Chestnut Chat: Evolution of the Genus *Castanea*

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Biological taxonomy (ideally) reflects evolutionary history

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Two main types of evidence used to study *Castanea* evolution

**Fossils**

PC: Burke Museum, Univ. Washington
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**Fossils**

**DNA sequence comparisons**

| Indiv 1: | AA|GGGATGCAAAGAGCTAAAGAAGAGGAATTTTAATATTGATTCT |
| Indiv 2: | AAGGGATGCAAAGAGCTAAAGAAGAGGAATTTTAATATTGATTCT |
| Indiv 3: | AAAGGATGAAAAGAGCTAAAGAAGAGGAATTTTAATATTGATTCT |

Polymorphisms (*i.e.*, mutations)

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- **Indiv 3**: AGGGATGCAAAAGAGCTAAAGAAGAGGGGAATTTTAATTTAATAGCATTCT
7-10 *Castanea* species currently exist.
Angiosperms had appeared by the early Cretaceous, ~130 mya

Montsechia vidalii from 130-125 mya
Gomez et al. (2015)

Leefructus mirus from 122.6-125.8 mya
Sun et al. (2011)

Micropetasos burmensis flowers in amber, from ~100 mya
Poinar et al. (2013)
Earliest Fagaceae fossils from:
Late Cretaceous, ~83-72 million years ago;
Paleocene-Eocene boundary, ~56 mya

Protofagacea allonensis,
~83-72 mya

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Trigonobalanoidea, ~56 mya

Castanopsoidea, ~56 mya

North America ~60 mya
(map by RC Blakey, NAU)

*Castaneoidea puryearensis*, the earliest Chestnut-like fossils
From the mid-Eocene, ~50-40 million years ago

Fossil bur

Fossil catkin

North America ~40 mya
(map by RC Blakey, NAU)

Castanea occurred in both eastern and western North America during the Eocene.

Claiborne Formation, TN
Allenby Formation, BC, Canada
Allenby Fm, BC, Canada

Clarno Formation, Oregon
Renova Formation, Montana
Florissant Formation, Colorado

North America ~40 mya (map by RC Blakey, NAU)

Data and images courtesy of Burke Museum (Univ. Washington), Yale Peabody Museum, Bouchal et al. (2014), Jaynes (1975)
Hypothesized origin of *Castanea* in eastern Asia

Ref: Jaynes (1975) *Advances in Fruit Breeding*
“Land bridges” have allowed migration of species across the globe ~40 million years ago, map by RC Blakey (NAU)
Castanea evolutionary tree inferred from chloroplast DNA
C. sativa is more closely related to N. American Castanea

Lang et al. (2007): a hypothesized westward migration of *Castanea* from eastern Asia
Castanea evolutionary tree inferred from chloroplast DNA
Pleistocene glaciation cycles from ~2.5 mya – 11,700 ya

Extent of ice at the last glacial maximum, ~20,000 ya
Migration of *Castanea* after last ice age inferred from the pollen record

...but new studies may add detail to the story

Species distribution modelling predictions (blue) and pollen records (red dots) from Spriggs and Fertakos (2021) Am J. Bot.
Hybridization between *Castanea* species in the wild

Fig. adapted from Sun et al. (2020) “Genomic basis of homoploid hybrid speciation in chestnut trees” *Nature Comm.*
North American *Castanea* species

- Allegheny chinquapin (*pumila*) in Florida: ~0.5 m
- Allegheny chinquapin (*pumila*) from Georgia: ~3 m
- Ozark chinquapin (*ozarkensis*) in Arkansas
- American chestnut in Tenn.
- *C. alabamensis* snag
Has hybridization contributed to morphological variation? (the case of *Castanea alabamensis*)

![Image of Allegheny chinquapin (pumila) × American chestnut (dentata) = Castanea alabamensis]

Castanea alabamensis is a distinct chinquapin clade
Allegheny chinquapin is more closely related to Ozark chinquapin than to American chestnut.
Prediction: C. alabamensis will have a reticulate pattern of descent in network analysis.
**Result**: C. alabamensis pattern of descent is **not** reticulate
Prediction: STRUCTURE will identify low levels of *C. dentata* ancestry in *C. alabamensis*.
Result: no evidence of C. dentata ancestry in C. alabamensis
STRUCTURE identifies potential *C. dentata* ancestry in population of *C. pumila* in Florida.
Admixture between different chinquapin taxa may be common.
Admixture between different chinquapin taxa may be common
Has hybridization contributed to this diversity? In the case of *C. alabamensis*...
Current research: whole genome re-sequencing of North American *Castanea* species

- Alex Sandercock, Jason Holliday (VA Tech)
- Jared Westbrook, Paul Sisco (TACF)
- Fred Paillet (U of Arkansas)
- Hill Craddock, Paola Zannini (UT-Chattanooga)
- Tatyana Zhebentyayeva (Penn State)

Whole genome sequences available
- **American chestnut** 388 plants
- **Allegheny chinquapin** 15 plants
- **Ozark chinquapin** 10 plants
- **C. alabamensis** 5 plants

We’re adding 228 samples
- **American chestnut** 27 plants (from 13 sites)
- **Allegheny chinquapin** 80 plants
- **Ozark chinquapin** 61 plants
- **C. alabamensis** 60 plants
Testing for gene flow between southern C. dentata and sympatric chinquapins: ABBA-BABA test
Future research questions:

1) Has chinquapin contributed to genetic diversity in American chestnut? Was there any adaptive significance?

2) When did American chestnut diverge from chinquapins?

3) What was the westernmost extent of *C. dentata* just before *Phytophthora* and *Cryphonectria* arrived?

4) Is the hypothesized westward migration of *Castanea* supported by genome sequencing data? Or was migration into North America more complex?
Questions?
(you can also email me at: tperkins2588@gmail.com)