

Repeated intercontinental migrations and recurring hybridizations characterise the evolutionary history of yew (*Taxus* L.)

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Объект исследования - род Тис (Taxus)



Сложности

- 1) Неочевидная и противоречивая таксономия
- 2) Противоречия в предыдущих филогенетических исследованиях
- 3) Сравнительно небольшое генетическое разнообразие между разными линиями
- 4) Предполагаемо много событий повторной гибридизации
- 5) Будем честны, кто вообще с хвойными работает и при этом получает удовольствие от того, как там все устроено и сколько доступно информации? Я точно нет.

Цели исследования

- 1) Реконструировать филогению рода *Taxus*
- 2) Проверить достоверность и попытаться объяснить конфликт между хлоропластными и ядерными маркерами
- 3) Датировать историческое расхождение разных ветвей
- 4) Реконструировать исторические ареалы и географию их распространения

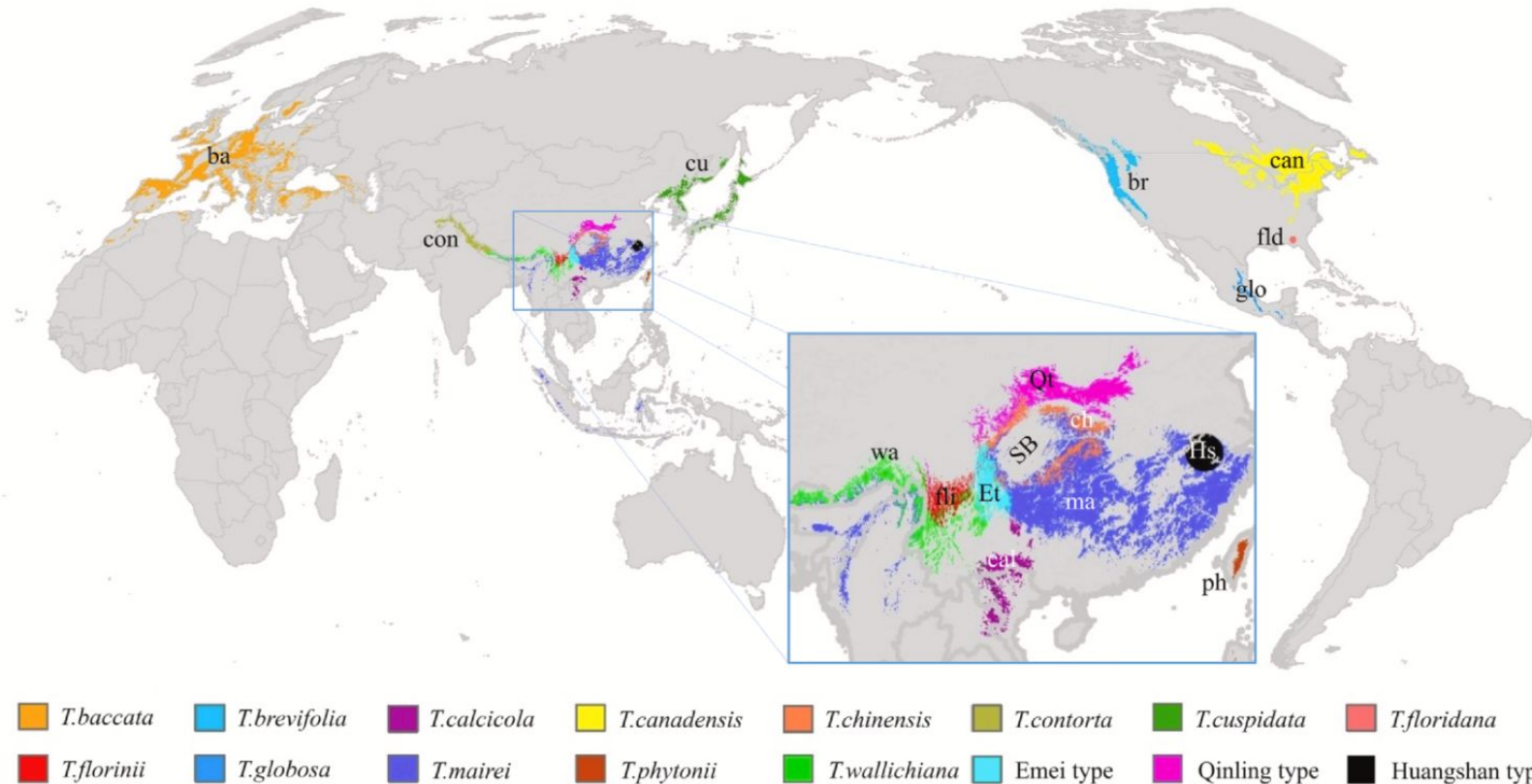


Fig. 1. Global distribution ranges of 16 *Taxus* lineages included in the study, on an Asia-centered map. The map was generated using a Robinson projection centred at the 150° East meridian in ArcGIS v9.3 (ESRI, Redlands, CA, USA). Abbreviations: ba – *T. baccata*; br – *T. brevifolia*; cal – *T. calcicola*; can – *T. canadensis*; ch – *T. chinensis*; con – *T. contorta*; cu – *T. cuspidata*; fld – *T. floridana*; glo – *T. globosa*; Hs – *T. Huangshan type*; ma – *T. mairei*; ph – *T. phytonii*; wa – *T. wallichiana*. Hybrid lineages: Et – Emei type; fli – *T. florinii*; Qt – Qinling type. SB – Sichuan basin.

Этапы исследования

1. Выделение ДНК СТАВ-методом
2. ПЦР двух ядерных маркеров (ITS и NEEDLY), а также тринадцати маркеров в хлоропластных генах
3. Секвенирование (по Сенгеру)
4. Конструирование матрицы
5. RAUP* для расчета деревьев – отдельно по ядерным маркерам и по хлоропластным
6. 6. Комбинирование матриц для общего анализа всех собранных маркеров
7. 7. BEAST для оценки временных рамок расхождения линий
8. 8. BioGeoBEARS для реконструкции ареалов

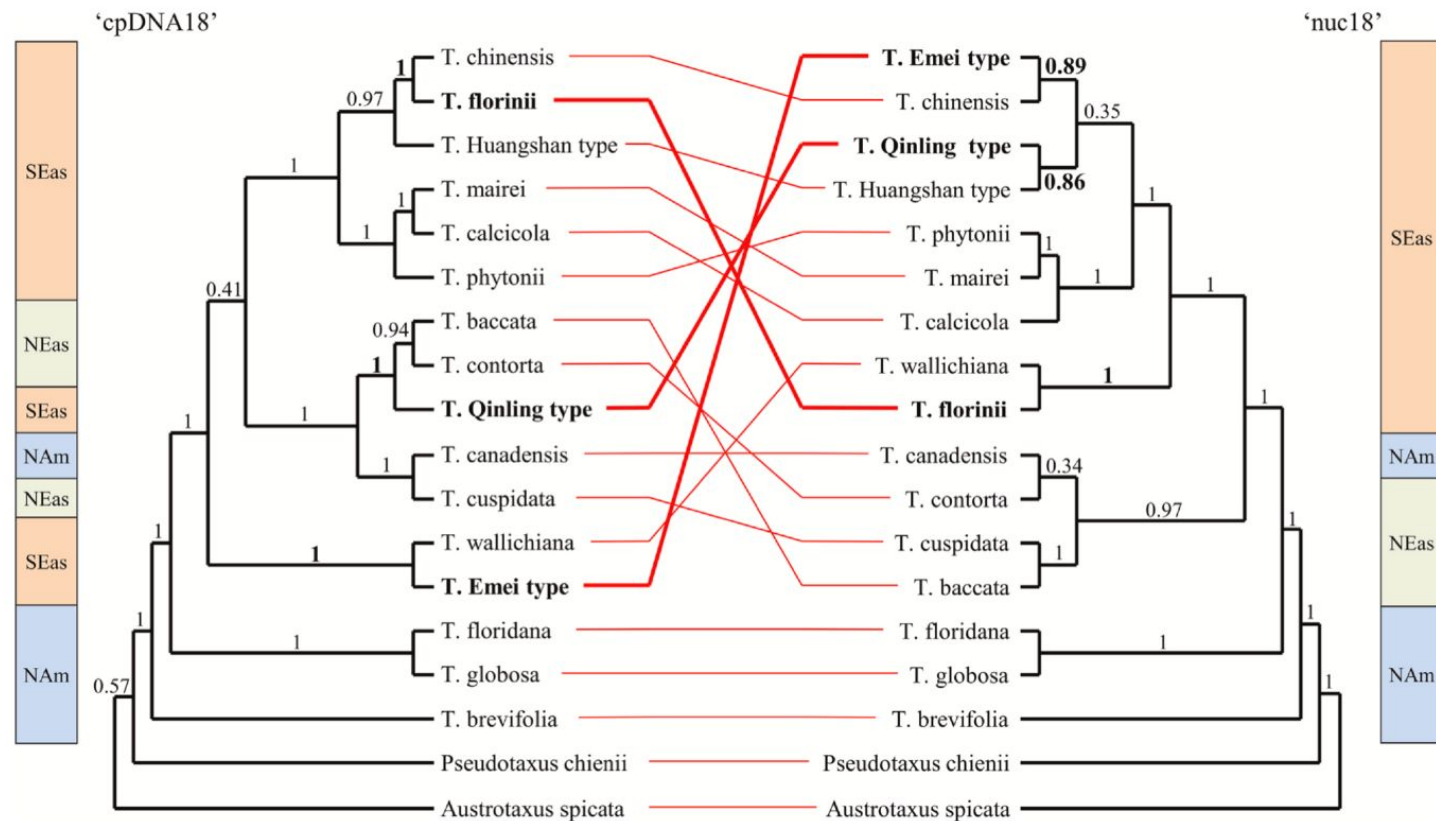


Fig. 2. Tanglegram based on 13 combined cpDNA marker sequences ('cpDNA18') and combined ITS and *NEEDLY* sequences ('nuc18') for 16 *Taxus* lineages with BEAST posterior probabilities along the branches. Bold red lines indicate inferred hybridization events, and bold names indicate lineages involved in the hybridization events based on their incongruent well-supported positions in the individual phylogenetic trees. The coloured bars left and right to the tanglegram indicate the main geographic regions of the *Taxus* lineages: NAm – North America; NEAs – North Eurasia; SEAs – South Eurasia. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

Повторы гибридизации

T. florinii = *T. wallichiana* (♀) × *T. chinensis* (♂)

T. Emei type = *T. chinensis* (♀) × *T. wallichiana* (♂)

T. Qinling type = *T. contorta* (♀) × *T. Huangshan type* (♂)

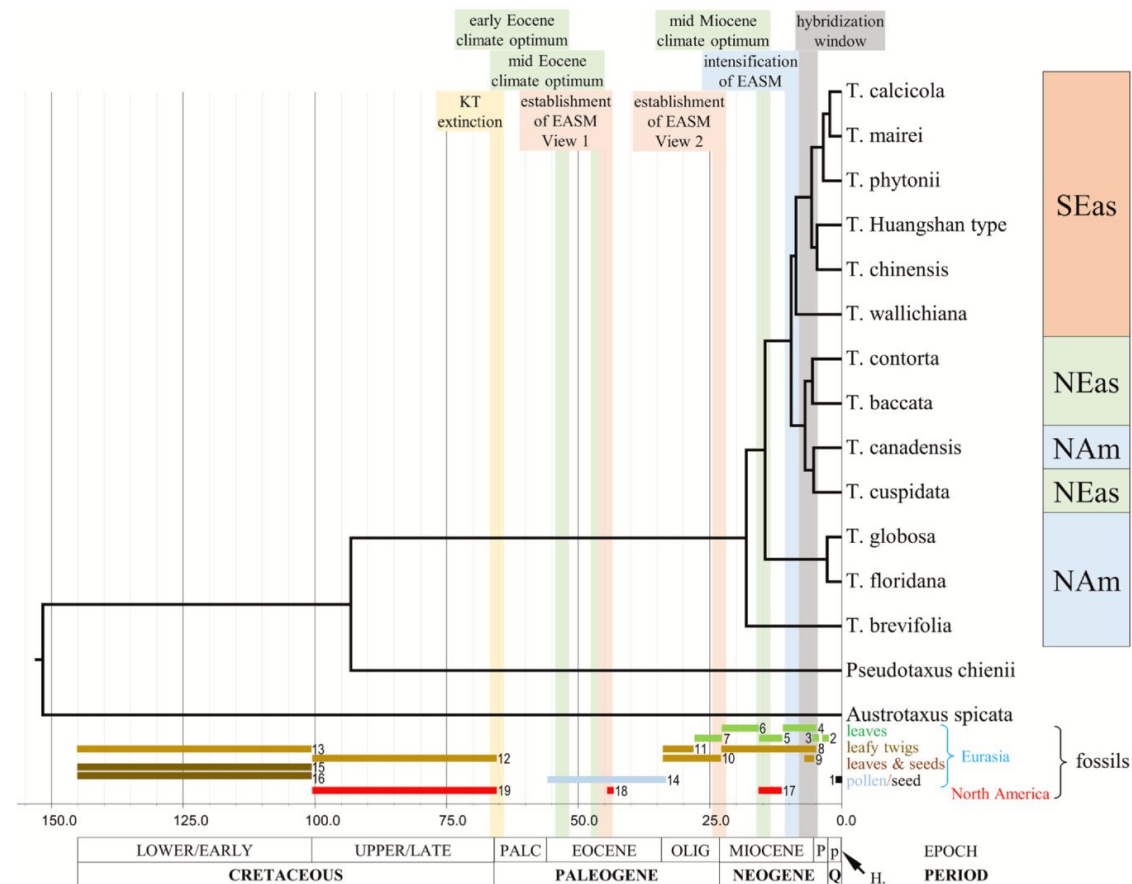


Fig. 3. BEAST chronogram (in Mya) based on combined 13 cpDNA markers, ITS and *NEEDLY* sequences for 13 *Taxus* lineages, with indication of timings for major climatic events and hybridization window. The coloured bars on the right indicate the main geographic regions of the *Taxus* lineages: NAM – North America; NEAs – North Eurasia; SEAs – South Eurasia. EASM – East Asian summer monsoon. PALC – Palaeocene; OLIG – Oligocene; P – Pliocene; p – Pleistocene; H – Holocene. Q – Quaternary. Fossils are coloured according to the plant fossil material: black – seed; dark brown – leaves & seeds; brown – leafy twigs; green – leaves; light blue – pollen/seed. Red indicates fossils from North America. Numbers along fossil bars refer to details given in Table A8. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

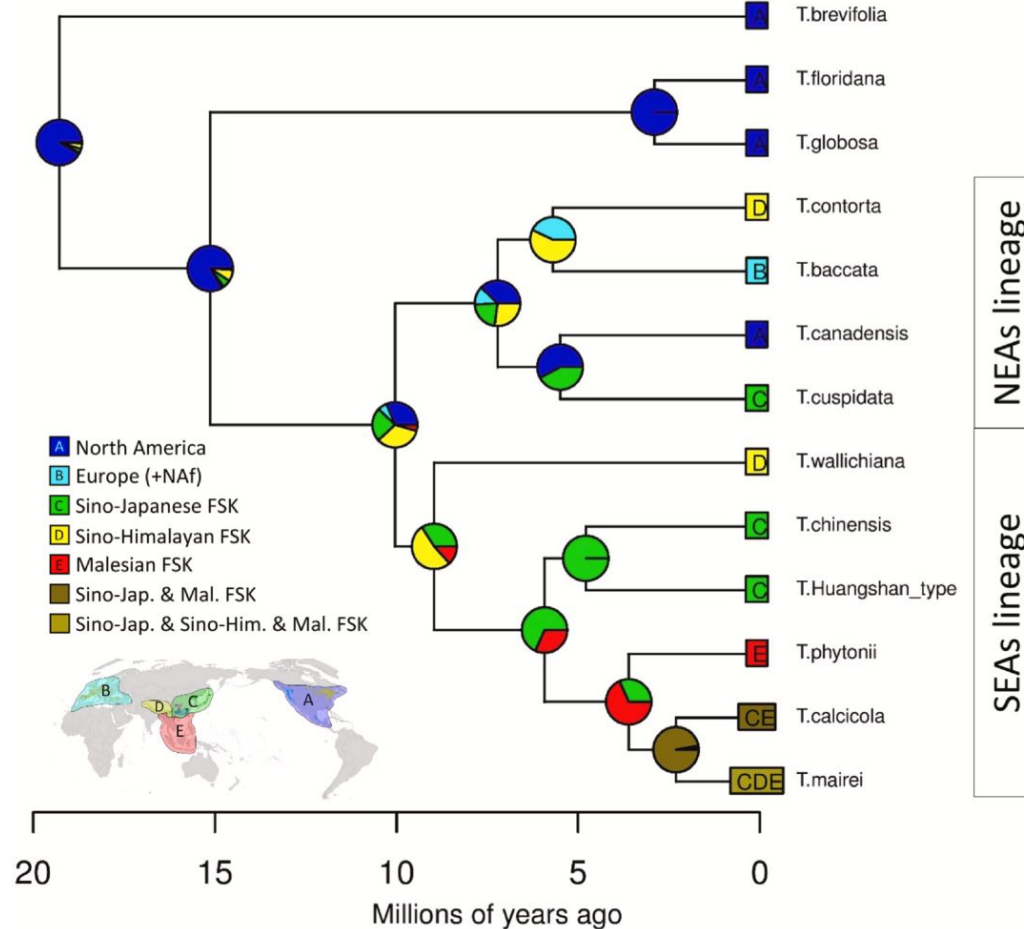


Fig. 5. Result of ancestral area reconstruction analyses in BioGeoBEARS based on the BEAST chronogram of extant *Taxus* lineages, with the best model under an 'Asia' geographic structuring, BAYAREA-LIKE + j. Areas are colour-coded as indicated in the legend. Pie graphs indicate the probabilities of any area or combined areas. A (dark blue) – North America; B (pale blue) – Europe (+NAf = North Africa); C (green) Sino-Japanese Forest Subkingdom; D (yellow) – Sino-Himalayan Forest Subkingdom; E (red) – Malaysian Forest Subkingdom; FSK – Forest Subkingdom. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

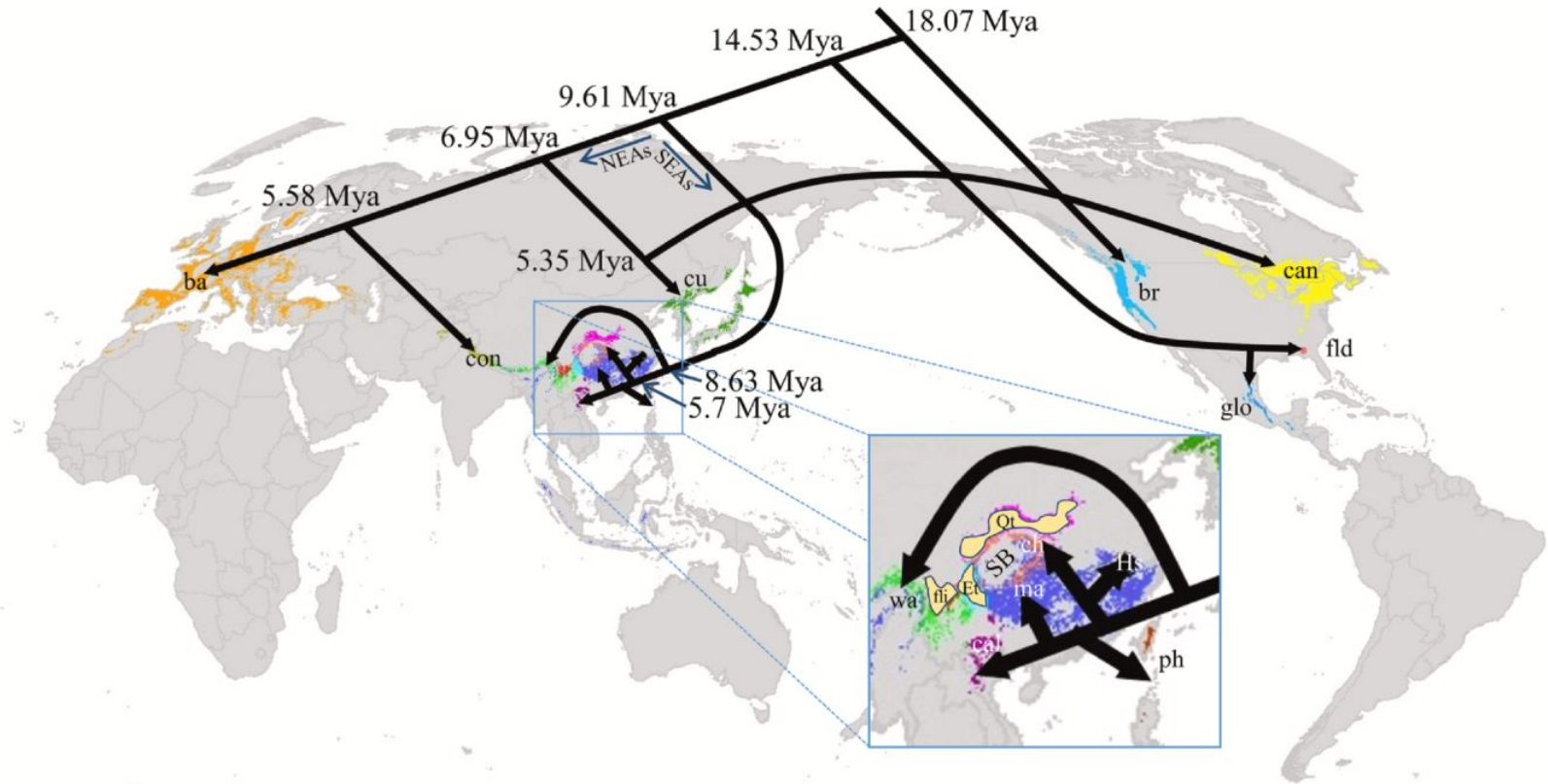


Fig. 6. Schematic distributions of the 13 *Taxus* lineages and three inferred hybrids globally, with superimposed phylogenetic tree given in Fig. 5. Abbreviations as in Fig. 1.