

sDiv Workshop Summary "sSTEP"

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The workshop examined patterns of trait evolution in vascular plants. We discussed three main topics:

1. Broad patterns of evolution in plant traits, such as constancy, changes in rate, and convergence.
2. Knowledge gaps and overlaps in plant trait (TRY), genetic (GenBank), distribution (GBIF), and taxonomic (The Plant List) databases
3. New analytical approaches for examining the evolution of spectral plant trait data

The first topic was the primary focus of discussion during the plenary sessions. Specifically, we addressed i) the diversification, direction and rate of change functional traits across the plant tree of life since the early history of vascular plants, ii) their evolutionary shifts in relation to climate under the constraints in form and function associated with specific lineages, and iii) the evolution of innovations in functional forms within lineages that seem to fall outside the major axes of trait variation.

The participants came from very different disciplines: ecology, evolution, plant physiology, bioinformatics, and spatial processing. Consequently we spent much time focusing on discussions to find cross-overs and linkages between these fields. Diverse career stages were represented, including graduate students, post docs, early career faculty and senior faculty. The group was also diverse in terms gender and geographic origins, with participants from Europe, the US, Canada and Latin America.

Several of our participants took part in the meeting over the Internet; we found this model to work very well for analytical work, and (with sDIV support) reasonably well for discussions. We would certainly encourage other groups to employ this 'greener' approach to meetings, but only if participants are familiar with remote participation tools such as GitHub and Slack. For single meetings, the focus that remote participation naturally produces on analysis was extremely useful in generating results and outputs quickly.

There are 4 major outputs expected from the meeting:

- Data publication covering the new trait cleaning bioinformatic pipeline developed for the meeting, currently led by *Jens Kattge*

- Manuscript describing the overlap between plant trait, genetic, distributional, and taxonomic databases, currently led by *Will Cornwell*
- Manuscript describing broad patterns in trait evolution, currently led by *Will Pearse*
- A proposal for a NIMBioS working group further developing models for the evolution of hyper-spectral data, currently led by *Jeannine Cavender-Bares*

Participants attending in-person included:

Will Pearse, Jeannine Cavender-Bares, Hans Cornellison, Jens Kattge, Sandra Diaz, Jose Meireles, Shan Kothari, Julia Joswig, Talie Musavi and Guido Kraemer



Participants attending remotely included:

Will Cornwell, Amy Zanne, Beth Forrestel and Liam Ravell. Phil Townsend and Greg Asner also joined for a one hour discussion on spectral traits.