



sPlot – the new global vegetation-plot database for addressing trait-environment relationships across the world's biomes

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2013

03/2013
1st sPlot
Workshop
at iDiv

06/2013
Collaboration
agreement
with EVA

07/2013
Governance and
Data Property
Rules approved

Invitation of
contributing
databases
started

12/2013
Implementation
of sPlot under
TURBOVEG 3
(S. Hennekens)

2014

04/2014
First databases
included
(official start of
sPlot)

11/2014
sPlot 1.0

04/2015
sPlot 2.0

Matching sPlot
1.0 with TRY
2.0

12/2014
2nd sPlot
Workshop at
iDiv

2015

04/2015
Release of sPlot
2.0

Future

Aims

1. Analysis of plant trait-environment relationships across the world's biomes (**global extent**) on the basis of vegetation-plot/community data (**small grain**).
2. Provide a global vegetation plot data base to address questions of **functional biodiversity research**.

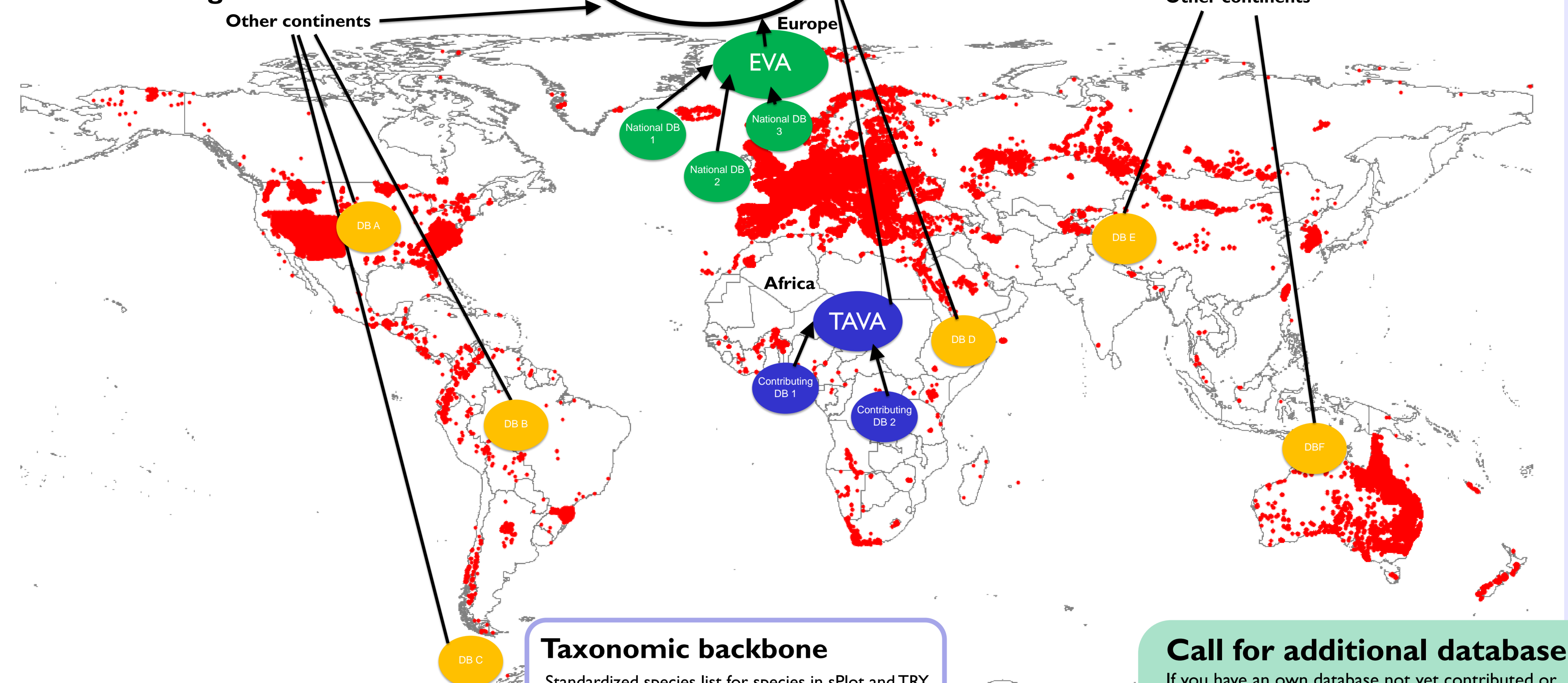
What is sPlot?

- Established by a working group **hosted by the Synthesis Centre (sDiv)** of the German Centre of Integrative Biodiversity Research Halle-Jena-Leipzig (iDiv).
- sPlot is a common vegetation-plot database for data from all continents in combination with **mean species trait values from the TRY database** and tools to match data from different sources taxonomically.

Content of sPlot 2.0 (to be released 19 April 2015)

- Total: 110 DBs, 130 countries, 1,117,762 relevés**
- All seven continents** represented
- Europe (including Turkey):** 54 DBs, 941,425 plot observations (relevés)
- Americas:** 20 DBs, 101,203 relevés
- Africa, Asia, Australasia, Antarctica:** 42 DBs, 73,036 relevés
- Increase compared to sPlot 1.0 (30 November 2014):** 57 DBs, 60 countries, c. 250,000 relevés
- Data handling in sPlot with prototype of **TURBOVEG 3**

sPlot data integration & current content



Call for additional databases!
If you have an own database not yet contributed or know of other colleagues and institutions with suitable databases **please contact**
Jürgen Dengler:
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Link to traits in TRY (based on sPlot 1.0 & TRY 2.0)

- Species-level **mean trait values** for **18 traits** in TRY 2.0 (Kattge et al. 2011).
- Fully **gap-filled** species trait matrix based on Hierarchical Matrix Factorization (Shan et al. 2012).
- 41% overall match** between species in sPlot and TRY.

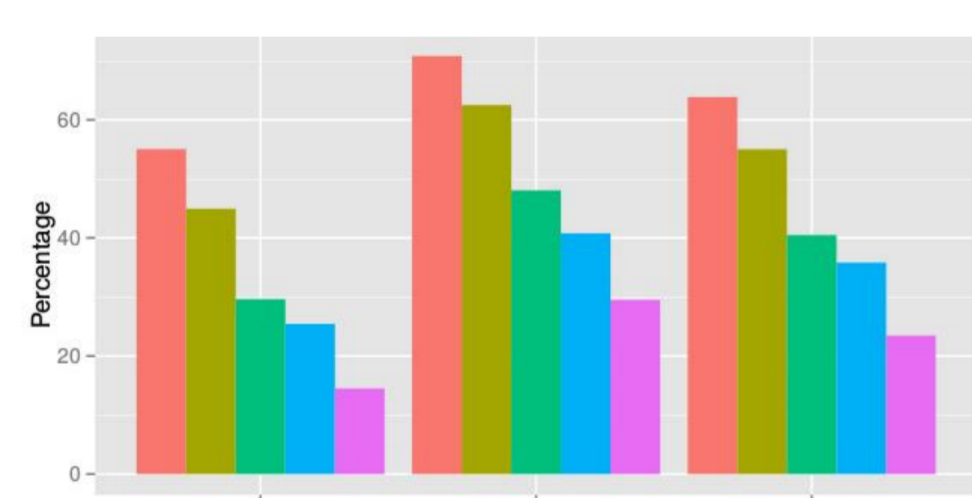


Fig. 2. Match (in %) between species (all, most frequent and dominant) in sPlot 1.0 and TRY 2.0; for all TRY-species, gap-filled and LHS-traits (height, seed mass, SLA), respectively.

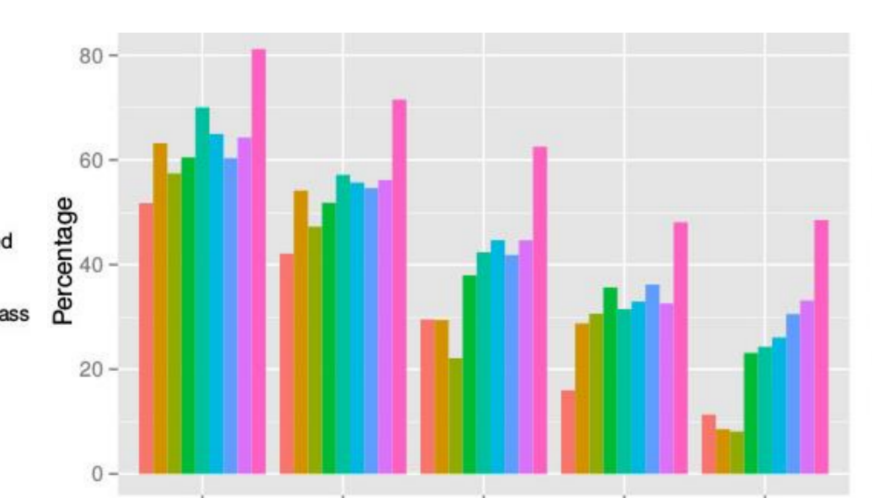


Fig. 3. Match (in %) between species in sPlot 1.0 and TRY 2.0; for all TRY-species, gap-filled and LHS-traits (height, seed mass, SLA), respectively across the nine biomes.

First results (based on sPlot 1.0 & TRY 2.0)

Global patterns of community-weighted SLA

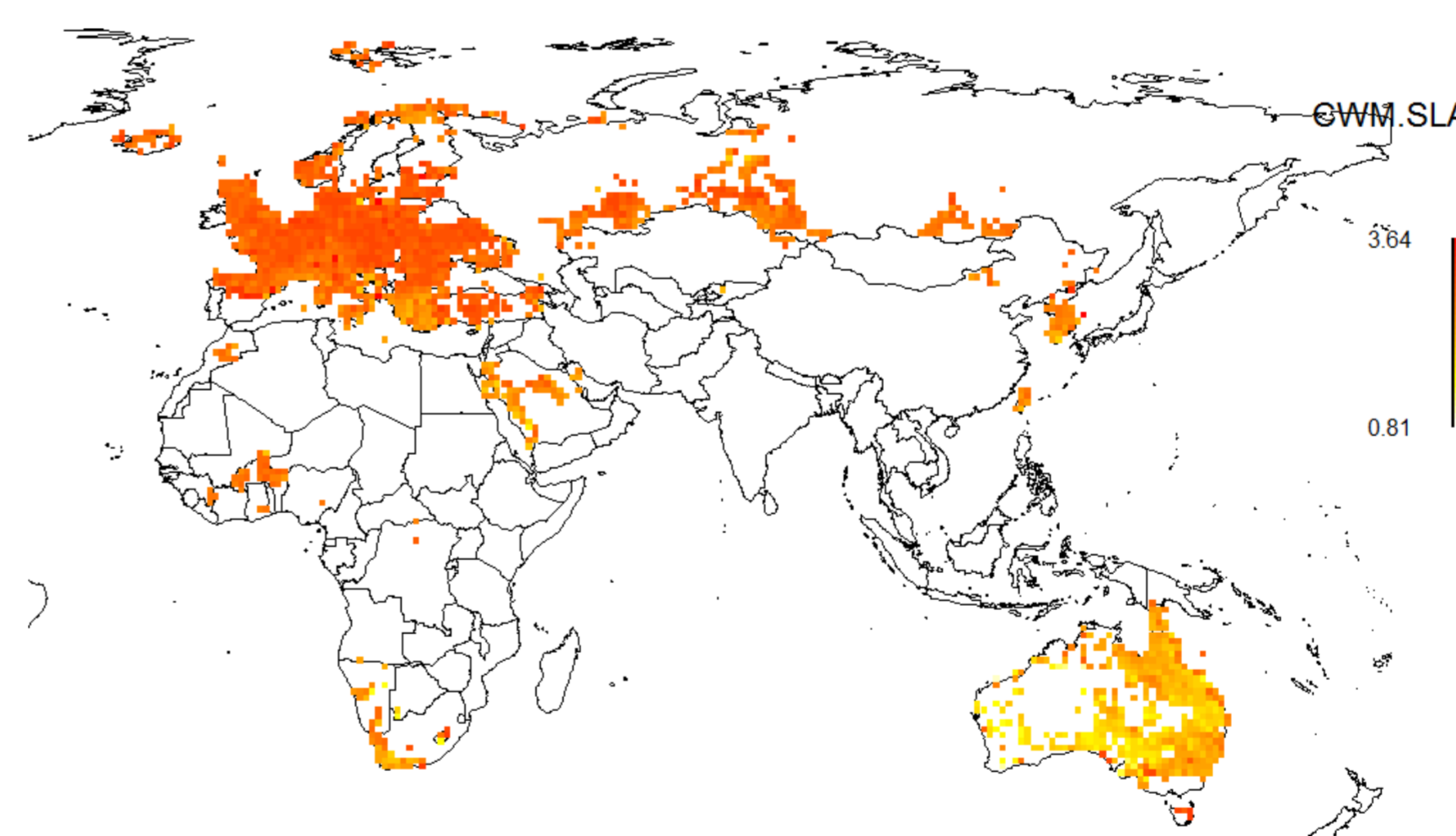


Fig. 4. Community-weighted means of specific-leaf area (SLA) in m²/kg (ln-transformed) averaged across all plots within a 1-degree grid cell.

SLA vs. Mean temperature

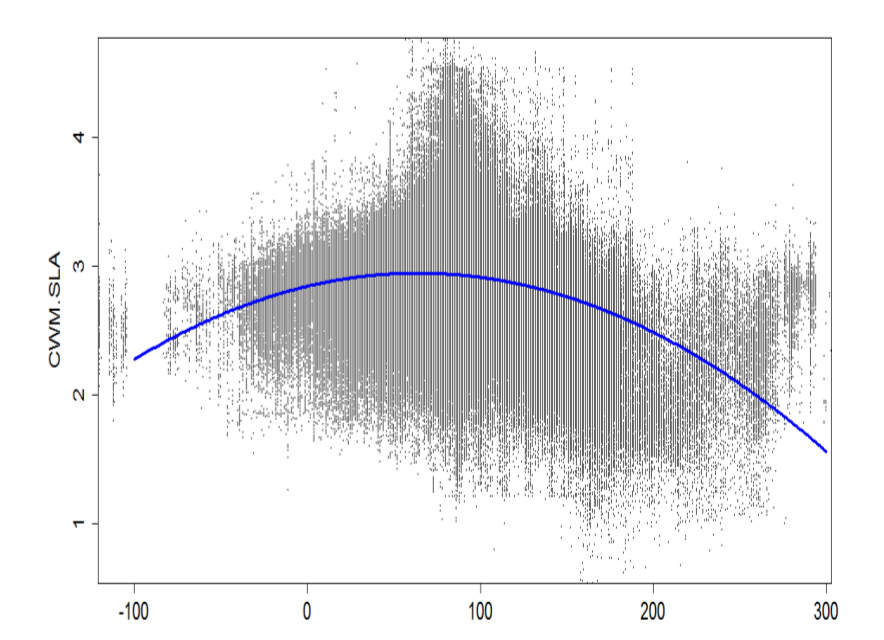


Fig. 5. Relationship between CWM of SLA and mean annual temperature (BIO_1). Fitted line indicates significant quadratic effect.

Outlook and next steps

- On 19 April 2015, **sPlot 2.0** (including the match with TRY 3.0) will be released.
- Content of sPlot 2.0 will be described in a database paper
- The sPlot Consortium is planning to write several analytical papers, based on sPlot 2.0/TRY 3.0 and topics such as trait-environment relationships, diversity patterns and plant invasions.
- sPlot 2.0 is available for other paper projects led by members of the sPlot Consortium and following the sPlot Rules.
- sPlot will continue to collect data and augment the contained data; the next release of a fixed version (sPlot 3.0) is planned in approximately one year from now.

Functional diversity explained by temporal climatic variability

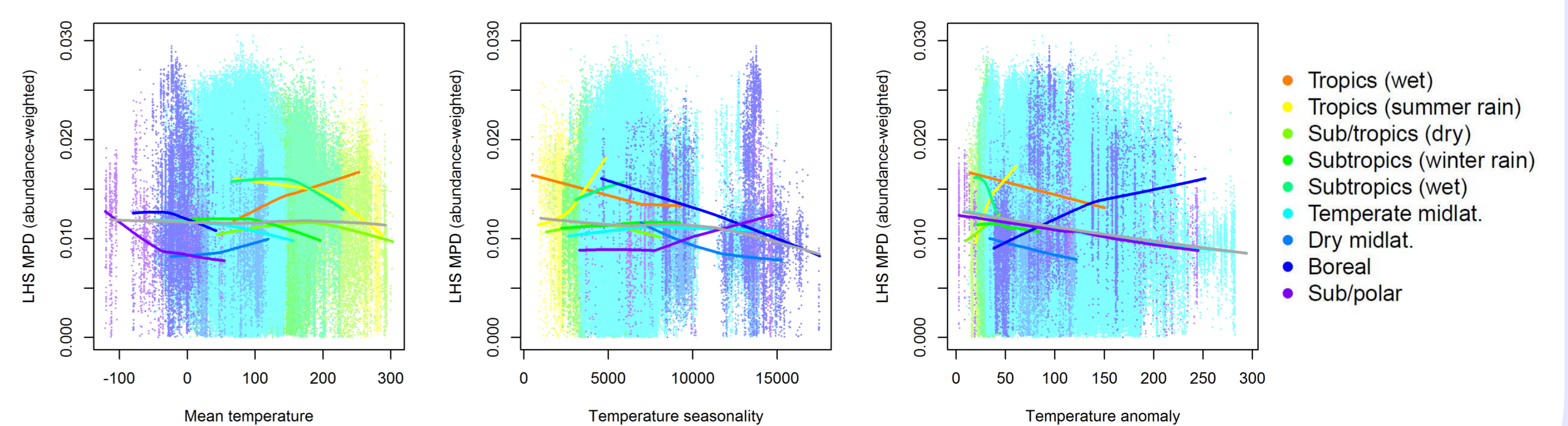


Fig. 6. Relationship between multi-trait (LHS: SLA, plant height, seed mass) functional diversity (abundance-weighted MPD) and (a) mean annual temperature, (b) temperature seasonality and (c) climate change velocity (temperature anomaly). Fitted regression splines indicate (i) overall relationships across all biomes (grey line) and (ii) relationships within each of the nine biomes (colored lines).

We thank those thousands of vegetation scientists who recorded relevés or measured plant traits and made these data available in common databases!

