimm GW. 2009b. Significance of pollen characteristics for infrageneric classification and phylogeny in Quercus (Fagaceae). International Journal of Plant Sciences, 170: 926–940.
CrossRefWeb of ScienceGoogle Scholar
7. ↵
Denk T, Grimm GW. 2010. The oaks of western Eurasia: traditional classifications and evidence from two nuclear markers. Taxon, 59: 351–366.
Web of ScienceGoogle Scholar
8. ↵

Denk T, Grimm GW, Grímsson F, Zetter R. 2013. Evidence from "Köppen signatures" of fossil plant assemblages for effective heat transport of Gulf Stream to subarctic North Atlantic during Miocene cooling. Biogeosciences, 10: 7927–7942.
CrossRefGoogle Scholar

9. ↲
Denk T, Grimm GW, Hemleben V. 2005. Patterns of molecular and morphological differentiation in Fagus: implications for phylogeny. American Journal of Botany, 92: 1006–1016.
Abstract/FREE Full TextGoogle Scholar

10. ↲
Denk T, Grímsson F, Zetter R, Símonarson LA. 2011. Late Cainozoic Floras of Iceland: 15 Million Years of Vegetation and Climate History in the Northern North Atlantic. Heidelberg, New York: Springer.
Google Scholar

11. ↲
Denk T, Güner HT, Grimm GW. 2014. From mesic to arid: Leaf epidermal features suggest preadaptation in Miocene dragon trees (Dracaena). Review of Palaeobotany and Palynology, 200: 211–228.
GeoRefGoogle Scholar

12. ↲
Earle CJ. 2010. The Gymnosperm Database.
Google Scholar

13. ↲
Eldrett JS, Greenwood DR, Polling M, Brinkhuis H, Sluijs A. 2014. A seasonality trigger for carbon injection at the Paleocene–Eocene Thermal Maximum. Climates of the Past, 10: 759–769.
Google Scholar

14. ↲
Elias SA. 2001. Mutual climatic range reconstructions of seasonal temperatures based on Late Pleistocene fossil beetle assemblages in Eastern Beringia. Quaternary Science Reviews, 20: 77–91.
CrossRefGeoRefWeb of ScienceGoogle Scholar

15. ↲
Fang J, Wang Z, Tang Z. 2009. Atlas of Woody Plants in China. Volumes 1 to 3 and index. Beijing: Higher Education Press.
Google Scholar

16. ↲
Flora of China. 2014. eFloras: Flora of China.: Missouri Botanical Garden, St. Louis, MO & Harvard University Herbaria, Cambridge, MA.
Google Scholar

17. ↲
Flora of North America. 2004 onwards. eFloras: Flora of North America. Missouri Botanical Garden, St. Louis, MO & Harvard University Herbaria, Cambridge, MA.
Google Scholar

18. ↲
Gao Z-f, Thomas BA. 1989a. Occurrence of earliest cycads in the Permian of China and its bearing on their evolution. Chinese Science Bulletin, 34: 766–769.
GeoRefGoogle Scholar

19. ↲
Gao Z-f, Thomas BA. 1989b. A review of fossil cycad megasporophylls, with new evidence of Crossozamia Pomel and its associated leaves from the Lower Permian of Taiyuan, China. Review of Palaebotany and Palynology, 60: 205–223.
Google Scholar

20. ↲
Greenwood DR, Archibald SB, Mathewes RW, Moss PT. 2005. Fossil biotas from the Okanagan Highlands, southern British Columbia and northeastern Washington State: climates and ecosystems across an Eocene landscape. Canadian Journal of Earth Sciences, 42: 167–185.
Abstract/FREE Full TextGoogle Scholar

21. ↲
Grimm GW, Denk T. 2012. Reliability and resolution of the coexistence approach — A revalidation using modern-day data. Review of Palaeobotany and Palynology, 172: 33–47.
CrossRefGeoRefGoogle Scholar

22. ↲

Grimm GW, Denk T, Hemleben V. 2007. Evolutionary history and systematic of Acer section Acer - a case study of low-level phylogenetics. Plant Systematics and Evolution, 267: 215–253.
CrossRefWeb of ScienceGoogle Scholar

23. ↵
Grímsson F, Zetter R, Grimm GW, Krarup Pedersen G, Pedersen AK, Denk T. 2015. Fagaceae pollen from the early Cenozoic of West Greenland: revisiting Engler’s and Chaney’s Arcto-Tertiary hypotheses. Plant Systematics and Evolution, 301: 809–832.
Google Scholar

24. ↵
Grímsson F, Zetter R, Halbritter H, Grimm GW. 2014. Aponogeton pollen from the Cretaceous and Paleogene of North America and West Greenland: Implications for the origin and palaeobiogeography of the genus. Review of Palaeobotany and Palynology, 200: 161–187.
GeoRefGoogle Scholar

25. ↵
Hijmans RJ, Cameron SE, Parra JL, Jones PG, Jarvis A. 2005. Very high resolution interpolated climate surfaces for global land areas. International Journal of Climatology, 25: 1965–1978.
CrossRefWeb of ScienceGoogle Scholar

26. ↵
Huang T-C. 1972. Pollen flora of Taiwan. Taipeh: National Taiwan University Botany Department Press.
Google Scholar

27. ↵
Hutchinson GE. 1957. Concluding Remarks. Cold Spring Harbor Symposia on Quantitative Biology, 22: 415–427.
Abstract/FREE Full TextGoogle Scholar

28. ↵
Jacques FMB, Guo S-X, Su T, Xing Y-W, Huang Y-J, Liu Y-S, Ferguson DK, Zhou Z-K. 2011. Quantitative reconstruction of the Late Miocene monsoon climates of southwest China: a case study of the Lincang flora from Yunnan Province. palaeogeography, Palaeoclimatology, Palaeoecology, 304: 318–327.
CrossRefGeoRefWeb of ScienceGoogle Scholar

29. ↵
Jones GD, Bryant VBJ, Lieux MH, Jones SD, Lingren PD. 1995. Pollen of the Southeastern United States: with emphasis on melissopalynology and entomopalynology. American Association of Stratigraphic Palynologists Foundation - Contributions, Series 30.
Google Scholar

30. ↵
Klotz S. 1999. Neue Methoden der Klimarekonstruktion - angewendet auf quartäre Pollensequenzen der französischen Alpen. Tübingen: Institut & Museum für Geologie & Paläontologie [know: Institute for Geosciences], Eberhard Karls University.
Google Scholar

31. ↵
Kottek M, Grieser J, Beck C, Rudolf B, Rubel F. 2006. World map of the Köppen-Geiger climate classification updated. Meteorol. Z., 15: 259–263.
CrossRefWeb of ScienceGoogle Scholar

32. ↵
Kotthoff U, Greenwood DR, McCarthy FMG, Müller-Navarra K, Prader S, Hesselbo SP. 2014. Late Eocene to middle Miocene (33 to 13 million years ago) vegetation and climate development on the North American Atlantic Coastal Plain (IODP Expedition 313, Site M0027). Climates of the Past, 10: 1523–1539.
Google Scholar

33. ↵
Kvaček Z. 2007. Do extant nearest relatives of thermophile European Cenozoic plant elements reliably reflect climatic signal? Palaeogeography, Palaeoclimatology, Palaeoecology, 253: 32–40.
GeoRefGoogle Scholar

34. ↵
Li T. 2011. Pollen Flora of China Woody Plants by SEM. Bejing: Chinese Cooperation for Promotion of Humanities.
Google Scholar

35. ↵
Manchester SR. 1987. The fossil history of the Juglandaceae. St. Louis: Missouri Botanical Garden.
Google Scholar

36. ↲
Manos PS, Soltis PS, Soltis DE, Manchester SR, Oh S-H, Bell CD, Dilcher DL, Stone DS. 2007. Phylogeny of extant and fossil Juglandaceae inferred from the integration of molecular and morphological data sets. Systematic Biology, 56: 412–430.
CrossRefGeoRefPubMedWeb of ScienceGoogle Scholar

37. ↲
Manum SB. 1962. Studies in the Tertiary flora of Spitsbergen,with notes on Tertiary floras of Ellesmere Island, Greenland, and Iceland. Norsk Polarinstitutt Skrifter, 125: 1–127.
Google Scholar

38. ↲
Martin PS, Drew CM. 1969. Scanning electron photographs of southwestern pollen grains. Journal of the Arizona Academy of Science, 5: 147–176.
Google Scholar

39. ↲
Miyoshi N, Fujiki T, Kimura H. 2011. Pollen flora of Japan. Sapporo: Hokkaido University Press.
Google Scholar

40. ↲
Mosbrugger V, Utescher T. 1997. The coexistence approach – a method for quantitative reconstructions of Tertiary terrestrial palaeoclimate data using plant fossils. Palaeogeography, Palaeoclimatology, Palaeoecology, 134: 61–86.
CrossRefGeoRefWeb of ScienceGoogle Scholar

41. ↲
Müller MJ, Hennings D. 2000. The Global Climate Data Atlas on CD Rom. Flensburg: Universität Flensburg, Institut für Geografie.
Google Scholar

42. ↲
Peel MC, Finlayson BL, McMahon TA. 2007. Updated world map of the Köppen-Geiger climate classification. Hydrology and Earth System Sciences, 11: 1633–1644.
CrossRefWeb of Science, Google Scholar

43. ↲
Pocknall DT, Crosbie YM. 1988. Pollen morphology of Beauprea (Proteaceae): Modern and fossil. Review of Palaeobotany and Palynology, 53: 305–327.
CrossRefGeoRefWeb of ScienceGoogle Scholar

44. ↲
Quan C, Liu Y-SC, Utescher T. 2012. Eocene monsoon prevalence over China: A paleobotanical perspective. Palaegeography, Palaeoclimatology, Palaeoecology, 365-366: 302–311.
Google Scholar

45. ↲
Solomon AM, King JE, Martin PS, Thomas J. 1973. Further scanning electron photomicrographs of southwestern pollen grains. Journal of the Arizona Academy of Science, 8: 103–157.
Google Scholar

46. ↲
Stevens PF. 2001 onwards. Angiosperm Phylogeny Website. Version 8, June 2007 [and more or less continuously updated since].
Google Scholar

47. ↲
Stuchlik L, Ziembińska-Tworzydło M, Kohlman-Adamska A, Grabowska I. B. S, Wazyńska, H., Sadowska A. 2009. Atlas of pollen and spores from the Polish Neogene. Vol. 3. Angiosperms (1). Kraków: W. Szafer Institute of Botany, Polish Academy of Science.
Google Scholar

48. ↲
Stuchlik L, Ziembińska-Tworzydło M, Kohlman-Adamska A, Grabowska I. B. S, Worobiec E, Durska E. 2014. Atlas of pollen and spores from the Polish Neogene. Vol. 4. Angiosperms (2). Kraków: W. Szafer Institute of Botany, Polish Academy of Science.
Google Scholar

49. ↲

Stuchlik L, Ziembińska-Tworzydło M, Kohlman-Adamska A, Grabowska I, Wazyńska, H., Sadowska A. 2002. Atlas of pollen and spores from the Polish Neogene. Vol. 2. Gymnosperms. Kraków: W. Szafer Institute of Botany, Polish Academy of Science.
Google Scholar

50. ↲
Stuchlik L, Ziembińska-Tworzydło M, Kohlman-Adamska A, Grabowska I, Wazyńska H. B. S, Sadowska A. 2001. Atlas of pollen and spores from the Polish Neogene. Vol. 1. Spores. Kraków: W. Szafer Institute of Botany, Polish Academy of Science.

51. ↲
Taylor TN, Taylor EL, Krings M. 2009. Paleobotany – The Biology and Evolution of Fossil Plants. Burlington: Academic Press.

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