This MossQuantGenreadme.txt file was generated on 2021-02-05 by Leslie M. Kollar

GENERAL INFORMATION

1. Moss growth, development, morphology, and physiology dataset and code:

2. Author Information

A. Principal Investigator Contact Information

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B. Associate or Co-investigator Contact Information

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3. Date of data collection (single date, range, approximate date): Spring 2016

4. Geographic location of data collection: Portland, OR (Portland State University)

5. Information about funding sources that supported the collection of the data: This work was supported by the National Science Foundation Doctoral Dissertation Improvement Grant (NSF DEB 1701915) to LMK and SFM, NSF grants to SFM (DEB 1541005 and 1542609); EDEN: Evo-Devo-Eco Network Training Grant to LMK, MicroMorph Cross-Disciplinary Training Grant to LMK, the University of Florida’s Biology Department grants to LMK, and by the Swedish Research Council (2018-06775 to KG).

SHARING/ACCESS INFORMATION

1. Licenses/restrictions placed on the data: N/A

2. Links to publications that cite or use the data:

3. Links to other publicly accessible locations of the data:

<https://doi.org/10.5061/dryad.59zw3r266>

4. Links/relationships to ancillary data sets: N/A

5. Was data derived from another source? No

6. Recommended citation for this dataset:

DATA & FILE OVERVIEW

1. File List:

LH.traits.data.NONA.csv

Data.homemade.traits.csv

Multivariate\_analyses\_Kollar.L.R

Univariate\_analyses\_Kollar.L.R

scaled.threeLHtraits.parexp.obj

Final.VOC.4.repro.obj

1. Relationship between files, if important:

LH.traits.data.NONA.csv contains traits categorized as “growth and development” and Data.homemade.traits.csv contains traits categorized and “morphology and physiology”. We fit models for each category of traits and included both of the models. Scaled.threeLHtraits.parexp.obj is the model fit for the growth and development traits while Final.VOC.4.repro.obj is the model for the morphology and physiology traits. The majority of analyses can be found in Multivariate\_analyses\_Kollar.L.R while testing for significant genetic variation can be found in the file Univariate\_analyses\_Kollar.L.R.

3. Additional related data collected that was not included in the current data package: NA

4. Are there multiple versions of the dataset? Not yet

METHODOLOGICAL INFORMATION

1. Description of methods used for collection/generation of data:

Please see manuscript and supplemental material.

2.Methods for processing the data:

Data collection and processing is discussed in detail in the manuscript and the supplemental methods. We include some brief points here to clarify.

**PTR Data:** We identified 75 different masses using the PTR-TOF-MS in mature sex expressing gametophytes. We represented the masses as total volatile output and as number of compounds. The raw PTR data files were analyzed using the PTR viewer and background/blank cuvette air was subtracted from the sample readings to account for noise in the signal.

**Leaf traits:** After leaves were mounted flat on a slide and images were taken, leaf traits including (length, area, and perimeter) were calculated using a custom script in ImageJ.

**Reproductive output:** For female reproduction we counted the number of archegonia (eggs) in each female sex structure. To account for possible differences in placement of the sex structure along the stem, we sampled sex structures from three different locations on the stem (top, middle, and bottom) per sample. For male reproduction, we counted the total number of male sex structures per 10 stems per sample. To make the male and female reproductive units comparable we combined male and female reproductive units into a single column and mean centered and variance standardized reproductive units. Standardization methods are in the R scripts.

**Growth and developmental data:** We collected many traits encompassing growth and development in juvenile moss tissue. These samples were grown in a growth chamber in 12 well plates. Images were taken every 7 days and analyzed using ImageJ software. Some measurements such as total number of gametophores were measured simply by counting the presence of mature gametophytes.

3. Instrument- or software-specific information needed to interpret the data:

Proton Transfer Reaction Time of Flight Mass Spectrometer (PTR-TOF-MS 1000, Ionicon)

PTR-MS Viewer 3.1 (Ionicon)

R (version 4.0.2; R Development Core Team 2020)

MCMCglmm’ (v. 2.29)

4. Standards and calibration information, if appropriate: See supplemental material

5. Environmental/experimental conditions: See supplemental material

6. Describe any quality-assurance procedures performed on the data: See supplemental material

DATA-SPECIFIC INFORMATION FOR: [FILENAME]

<repeat this section for each dataset, folder or file, as appropriate>

1. Number of variables:

LH.traits.data.NONA.csv: 10

Data.homemade.traits.csv: 18

1. Number of cases/rows:

LH.traits.data.NONA.csv: 1070

Data.homemade.traits.csv: 580

3. Variable List:

LH.traits.data.NONA.csv: "sampid", "famid", "ssex", "Plate", "Tray", "area\_wk3", "perim\_wk3", "circ\_wk3",

"Days\_gam", "Total\_gam"

Data.homemade.traits.csv: "famid", "sampid", "Date.PTR", "ssex", "Total.conc", "Total.masses", "Avg.conc.raw", "Total.conc.stand.mean", "Avg.conc.divmean", "low.end.sum.Total.conc", "high.end.sum.Total.conc", "low.end.Total.masses", "high.end.Total.masses", "high.avg.conc”, "low.avg.conc", "data.Leaf\_Length\_Average", "data.repro"

4. Missing data codes: We removed samples with missing data.

5. Specialized formats or other abbreviations used: NA