

sDiv Workshop
***“ 5th workshop of the TRY initiative:
Quantifying and scaling global plant trait diversity”***
3 – 5 September 2013
Workshop Summary

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Aim of the 5th workshop of the Global Plant Trait Initiative (TRY – www.try-db.org) was to examine the recent developments in the context of the TRY initiative, to initiate and support cooperation on core research topics and to further refine the TRY initiative, in particular the access to data stored in the trait data base.

The TRY initiative started in 2007 as IGBP fast-track initiative on “refining plant functional classifications” (PFT-FTI). In 2008, name was changed to TRY, and a new goal was developed: the development of a global plant trait database to make data available for trait-based approaches in ecology and the design of a new generation of DGVMs. In conjunction with this, Intellectual Property Guidelines were developed to overcome psychological barriers, and to provide incentives for data contributions. Over the last few years, TRY has gained considerable momentum, it is now a global research network with 591 participants from more than 200 institutes worldwide.

Perspectives for 2013/2014 include the improvement of data processing and process of data release, as well as further development of TRY as “role model” in the ecological community.

The open day of the workshop started with an introduction to the TRY initiative and its data base, and plans for the future. This was followed by presentations on lessons learned and opportunities for the future from data sharing initiatives related to TRY by Bill Michener (DATA One), Michael Kleyer (LEDA), Eamon O’Tuama (GBIF), Hendrik Poorter (MetaPhenomics) and Markus Reichstein (FLUXNET). These presentations also provided the background for discussion on the integration of TRY with these efforts.

A number of participants were given the opportunity to present their latest research based on using data from the TRY data base either in talks or in a poster session. Topics covered functional biogeography of traits, trait – environment relationships, and integration of trait data into dynamic vegetation modelling.

The second day of the workshop was dedicated to in-depth discussions in working groups on

- Plant traits and vegetation modelling (lead: Colin Prentice, Nicolas Viovy)
- Plant trait prediction and gap-filling (lead: Arindam Banerjee)
- The global spectrum of plant function (lead: Sandra Diaz, Sandra Lavorel)
- Plant traits and phylogenetic analyses (lead: William Pearse)
- Next generation trait screening projects (lead: Joe Craine)
- Tropical Forest Traits (lead: Christopher Baratolo)
- Linking Plant traits to plot data (lead: Oliver Purschke)

A number of collaborations have arisen from these working groups, and a manuscript on the global spectrum of plant functional traits is in preparation.

The final day of the workshop focused on further refining the TRY initiative, in particular on data availability and access, data quality and the integration of TRY with other data sharing initiatives. The suggested way forward for the trait data base includes a move towards open access, but with some restrictions on certain types of data. Public access data will have guidelines for good practice attached, which are facilitated by TRY. Handling of acknowledgement of data with restricted access is responsibility of both data owner and data user, they will need come to an agreement.

There is a need to find ways to make data sets "*citable*", e.g. via assigning DOIs or publishing data papers. The intellectual property guidelines will be updated accordingly, and the draft document to be circulated to work shop participants and TRY community. Data quality will be improved by including (and improving already existing) meta data and auxiliary data, as well as taxonomic information. There are currently efforts under way on standardising terminology within TRY.

The TRY data base can further be amended and expanded by

- Directly linking a plant thesaurus to the TRY data base
- Link traits to plot data (e.g. via plot id)
- Linking specimens to traits
- Complementing trait data currently included (e.g. adding root traits and conducting gap analysis)
- Integration of "Pseudo-traits", i.e. modelled trait values (these need to be labelled clearly)
- Inclusion of remote sensing measurements

Participants

	Name	Affiliation
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