Dataset Title

1. Predawn, LMA and Carbon Isotope Data from three common gardens located on the North Kaibab Ranger District, Kaibab National Forest, Arizona: 2015-2019
2. Mortality and Treatment Differential Database from three common gardens located on the North Kaibab Ranger District, Kaibab National Forest, Arizona: 2015-2019

Abstract

Abstract from: Bucholz E, Waring KM, Kolb TE, Swenson J, and Whipple A. (2020). Water relations and drought response of *Pinus strobiformis*. *Canadian Journal of Forest Research*. 50(9): 905-916. https://doi.org/10.1139/cjfr-2019-0423

Southwestern white pine (*Pinus strobiformis* Engelm.) faces dual threats of climate change shifting its environmental niche and mortality due to a nonnative, invasive fungal pathogen. To inform efforts to sustain this species, we established experimental field trials in three common gardens along an elevational gradient with drought treatments to assess trait responses in southwestern white pine. We measured predawn and midday water potential on 44 maternal families from 10 populations at each garden. We used regression between predawn and midday water potentials to estimate hydroscape area, an index of stomatal regulation of transpiration. We measured leaf carbon isotope ratio and estimated carbon isotope discrimination and leaf mass per area to understand the effects of gardens and treatments on stomatal aperture and leaf structure. Water stress caused by experimental drought and temperature decreased leaf carbon isotope discrimination and leaf mass per area, indicating formation of thin leaves with low stomatal conductance in response to heat and drought. The hydroscape area of southwestern white pine suggests tight control of transpiration via stomatal closure, similar to other isohydric pines. Families with greater stomatal closure (inferred from carbon isotope ratio) at the warm, dry garden had higher survival than other families, suggesting an important role of isohydry in acclimation of southwestern white pine to expected habitat drying and warming.

-Creators

(These are the people who will show up as authors in the dataset citation. These are the individuals who have provided intellectual or other significant contributions to the creation of this dataset, much like the authors of a research paper.)

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(Who should a data user contact with questions about these data? You **must** enter a person or organization name to serve as the **contact** for this dataset. You may also list other personnel who participated in the project (such as field crew, lab tech, data entry etc.) in this table with optional fields e-mail addresses, organization and ORCID ID.)

First Name	Middle Initial	Last Name	Organization	e-mail address	ORCID ID (optional)	Role in project
Ethan	R	Bucholz	Northern Arizona University; Colorado	ethanbucholz@gmail.com		Contact

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License

(Select a license for release of your data. We have 2 recommendations: CCO – most accommodating of data reuse, & CCBY – requires attribution).

License: CCBY

Keywords

(**List keywords below and separate with commas.** Using keywords from a controlled vocabulary (CV) will improve the future discovery and reuse of your data. The LTER CV is a good source for keywords. **Access the LTER CV here**. Also, please determine one or two keywords that best describe your lab, station, and/or project (e.g., Trout Lake Station, NTL LTER).)

Plant properties (Predawn water potential, midday water potential, carbon isotope discrimination, hydroscape area), *Pinus strobiformis*, NAU Department of Biological Sciences, NAU School of Forestry, NAU Silviculture and Applied Forest Health Lab, drought, climate change, common garden, adaptive traits

Funding of this work:

List only the **main PI of a grant** that supported this project, starting with the main grant first. Add rows to the table if several grants were involved.

PI First Name	PI Middle Initial	PI Last Name	PI ORCID ID (optional)	Title of Grant	Funding Agency	Funding Identification Number
Kristen	M	Waring	0000-0001-9935-9432	NSF Grant 1	National Science Foundation	EF-1442597

Timeframe

- Begin date: 06/2015
- End date: 06/2020

- Data collection ongoing/completed: Summer 2021

Geographic location

(Use **decimal degrees** to define a point or a bounding box. Use a negative symbol (-) to indicate a west longitude. Copy this block to add multiple points or areas.)

- Verbal description: All individuals measured were located in Common Gardens within the Kaibab National Forest, AZ. All populations tested came from seed collected in New Mexico, Arizona, Colorado and Texas.
- North bounding coordinate: 40.0
- South bounding coordinate: 30.0
- East bounding coordinate: -102.5
- West bounding coordinate:-112.5

Taxonomic species or groups

Pinus strobiformis Engelm.

Methods

(Be specific about the study design and field and lab methods for collecting and processing the data. Include instrument descriptions and protocol citations.)

From: Bucholz et al. 2020. Water relations and drought response of Pinus strobiformis, Canadian

Journal of Forest Research

Experimental Sites, Design and Seed Source

We utilized three Southwest Experimental Garden Array (SEGA) common garden sites on the Kaibab National Forest, Arizona, USA (Figure 1; https://sega.nau.edu). Common gardens are used to minimize environmental variation to facilitate investigation of genetic variation and phenotypic plasticity (e.g. Gonzalez-Martinez et al. 2006). The three common gardens we used are located along a 631-m elevational gradient, with gardens located at 2688 m (high elevation; cool, wet), 2276 m (middle elevation; intermediate), and 2057 m (low elevation; warm, dry) (Figure 1). These three gardens span 4°C in mean annual temperature, allowing us to test for effects of climate warming on phenotypic expression in PIST. Each SEGA garden was equipped with a weather station consisting of a 10-meter tower, solar power, a Campbell Scientific datalogger and instrumentation to record weather and climate parameters at 1-minute, 30-minute and 1-hour intervals. The parameters measured include air temperature using redundant sensors at 2 meters and 10 meters, relative humidity at 2 meters, soil temperature at 5, 10, and 15 centimeters, soil moisture at 0-30 and 30-60 centimeters, wind speed and direction at 10 meters, total sky plus sun solar radiation, photosynthetically active radiation, and precipitation.

Between 2012-2015 we collected open-pollinated PIST seed from populations in Colorado, Arizona, New Mexico, and Texas. Following collection, cones were dried, and seeds extracted, cleaned

and placed in long-term freezer storage until used in this study. A population consisted of 3-5 maternal trees, and progeny derived from seed of a single maternal tree was considered a family. Up to 25 seedlings family^{-1} were sown per garden (n=75 total per family). Seeds were sown in the Northern Arizona University Research Greenhouse in January 2015 and 2016. This study was part of a larger umbrella project and two sow years were used due to resource limitations and the logistical constraints of rapidly collecting seeds from many locations. Prior to sowing, seeds were surface sterilized for 24 hours in a 1% hydrogen peroxide solution followed by cold stratification for 4 weeks at 4°C. Forty-cell Tinus book planters (individual cell dimensions: 20cm x 6cm x 4cm) were randomly allocated to one of 3 common gardens, and seeds were then randomized and sown within each planter. Depending on expected germination from seed x-rays (data provided by collaborators at the Dorena Genetic Resource Center for seed from the same families and collection year), and knowledge of family and collection year germination performance in previous research (e.g. Goodrich et al. 2016), either one, two, or three seeds were sown. Greenhouse temperatures were maintained at 15°C (nighttime) and 26°C (daytime), at a near constant relative humidity of 50%. Seedlings were watered three times weekly to soil capacity. In May, at the start of the growing season, plants were fertilized twice weekly with a 20-20-20 N-P-K solution starting at 15 ppm. Each week following, the solution was increased by 15 ppm until it reached 60 ppm (4 weeks).

In August of 2015 and 2016, seedlings were transplanted to raised-bed boxes at each of the three common gardens. Boxes were 107cm x 117cm x 91cm, with individual boxes separated from each other by approximately 90 cm. Seedlings were randomly planted within the boxes, mirroring the sowing in the greenhouse, in 10 rows of 10 seedlings each. Approximately 2200 seedlings were sown in 2015 per garden, and an additional 1700 were sown per garden in 2016. We provided irrigation on a bi-weekly basis throughout each growing season (May-October) (see additional irrigation details below). From populations and families comprising these sow years, we selected a subsample of populations for this study. Selection criteria included geographic location of source populations and source environmental heterogeneity of precipitation and temperature. Ultimately, a subset of 10 populations comprised of 44 maternal families representing nearly the entire US range of PIST (Figure 1) was included. Population source location spanned a latitudinal gradient of 5.5 degrees and 6.8 degrees of longitude (Table 1; Figure 1). From this subset of populations, we randomly selected 2-3 individuals x 2 drought treatments (described below) x 44 families x 3 gardens for sampling (Table 1; n=783). All populations were comprised of 4 or 5 families; if the 5th family had at least 2 living individuals per treatment, it was included in this study, otherwise that family was excluded (Table 1).

Mortality was assessed on each box of seedlings biannually starting in 2017. Trees were considered dead when their needles were completely brown, no turgidity remained within their main stems, and any buds were dry and brown. We assessed mortality on a binomial basis (1,0) after winter snowmelt in March, April or May, depending on garden elevation, and then again in October prior to the onset of winter. Family-level survival was calculated as the proportion of living individuals to the total number of individuals present within a given family.

Irrigation and Drought Treatments

From May-November, 2017, 2018, and 2019, we irrigated all boxes and implemented a non-lethal drought treatment at all three common gardens. The goal of this drought treatment was to stress seedlings without killing them. We provided irrigation on a bi-weekly basis for the same amount of time at each garden (1.5 hours for non-drought boxes, 45 minutes for drought boxes). This equated to 56 mm

of water every watering in the non-drought treatment, and 28 mm of water for the drought treatment (Table 2). The drought treatment encompassed half the planted boxes, 20 out of 40 boxes total at each garden (n=120 total across gardens). Drought treatments included both a reduction by 50% of irrigation received in non-drought boxes, with an additional reduction of 49% of ambient precipitation by rain-out shelters. Design of the rain-out shelters followed the design of Yahdjian and Sala (2000). Each shelter was 86 cm tall at one end, and 56 cm tall at the other, to create a water drainage slope. Five V-shaped plastic gutters, spaced at 23 cm intervals, were installed over each box (E-plastics, San Diego, CA). Gardens were winterized in November of each year and rain-out shelters removed and stored. This study used foliage formed during the 2017 and 2018 growing seasons for all tissue samples collected (described below), with data collected during the 2018 and 2019 field seasons.

Leaf Mass per Area Measurement

During the summer of 2019, we collected foliage and calculated leaf mass per area (LMA). LMA data were used to address research questions 1 and 2 because this trait addresses the leaf-building economic trade-off (Westoby et al. 2002). Three fascicles formed during the 2018 growing season drought treatment period were randomly sampled from each individual in our subsample, transported on ice in a cooler, and stored in a 2ºC refrigerator until analyses. Individual fascicles were disarticulated into all needle components, placed on a flat-bed scanner (Epson 4990) and surface area estimated using WinFolia PRO (2006; Regent Instruments Inc.). Samples were then oven dried at 65°C for 72 hours before weighing on an Explorer analytical balance (Ohaus Corp, Switzerland). Leaf area was converted from cm^2 to m^2 and leaf mass (g) was then divided by leaf area for each individual fascicle to determine LMA. After calculation, data were averaged to the individual seedling level, and then to the population level for further analyses.

Carbon and Nitrogen Isotope Ratio

At the completion of the 2018 growing season, we collected current-year fascicles from all selected individuals for measurement of leaf carbon isotope ratio ($\delta^{13}C$) and percent nitrogen concentration (%N). $\delta^{13}C$ is related to leaf intracellular CO_2 concentration, which is regulated by stomatal conductance and carboxylation efficiency (e.g. Farquhar et al. 1989; research questions 1 and 2), and %N is related to maximum carboxylation efficiency (e.g. Wong et al. 1985). Collected fascicles were placed in labeled envelopes and dried in a JUMO DTRON 308 drying oven at 65°C for 72 hours. Foliage from each sample was combined in 2 mL conical microcentrifuge tubes with five 2.3 mm stainless steel balls and ground to an even consistency in a 2000 Geno Grinder (SPEX Sample Prep, NJ, USA) for 3 minutes at 1500 rpm. We packaged samples in 6 x 4 mm pressed tin capsules (Elemental Microanalysis Inc, UK) for isotopic measurement at the Colorado Plateau Stable Isotopes Lab (CPSIL-NAU). Samples were processed on a Thermo-Electron Delta V Advantage IRMS. This equipment is configured through a Finnigan CONFLO III for automated continuous-flow analysis of $\delta^{13}C$ and %N using a Carlo Erba NC2100 elemental analyzer for combustion and separation of carbon and nitrogen. We then calculated carbon isotope discrimination ($\Delta^{13}C$) from $\delta^{13}C$ using equation 1 (Farquhar et al. 1989).

$$\frac{-0.008 + (\frac{\delta^{13}C}{-1000})}{1 - (\frac{\delta^{13}C}{-1000})} \times 1000 \quad \textbf{(1)}$$

Where $\delta^{13}C$ represents the isotopic ratio of ^{13}C in needle tissues, and -0.008 is an approximation of the $\delta^{13}C$ of atmospheric CO_2, compared to the standard pee-dee belemnite.

Predawn and Midday Water Potentials

Between mid-June and early July 2018, we measured xylem water potential on fully-developed foliage formed during the previous year (2017), before dawn and at midday. For predawn measurements, we started between 2:30-3:30am, and removed whole fascicles by cutting with a razor close to the stem. After removal, samples were wrapped in aluminum foil and placed in a bag with damp paper towels and stored on ice in a shaded cooler. This method is appropriate for sample storage to minimize water potential variation prior to testing (Kaufmann and Thor (1982). A total of 90-100 samples were measured each day (n=9-15 per population per treatment, 18-30 total per population per garden). After all samples were collected, water potential of fascicles was measured using a PMS Pressure Chamber (PMS Instruments, Corvallis, OR) following the protocol of Scholander et al. (1965). This process was repeated starting between 12:30-13:30 for midday water potential measurements. Measurements took approximately 2 hours for each measurement period.

Determination of Sigma and Hydroscape Area

To address research question 1, we calculated sigma (Martinez-Vilalta et al. 2014) and hydroscape area (Meinzer et al. 2016) based on the regression between predawn and midday water potentials. Sigma represents the difference between soil water potential and leaf water potential, where sigma values between 0 and 1 indicate a reduction in the difference between soil and leaf water potential as soil water potential decreases (Martinez-Vilalta et al. 2014).We calculated sigma for each treatment at each garden. We fit a linear model using midday water potential as our response with the three-way interaction between garden, treatment, and predawn water potential to test whether slopes between predawn and midday water potentials were different across treatments and gardens (alpha=0.05).

We calculated hydroscape area following the methods of Meinzer et al. (2016). Hydroscape area represents the potential range of water potentials in which a species operates, and its magnitude reflects the continuum between isohydry and anisohydry (Meinzer et al. 2016). We determined the most negative values of predawn and midday water potentials, with special emphasis placed on determining the water potential at which stomates do not open ($\Psi_{Predawn}=\Psi_{Midday}$), and then removed all less-negative values. For our sampled seedlings, this occurred between -1.8 MPa and -2.2 MPa. We then fit a regression between predawn and midday water potential and iteratively added in less negative values of water potential measurements. At the point where the r^2 was maximized, we took the intercept of the regression line. We fit a 1:1 line and calculated the area between the 1:1 line and the regression line as the hydroscape area.

Data Analysis

In order to address our first research question and hypothesized isohydric behavior, we used linear-mixed effects models to test the impact of the two-way interaction between garden and treatment on traits. In these models, garden and treatment were treated as fixed effects, while population, family-within-population, sow year and planting location were random effects. We used the rand() function in package lmtest to approximate the significance of family-within population variance and population variance on our response variables. We used package emmeans to conduct posthoc tests across levels of garden and treatment with a Tukey adjustment to the p-value. QQ-plots revealed that residuals were normally distrusted for each model. All model testing was conducted within the R statistical software platform (v. 3.4.2 R Core Development Team, 2019).

To address our second research question, we calculated the heritability of each trait by subsetting our data by treatment to determine variance components attributable to family-within population and population. Each measured trait ($\Delta^{13}C$ and LMA) was analyzed separately. Family-narrow sense heritability was calculated as $\sigma^2_w/\sigma^2_{Total}$ where σ^2_w is estimated as 3*within-family variance, and σ^2_{Total} represents the total phenotypic variance for each of our measured traits (Lynch and Walsh 1998). We used 3 as our multiplier for within-family variance instead of 4, as the seedlings from a common maternal tree likely were a mixture of half-sibs and full-sibs, and 3 has been shown to be a better estimate of the degree of mixing of open-pollinated maternal sources (e.g. Bower and Aitken 2008).

We assessed the relationship between treatment differential and survival of maternal families at each garden. We hypothesized that increased survival would be related to higher treatment differential in $\Delta^{13}C$ ($\Delta^{13}C_{ND-D}$; where ND=Non-Drought Treatment and D=Drought Treatment) and a lower treatment differential for LMA (LMA_{ND-D}). Increased $\Delta^{13}C_{ND-D}$ indicated a greater decrease in carbon isotope discrimination between the two treatments and therefore increased incorporation of ^{13}C into foliar tissues. Increased LMA_{ND-D} reflected the same change with LMA between the same non-droughted and droughted families. Following the methods of Goodrich et al. (2016), we calculated the treatment differential for an individual family at an individual garden by subtracting the family-average trait value in the drought treatment from the value in the non-drought treatment. We calculated the average trait value for each family (n=44) at each garden (n=3) and combined this data with the individual survival data for all members of these families (both selected individuals and non-selected individuals) at each garden in binary format (1,0). We then used a generalized linear mixed model (package glmmTMB), with a binomial distribution, and assessed survival and the two-way interaction between garden and treatment differential value. We considered treatment differential and garden as fixed effects, while population, family within population, sow year and planted positioning variables were random effects. All model testing was conducted within the R statistical software platform (v. 3.4.2 R Core Development Team, 2019).

Data Provenance

(Were these data derived from other data? If so, you will want to document this information so users know where these data came from. Please specify the source datasets used in the below **provenance table**, preferably with their DOI or URL. An example of a dataset derived from several others is here.)

Dataset title	Dataset DOI or URL	Creator (name & email)	Contact (name & email)

Data Table

(Provide a Table Name and Table Description. Each row in the below table describes one column in your data table. Complete each row as follows:

- **Column name**: This name must be exactly as it appears in the dataset. Please avoid special characters (like & or \), dashes and spaces. Underscores are permissible. Do not begin a column name with a number.
- **Description**: Please give a specific definition of the column name. This can be lengthy.
- **Unit:** Identify units for all numeric variables. Please avoid special characters and describe units in this pattern: e.g. microSiemenPerCentimeter, microgramsPerLiter, absorptionPerMolePerCentimeter
- **Code explanation**: If you use codes in your column, please explain in this way: e.g., LR=Little Rock Lake, A=Sample suspect, J=Nonstandard routine followed
- **Date format**: Please tell us exactly how the date and time is formatted: e.g. mm/dd/yyyy hh:mm:ss plus the time zone and whether or not daylight savings was observed. ISO date format of YYYY-MM-DD or YYYY-MM-DD hh:mm:ss is preferred.
- **Missing value code**: If a code for 'no data' is used, please specify: e.g., -99999

Table name: Predawn, LMA, Carbon Isotope Database
Table description: All data included in above analysis of carbon isotope discrimination, leaf mass per area and predawn and midday water potential measurements taken at common gardens.

Column name	Description	Unit or code explanation or date format	Missing value code
Tree_ID	Concatenation of population abbreviation and maternal tree number (IE: MUS299, MUS is the population, 299 is the maternal tree)	NA	No missing values
Garden_Tag	unique aluminum tag given to each individual seedling planted at our gardens	NA	No missing values
Site_Code	2, 3 or 4 letter abbreviation of the population name (ie GUMO=Guadalupe Mountains)	NA	No missing values
Family	numerical designation of maternal tree, all progeny derived from a single maternal tree are considered a family	NA	No missing values
Garden_Planted_Date	Date on which individual seedling was planted in one of 3 common gardens	MonthDayYear	No missing values
Garden	Garden in which individual seedling is planted (WP=white	NA	No missing values

	pockets, LM=little mountain, BS=bear springs)		
Box	Box (1-75) at garden in which tree is planted	NA	No missing values
Row	Row (1-10) in box in which seedling is planted	NA	No missing values
Position_in_Row	Position (1-10) in row in box in which seedling is planted	NA	No missing values
Treatment	Drought (L) or nondrought (H) treatment, treatments implemented in May 2018 on half the boxes at each garden	NA	No missing values
SY	Sow year (2015, 2016 or 2017)	year	No missing values
PDWP	Predawn Water Potential (Mpa)	megapascal	NA
MDWP	Midday Water Potential (Mpa)	megapascal	NA
Difference	difference between MDWP and PDWP	megapascal	NA
PD_Coll_Time	Time at which predawn water potential data collected	hour	NA
MD_Coll_Time	time at which midday water potential data collected	hour	NA
PDMD_Meas_Date	Date on which predawn and midday water potentials collected	MonthDayYear	NA
Height_SP18	Spring 2018 Height (cm)	centimeter	NA
DRC_SP18	Spring 2018 Diameter at root collar (DRC) (mm)	millimeter	NA
Phenology_SP18	Bud burst score given in the spring of 2018	0= dormant, 1=thickening, 2=elongating, 3=needle formation, 4= advanced needle formation, 5= fully formed needles	NA
Status_SP18	alive=1, dead=0 status as of spring 2018	NA	NA
SP18_MeasDate	Measurement date on which height, DRC and phenology were collected	MonthDayYear	NA
Mass (mg)	Ground foliage tissue sample mass (mg)	gram	NA
d13C	Carbon isotope ratio (per mille)	per mille	NA

d15N	Nitrogen isotope ratio (per mille)	per mille	NA
%C	% carbon contained within sample	percent	NA
%N	% nitrogen contained within sample	percent	NA
C/N ratio	carbon/nitrogen ratio	percent ratio	NA
CID	Carbon isotope discrimination (calculated from carbon isotope ratio)	per mille	NA
F1.Area (sq.m)	Fascicle 1 foliage leaf area in square meters	squareMeter	NA
F2.area (sq.m)	Fascicle 2 foliage leaf area in square meters	squareMeter	NA
F3.area(sq.m)	Fascicle 3 foliage leaf area in square meters	squareMeter	NA
F1.Area(sq.cm)	Fascicle 1 foliage leaf area in square cm	squareCentimeter	NA
F2.Area (sq.cm)	Fascicle 2 foliage leaf area in square cm	squareCentimeter	NA
F3.Area (sq.cm)	Fascicle 3 foliage leaf area in square cm	squareCentimeter	NA
F1.Dry.Weight	Fascicle 1 dry weight (g)	gram	NA
F2.Dry.Weight	Fascicle 2 dry weight (g)	gram	NA
F3.Dry.Weight	Fascicle 3 dry weight (g)	gram	NA
F1.SLA	Fascicle 1 specific leaf area (leaf area/mass)	squareMeterpergram	NA
F2.SLA	Fascicle 2 specific leaf area (leaf area/mass)	squareMeterpergram	NA
F3.SLA	Fascicle 3 specific leaf area (leaf area/mass)	squareMeterpergram	NA
AVG.IND.SLA	Average of 3 fascicles specific leaf area for an individual seedling	squareMeterpergram	NA
F1.LMA	Fascicle 1 leaf mass per area (1/SLA) (g/sq. m)	grampersquareMeter	NA
F2.LMA	Fascicle 2 leaf mass per area (1/SLA) (g/sq.m)	grampersquareMeter	NA
F3.LMA	Fascicle 3 leaf mass per area (1/SLA) (g/sq. m)	grampersquareMeter	NA

AVGLMA	Average of 3 fascicles leaf mass per area for an individual seedling	grampersquareMeter	NA

(Copy this table to document more than one data table.)

Table name: (A short name for this table)
Table description: (Add brief description of table contents)

Column name	Description	Unit or code explanation or date format	Missing value code
Tree_ID	Concatenation of 3-Letter Population and Maternal Tree ID (number)	NA	NA
Garden_Tag	Unique aluminum tag given to each individual planted at North Rim Gardens	NA	NA
GH_ID	Original unique ID number given to each individual sown in greenhouse	NA	NA
Epi_GH_ID	Original unique ID number given to each individual sown in greenhouse for epigen trees	NA	NA
GH_Transplant_ID	Unique ID number with a -2 or -3 to signify that the new individual in the greenhouse cell is from a cell wherein multiple germinants emerged	NA	NA
Epi_GH_Transplant_ID	Unique ID number to signify that the new individual in the greenhouse cell is from a cell wherein multiple germinants emerged for epigen trees	NA	NA
Population	Three or Four letter code abbreviating population name	NA	NA
Family	Maternal tree number	NA	NA
Epi_Trt	Epigenetic treatment (bubble=b, control=C, no epigen treatment=NA)	NA	NA
Germ_Boost_Plant_Date	Germ boost was conducted to increase certain family numbers, this date signifies when a germinated seed was put into empty cell belonging to same family	MonthDayYear	NA

Assigned_Site	assigned common garden (assignments made when trees were still in greenhoouse) (WP=White Pockets, LM=Little Mountain, BS=Bear Springs)	NA	NA
Rep_w_in_Fam	up to 25 individuals/garden (75 total) sown, this keeps track on which rep this individual comprised	NA	NA
GH_Planter	Planter number in which seeds were sown in the greenhouse	NA	NA
GH_Planter_Slot	Planter slot number (1-40) in which seeds were originally sown in the greenhouse	NA	NA
Germination	1=germinant present, 0=none present, tracking gerrmination through time in the greenhouse	NA	NA
GH_Transplant_planter_1	Planter from which a transplant was pulled	NA	NA
GH_Transplant_Planter_Slot_1	Planter slot from which a transplant was pulled	NA	NA
Orig_ID_1	original ID of transplant	NA	NA
GH_Transplant_ID_1	New ID created when transplant occurred	NA	NA
GH_Transplant_Date_1	date on which transplant occurred	NA	NA
Site_Planted_Date	Date on which seedling was planted at garden	MonthDayYear	NA
Site	Common Garden location (see assigned site for abbreviations)	NA	NA
Fall17_Status	Status (1=alive, 0=dead) at mortality census in the Fall of 2017	NA	NA
SY	SY to which this seedling belongs (2015, 2016 or 2017)	NA	NA
Garden	Garden site in which the tree is planted	NA	NA
Garden_Tag2	duplicate of garden tag (see above)	NA	NA
Box	Box at garden (1-75) in which seedling is planted	NA	NA
Row	Row within box (1-10) in which seedling is planted	NA	NA
Position_in_Row	Position within row (1-10) in which seedling is planted	NA	NA

Edge	seedlings are either edge trees (E) or interior (I)	NA	NA
Treatment	drought (L) or non-drought (H) treatment on box	NA	NA
SP18_Height	Height as recorded in the Spring of 2018	centimeter	NA
SP18_DRC	Diameter at root collar (DRC) as recorded in the Spring of 2018	millimeter	NA
SP18_Phen1	Phenology (bud burst) as recorded in the spring of 2018	NA	NA
SP18_Status	Alive=1, dead=0 status recorded in the Spring of 2018	NA	NA
SP18_Meas_Date	Measurement date on which above spring 2018 measurements were recorded	MonthDayYear	NA
SP18_phen2	second phenology measurement in the spring of 2018	NA	NA
SP18_phen2Status	Status (1=alive, 0=dead) at the second phenology census in the spring of 2018	NA	NA
SP18_phen2_meas_date	Date on which second phenology and status measurements taken	MonthDayYear	NA
F18_MeasDate	date on which fall 2018 measurements were recorded on an individual seedling	MonthDayYear	NA
F18_Status	Status (1=alive, 0=dead) at mortality census in the Fall of 2018	NA	NA
F18_Height	Height as recorded in the Fall of 2018	centimeter	NA
F18_DRC	Diameter at root collar (DRC) as recorded in the Fall of 2018	millimeter	NA
F18_Budscore	budscore as recorded in the fall of 2018	NA	NA
F18_Lammas	lammas growth present? (1=yes, NA=no)	NA	NA
F18_Browning	Browning of over 50% foliage=1, NA=no	NA	NA
F18_Clipped	Is tree clipped? 1=yes, NA=no	NA	NA
F18_Chlorotic	Is tree chlorotic? 1=yes, NA=no	NA	NA
HLCID	Family value for the change in carbon isotope discrimination (as derived	permille	NA

	from carbon isotope ratio) between individuals of that family measured in the non-drought treatment minus individuals of that family measured in the drought treatment		
HLLMA	family value for the change in leaf mass per area (LMA) between individuals of that family measured in the non-drought treatment minus individuals of that family measured in the drought treatment	gramspersquaremeter	NA
HLd13C	Family value for the change in carbon isotope ratio between individuals of that family measured in the non-drought treatment minus individuals of that family measured in the drought treatment	permille	NA
HLd15N	Family value for the change in nitrogen isotope ratio between individuals of that family measured in the non-drought treatment minus individuals of that family measured in the drought treatment	permille	NA

(Copy this table to document more than one data table.)

Spatial data objects

(List any geospatial data objects you would like to archive. Organize spatial data into .zip directories and describe each.)

Directory name: (A short name for the data)
Directory description: (A brief description of the data)

Attribute	Value
Horizontal Coordinate System Name (e.g. WGS_1984_UTM_Zone_12N)	
Horizontal Accuracy Report	
Vertical Accuracy Report	
Cell Size X Direction	
Cell Size Y Direction	
Raster Origin (e.g. Upper Left)	
Number of Rows	

Number of Columns	
Number of Verticals	
Cell Geometry (e.g. pixel)	

Scripts/code (software)

(List any software scripts/code you would like to archive along with your data. These may include processing scripts you wrote to create, clean, or analyze the data.)

File name	Description	Scripting language

Other objects (misc.)

(List any other objects (e.g. .zip, .pdf, etc.) you would like to archive.

File name	Description	Data type

Articles

(List articles citing this dataset)

Article DOI or URL (DOI is preferred)	Article title	Journal title
https://cdnsciencepub.com/doi/10.1139/cjfr-2019-0423	Water Relations and Drought Response of Pinus strobiformis	Canadian Journal of Forest Research

Notes and Comments