UNIVERSITY OF BIRMINGHAM

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BIRMINGHAM INSTITUTE OF FOREST RESEARCH

Using BIFoR to investigate the evolution of plant reproduction

Dr. Andy Plackett

University of Birmingham, School of Biosciences

A very simple question that's hard to answer

- "How does a plant's genetic program (their 'software') control how they grow?"
  - Until now, plant developmental genetics has been based on the intensive investigation of **model species.**
  - We now know a lot about how one or two plants work, much less about any other.

Arabidopsis thaliana
(Thale cress)

Oryza sativa
(Rice)

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Environment cabinet
(fridge-freezer)

Growth room
(walk in)

Limited by what will grow in a lab…

Laboratory-based models have their limits

- "How does a plant's genetic program (their 'software') control how they **reproduce?"**

Arabidopsis thaliana

Arabidopsis

- Highly complex, many genes involved
- Highly responsive to the environment!

Laboratory-based models have their limits

- "How does a plant's genetic program (their 'software') control how they **reproduce?**"

Arabidopsis thaliana

Arabidopsis

Passionfruit

Orchid

Laboratory-based models have their limits

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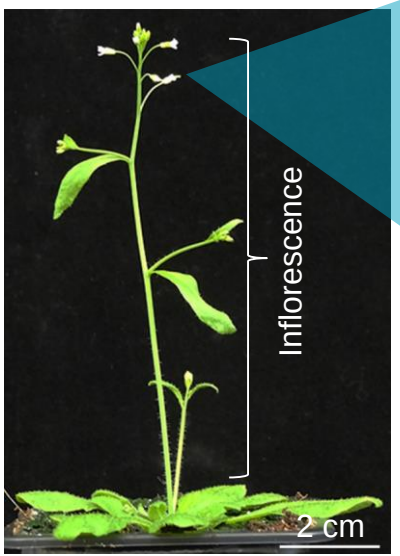

Arabidopsis thaliana

Arabidopsis

Passionfruit

Orchid

Sunflower (inflorescence)

Pineapple (inflorescence)

Laboratory-based models have their limits

- "How does a plant's genetic program (their 'software') control how they **reproduce?"**

Arabidopsis thaliana

Arabidopsis

Passionfruit

Orchid

Sunflower

Pineapple

Cacao

Coffee

Cherry

Banana

And what about **tree-forms**?

Laboratory-based models have their limits

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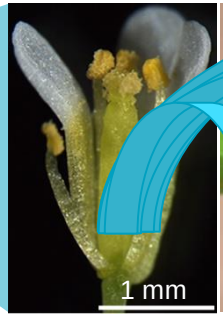
Arabidopsis thaliana



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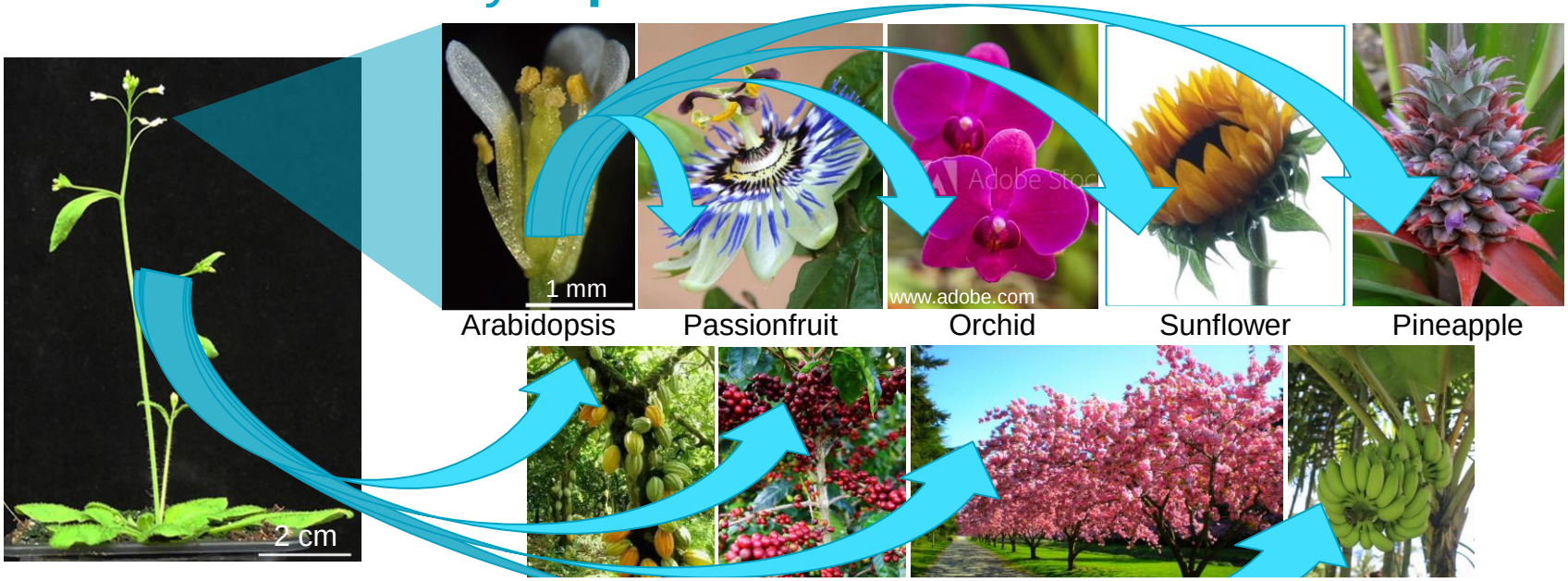
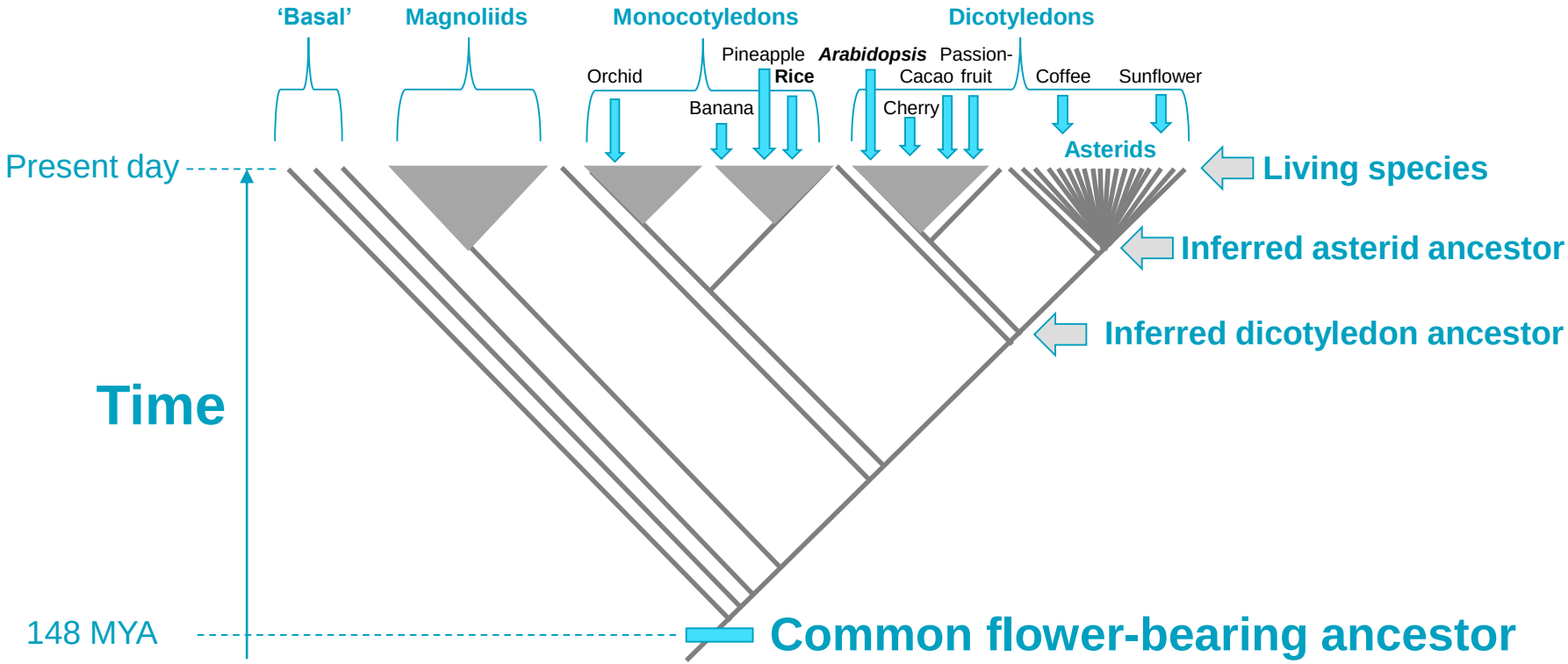


Our lab-derived knowledge struggles to predict reproductive **diversity**

Evolution can be used to leverage more from existing data

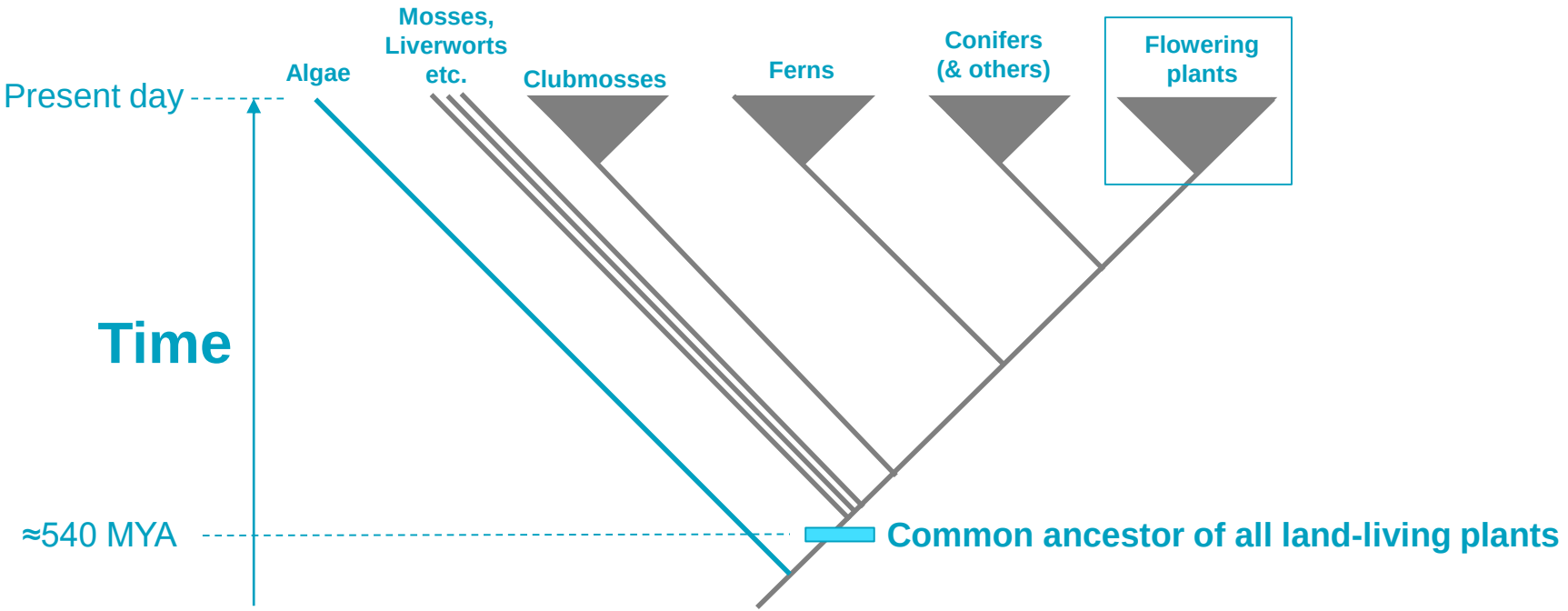
- Evolutionary relationships between flowering plants (‘angiosperms’):



Based on Chase et al., *Bot. J. Linn. Soc. 2016*

Evolution can be used to leverage more from existing data

- Evolutionary relationships between all **land-living plants** (‘embryophytes’):



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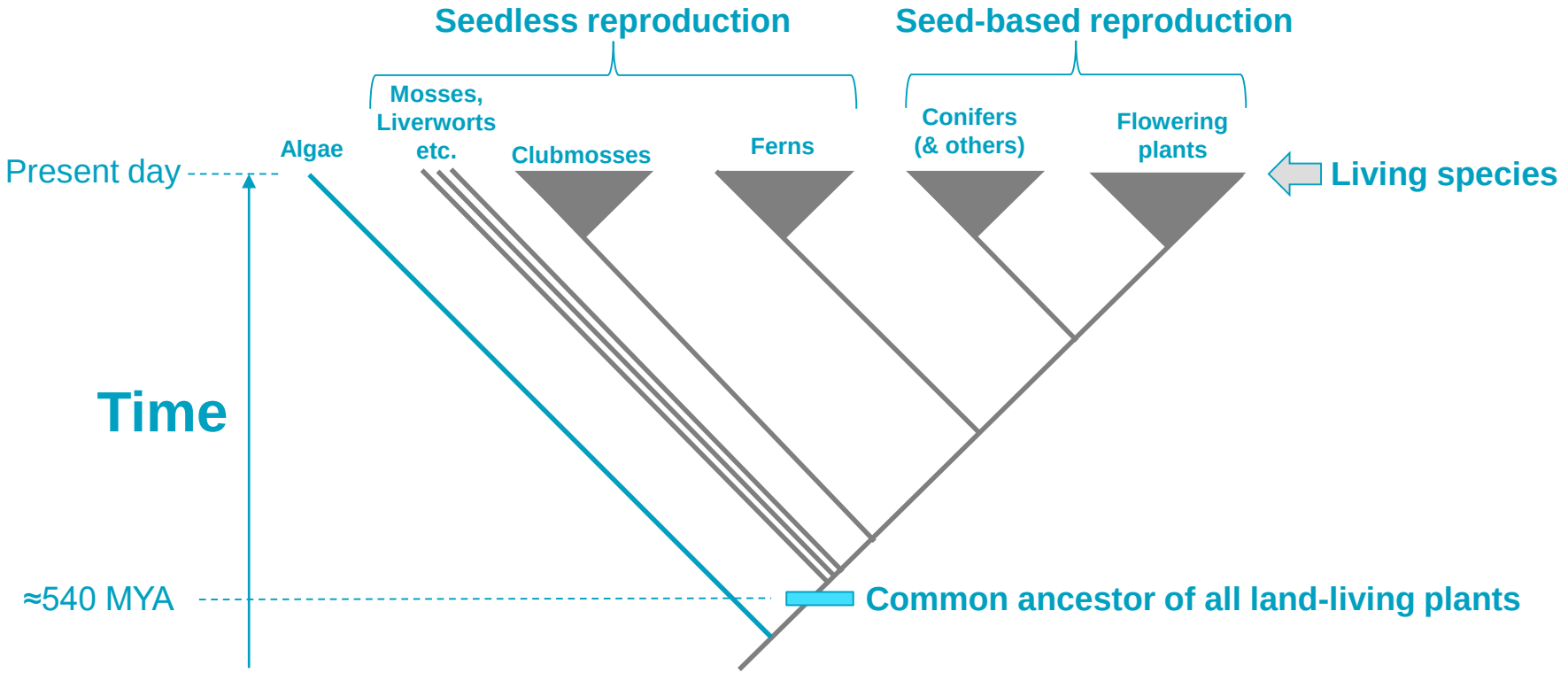

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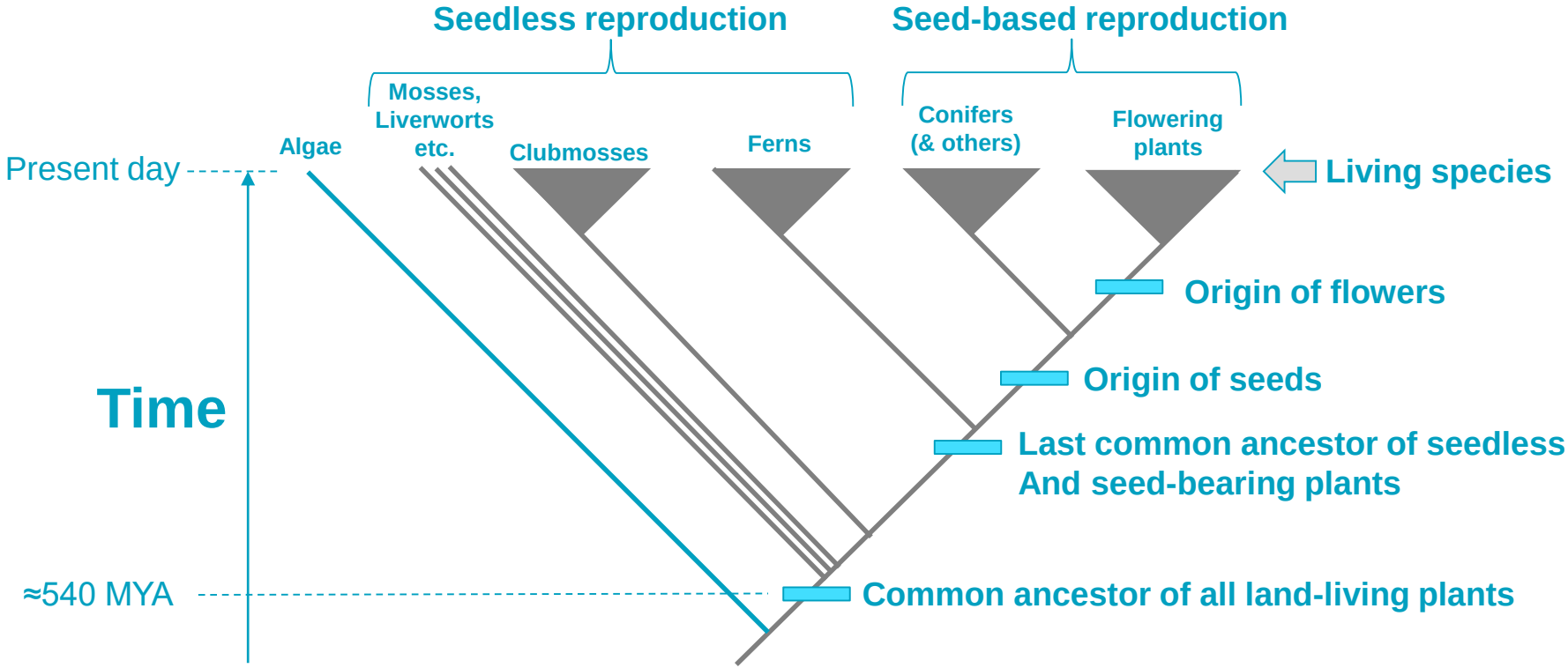

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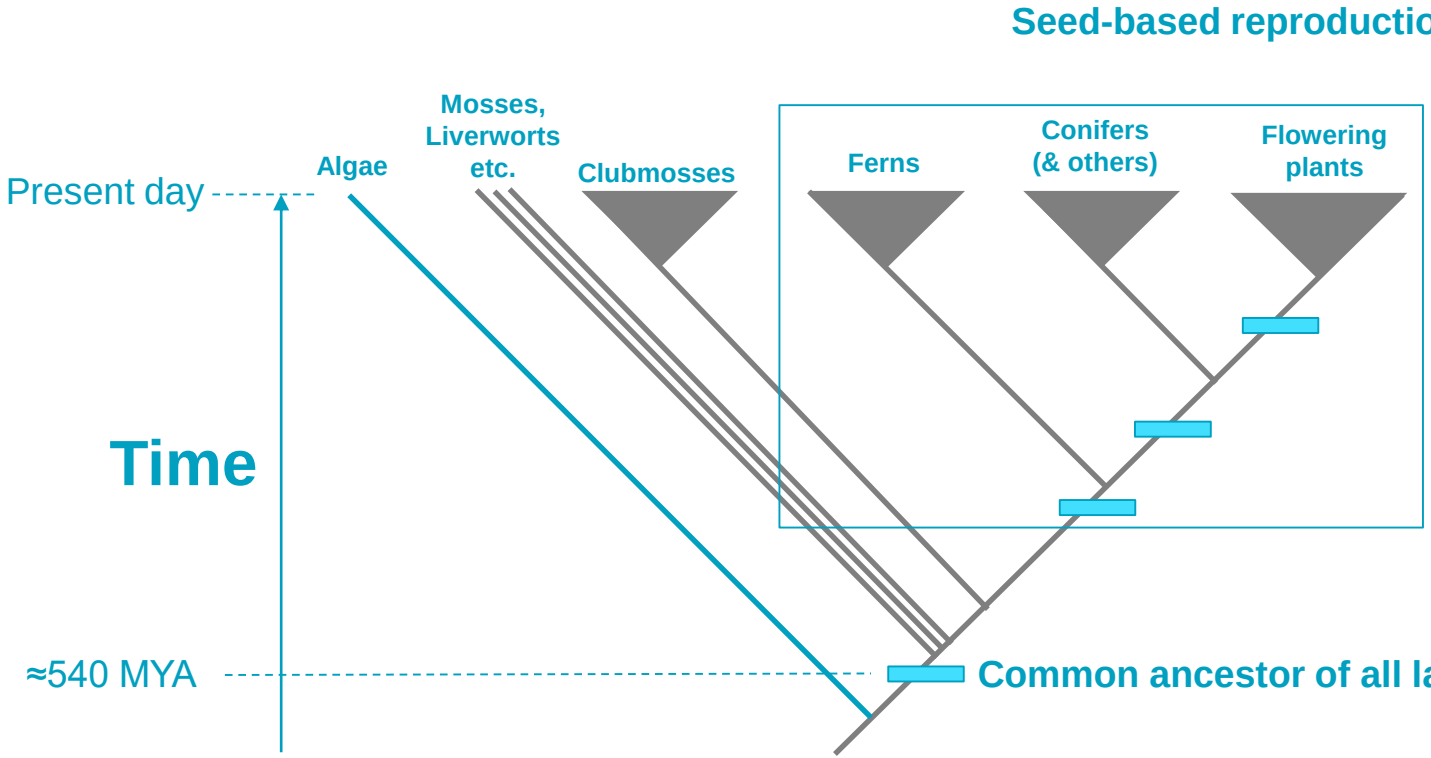
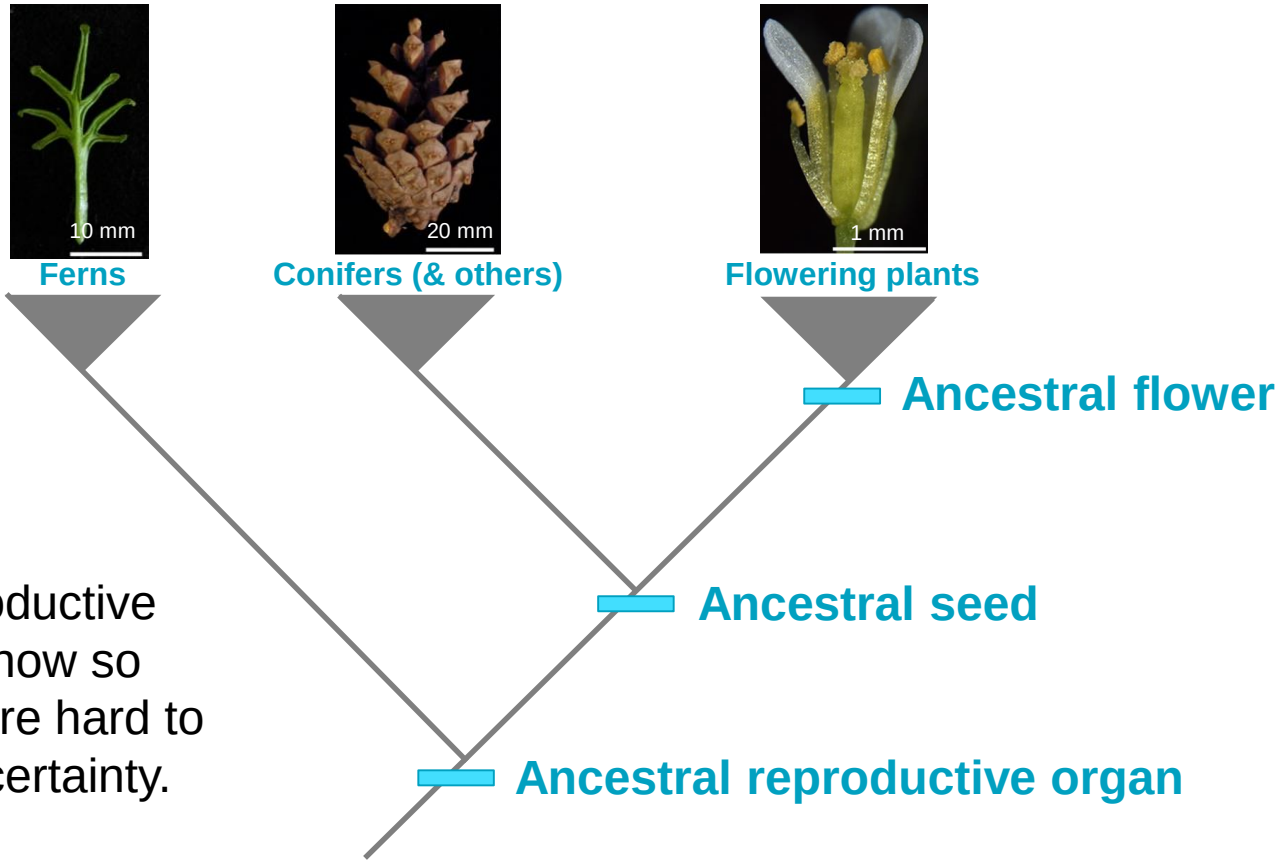


Comparing these will explain the **origin** of modern plant reproductive systems.

‘Keystone points’

Based on Wickett et al. *PNAS 2016*

We can now build a genetic roadmap to plant diversity…

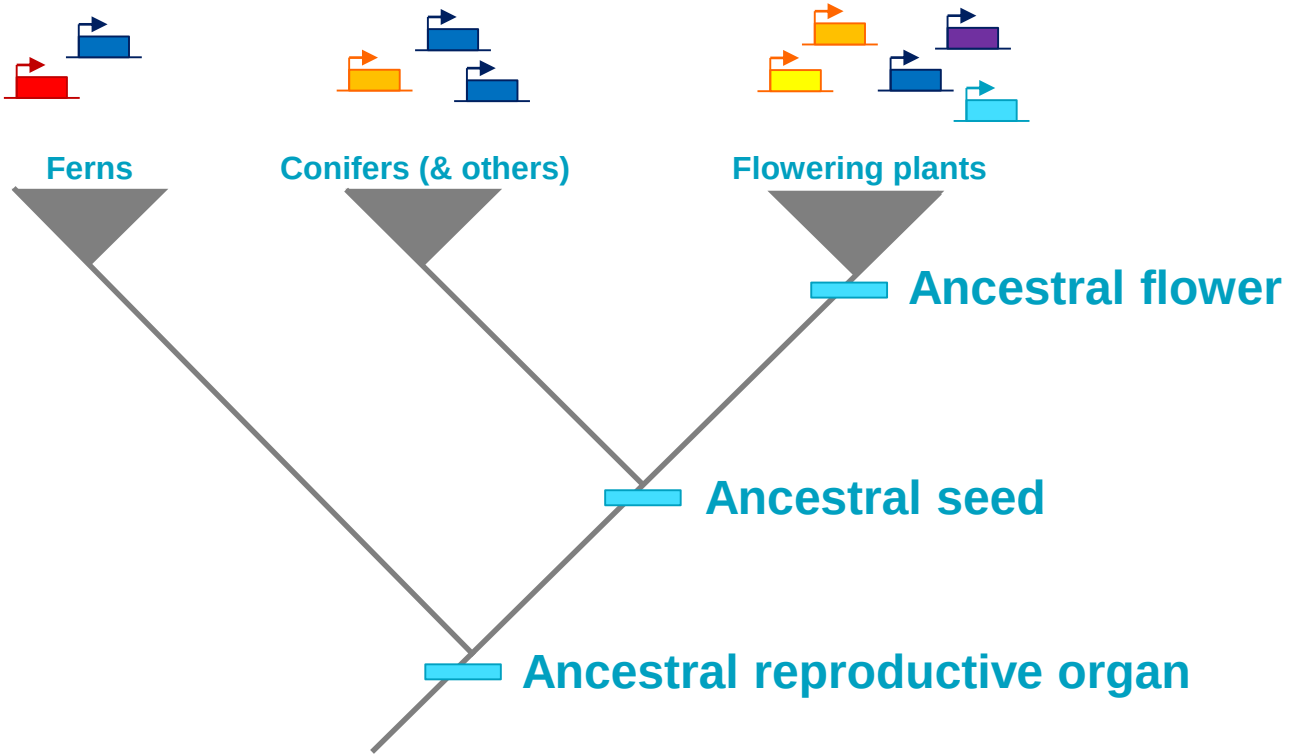


- Surviving reproductive structures are now so different they are hard to compare with certainty.

We can now build a genetic roadmap to plant diversity…

- At the **DNA level**, comparisons are actually **easier**:

- The same ‘families’ of genes are found in ferns, conifers and flowering plants



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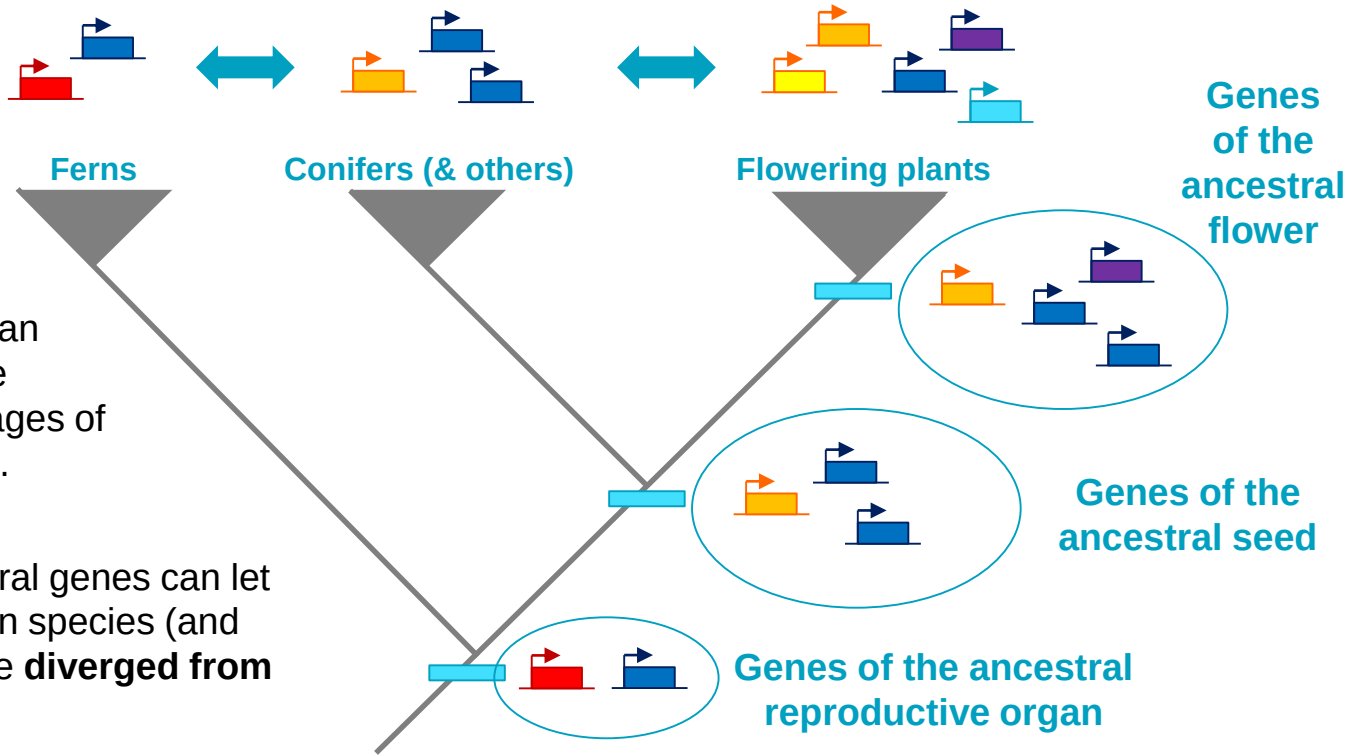
- At the **DNA level**, comparisons are actually **easier**:

- The same ‘families’ of genes are found in ferns, conifers and flowering plants

- By **comparison**, we can **infer** what genes were present at different stages of reproductive evolution.

- Reconstructing ancestral genes can let us **predict** how modern species (and their genes) have since **diverged from one another.**



…But first we need accessible samples!

- The only surviving gymnosperms (conifers and others) are **TREE-FORMS!**

E.g. Norway Spruce (*Picea abies*)

Why use this species?

- Reproduction has been previously studied
- Sequenced genome

BUT:

- Large size (> 20 metres)
- Only ‘flowers’ after 30-40 years (!)

Sexually-mature trees growing on the BIFoR site!

In conclusion

Resources like BIFoR enable fundamental research into plant development not otherwise possible with conventional lab-based approaches

- BIFoR conifer specimens will provide important keystone information about ancestral genes during the evolution of seed-based reproduction

- **Not just conifers!** (Oak, Sycamore, Hazelnut)

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THE ROYAL SOCIETY

Project collaborators:

Juliet Coates (Birmingham)
Steven Kelly (Oxford)
David Emms (Oxford)

Thank you for your attention!

Dr. Andy Plackett
University of Birmingham, School of Biosciences