Table S1. Experimental design for drought stress trials in bigbags in a polytunnel (52°23′55″ N 13°3′56″ E). Trial-Id = Trial-Identifier. Culture Id = experiment reference Id in the plant database (Köhl *et al.* 2008). Four treatments per experiment. n = number of replicate plants per treatment. Plantd = date of planting. Treat1 = start of drought stress treatment SS , Treatd2 = start of treatment SC, Treatd3 start of treatment CS, Harvestd = date of haulm destruction.

Trial_id	culture_id	n	Plantd	Treatd1	Treatd2	Treatd3	Harvestd
B2017	81251	8	11.04.2017	05.05.2017	05.05.2017	25.05.2017	21.07.2017
B2018	85178	8	17.04.2018	08.05.2018	08.05.2018	24.05.2018	08.07.2018
B2019	88022	6	02.05.2019	24.05.2019	24.05.2019	15.06.2019	26.07.2019

Table S2. Pedigree for lines that were used in phenotyping experiments B2017 to B2019. Plant line reference Id in the MPI-MP plant database (Köhl et al. 2008) (Sample_id), Genotype name of the crossings and cultivar names

Sample_id	Genotype name
899486	Albatros x Ramses 23
899519	Albatros x Ramses 56
899522	Albatros x Ramses 59
899665	Albatros x Ramses 202
899748	Albatros x Ramses 285
899822	Euroresa x Albatros 62
899831	Euroresa x Albatros 71
899834	Euroresa x Albatros 74
899922	Euroresa x Albatros 162
900024	Euroresa x Albatros 264
22497	Desirée
858638	Priamos
858641	Ramses
866296	Albatros
866303	Pirol
866306	Maxi
866309	Karlena
869004	Euroresa
872474	Eldena
872477	Eurostarch

Table S3. QC for laser scanner measurements. Measurement period, interruptions (break) due to power outage and QC criteria that lead to the exclusion of observation. Days 30 and 23 were excluded in 2018 as data were collected only for part of the diurnal cycle.

Year	**2017**	**2018**	**2019**
Start	27.04.2017	08.05.2018	10.05.2019
Stop	23.06.2018	29.06.2018	30.06.2019
Breaks		1.6.2018 - 4.6.2018	
Exclude observation if	PH outside 3SD range	PH outside 3SD range	PH outside of 2SD range
	LPD < 5	LPD < 5	LPD < 5
	LA < 40	LA < 25	DFP > 59
	DFP < 30 and PH > 500	LA > 60	
	DFP < 21	DFP = 30	
		DFP = 23	

Table S4. Result of an ANOVA on the effect of genotype (G), treatment interval (I), the diurnal time interval classtime (CT), treatment (E) and their interaction on leaf angle (LA), leaf inclination (LI) and light penetration depth (LPD). Bold: p< 0.001.

		Year		
Feature	**Independet variable**	**2017**	**2018**	**2019**
LA	Genotype (G)	**432.2**	**413.7**	**62.7**
	Interval (I)	**3216.5**	**259.8**	**12519.7**
	Classtime (CT)	**11.6**	**616.7**	**165.9**
	Treatment (E)	**7.7**	**3696.0**	**36.3**
	I x E	**106.7**	**3315.6**	**281.8**
	I x CT	**455.4**	**14.8**	**62.3**
	CT x E	**16.2**	**17.2**	**23.6**
LI	Genotype (G)	**556.3**	**378.1**	**54.0**
	Interval (I)	**1241.9**	**719.8**	**12149.4**
	Classtime (CT)	**15.2**	**627.7**	**172.2**
	Treatment (E)	**25.8**	**3838.7**	**26.7**
	I x E	**555.7**	**3567.3**	**290.5**
	I x CT	**83.9**	**12.2**	**77.7**
	CT x E	**19.6**	**17.2**	**20.6**
LPD	Genotype (G)	**1333.0**	**515.8**	**143.6**
	Interval (I)	**27392.6**	**84528.5**	**38245.9**
	Classtime (CT)	1.5	**73.6**	**166.7**
	Treatment (E)	**36.2**	**1751.9**	**169.1**
	I x E	**392.4**	**1192.9**	**364.6**
	I x CT	**16.8**	**25.1**	**10.9**
	CT x E	2.2	2.2	**4.2**

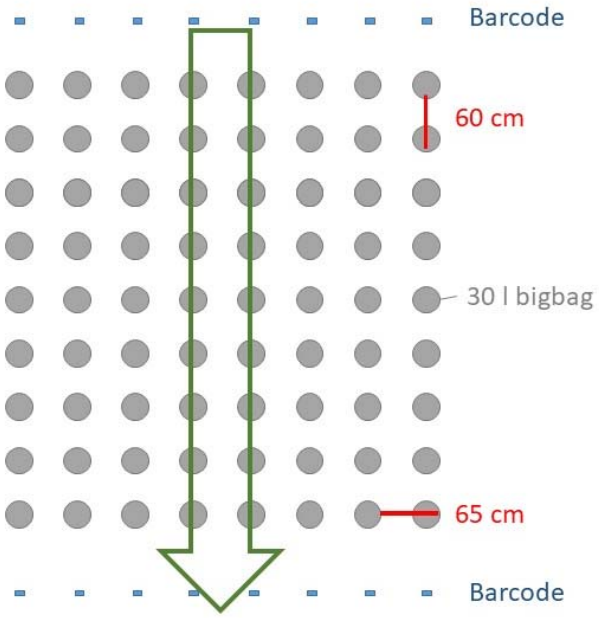


Figure S1. Spatial design of the bigbag system that was used for phenotyping potato genotypes. The image shows one of eight subplots that consist of eight columns (left to right) and nine rows. Each column in a subplot is identified by the barcodes at the beginning and end of the column. Each treatment block consisted of two of these subplots. The green arrow indicates the direction, in which the laser scanner is moved.

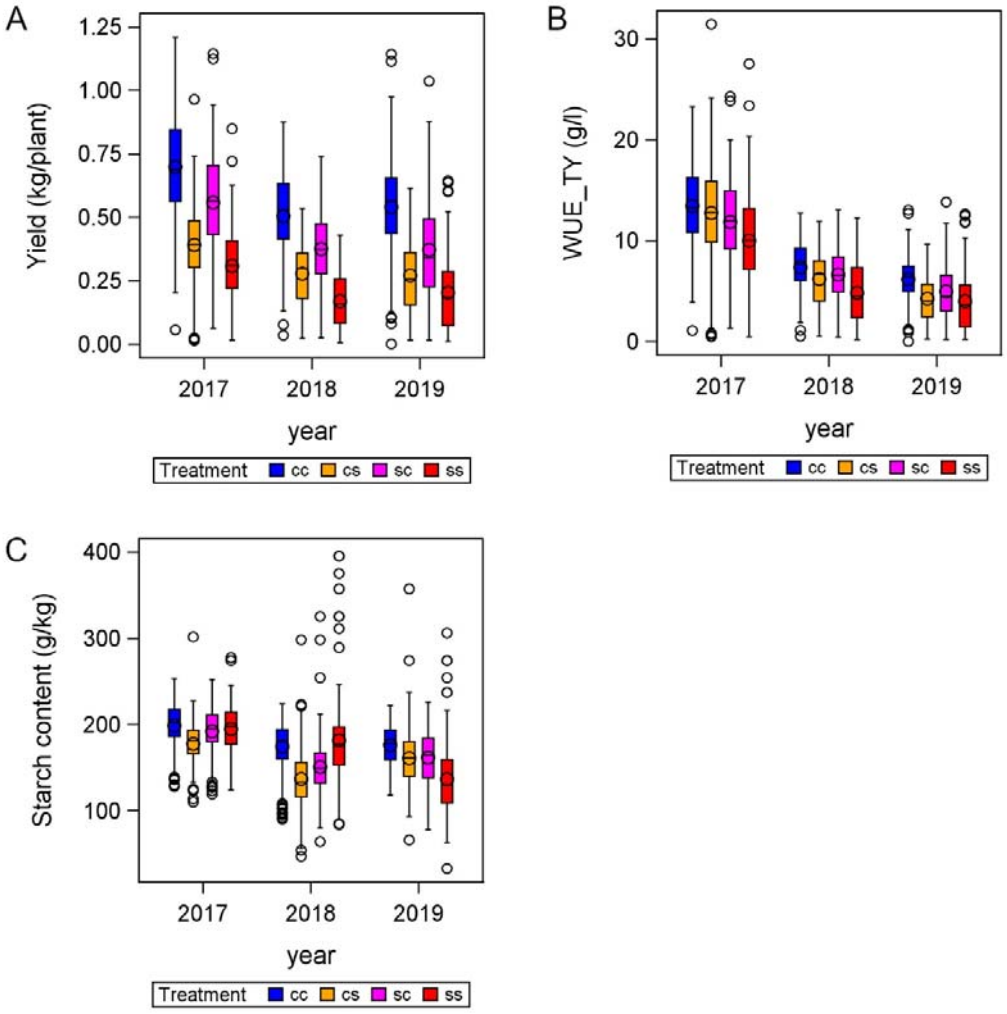


Figure S2. (A) Distribution of tuber fresh weight per plant in 20 potato genotypes cultivated at optimal water supply (cc), late drought (cs), early drought (sc) and long-term drought in experiments 2017, 2018 and 2019. (B) Distribution of water use efficiency of tuber fresh weight yield in 20 potato genotypes cultivated in different water regimes (see A). (C) Distribution of tuber starch content in 20 potato cultivars grown at different water regimes (see A). Result of ANOVA see table 1.

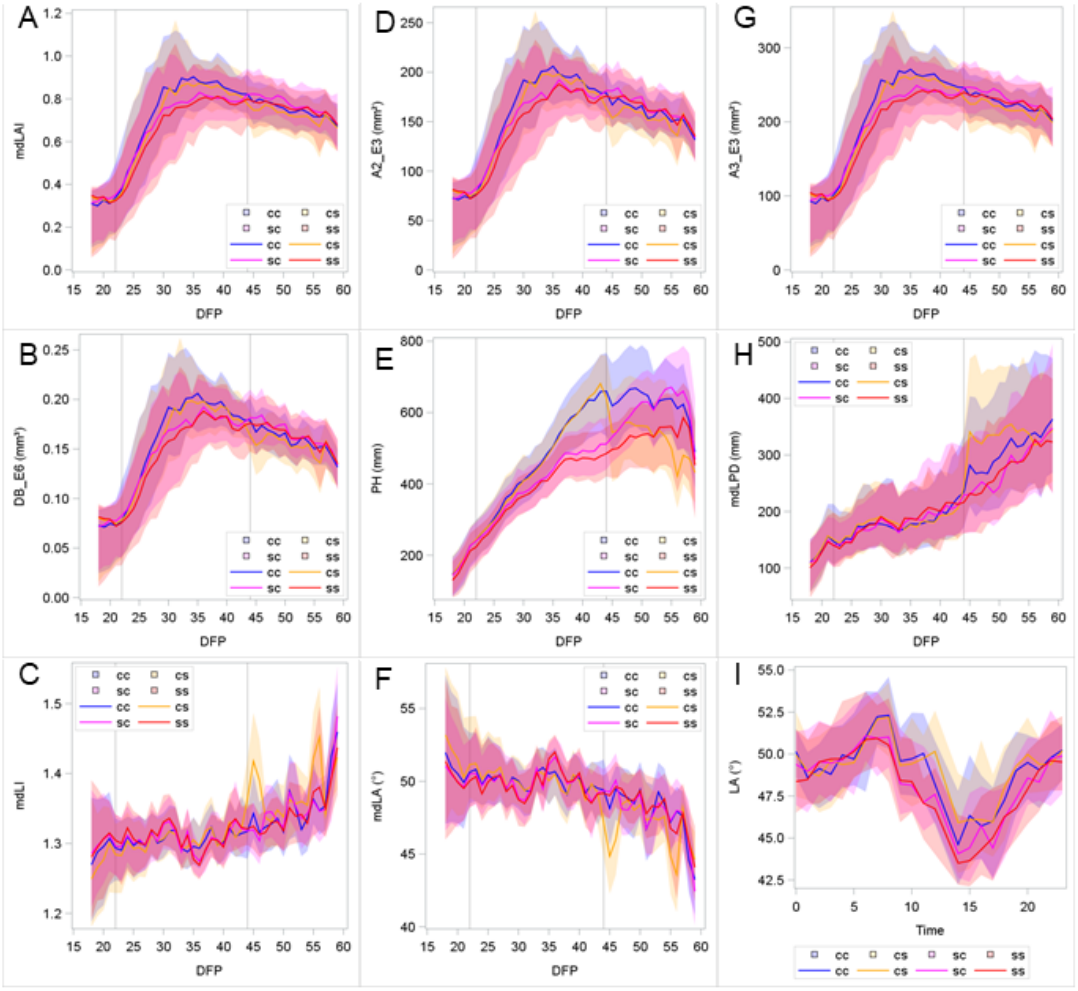


Figure S3. Effect of plant age, treatment and treatment interval on phenotypic features. Distribution of daily genotypic median of (A) leaf area index (mdLAI), (D)projected leaf area (mdA2_E3 = mdA2/10^3), (G)
leaf area (mdA3_E3 = mdA3/10^3), (B) digital biomass (mdDB_E6 = mdDB/10^6), (E) plant height (mdPH), (H) light penetration depth (mdLPD), (C) leaf inclination (mdLI) and (F) leaf angle (mdLA) is plotted against plant age (DFP) for the experiment 2019. The left reference line in image A to H indicates the start of the first treatment interval (phase 2), the right reference line the start of the second treatment interval (phase 3). Image (I) shows the diurnal course of the leaf angle distribution for day 31. The line plot indicates the median, the shaded area between percentile10 and percentile90.

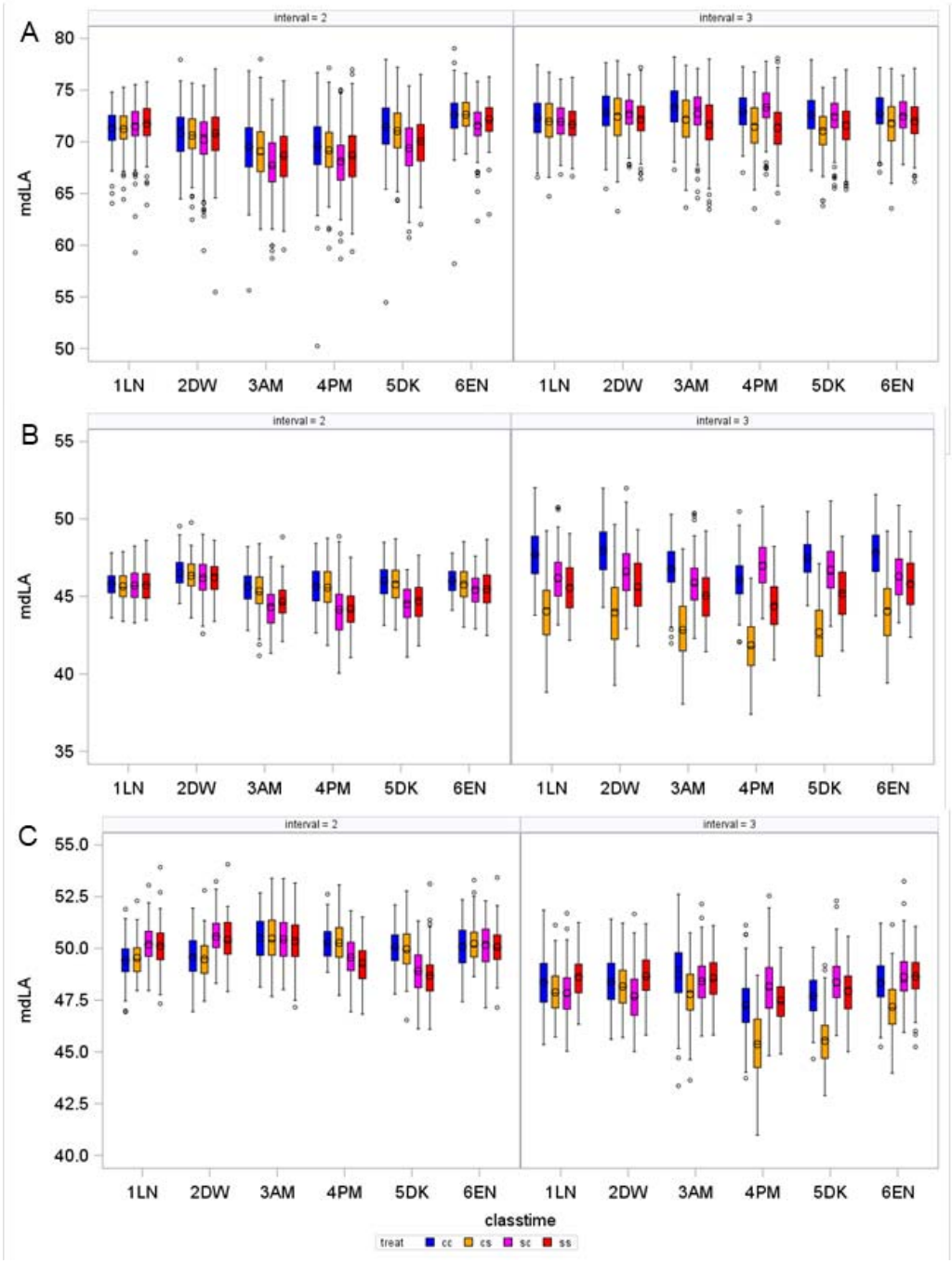


Figure S4. Distribution of genotypic median of leaf angles in different diurnal time classes (classtime CT). Interval 2 is the first treatment period before flowering, interval 3 the second treatment period after flowering. (A) experiment 2017, (B) experiment 2018, (C) experiment 2019. The box indicates the interquartile range IQR, the whiskers the mean and +/- 1.5 IQR.

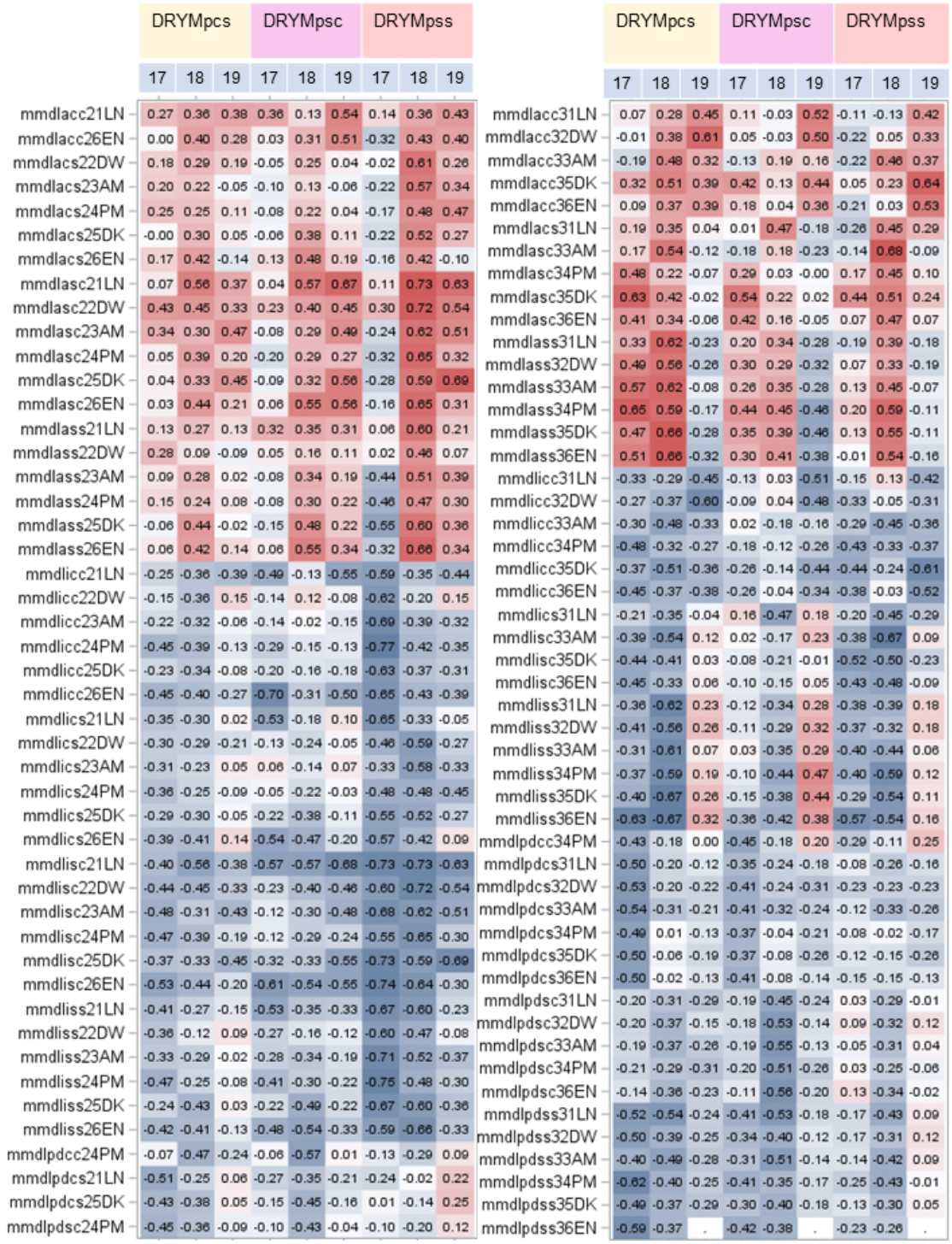
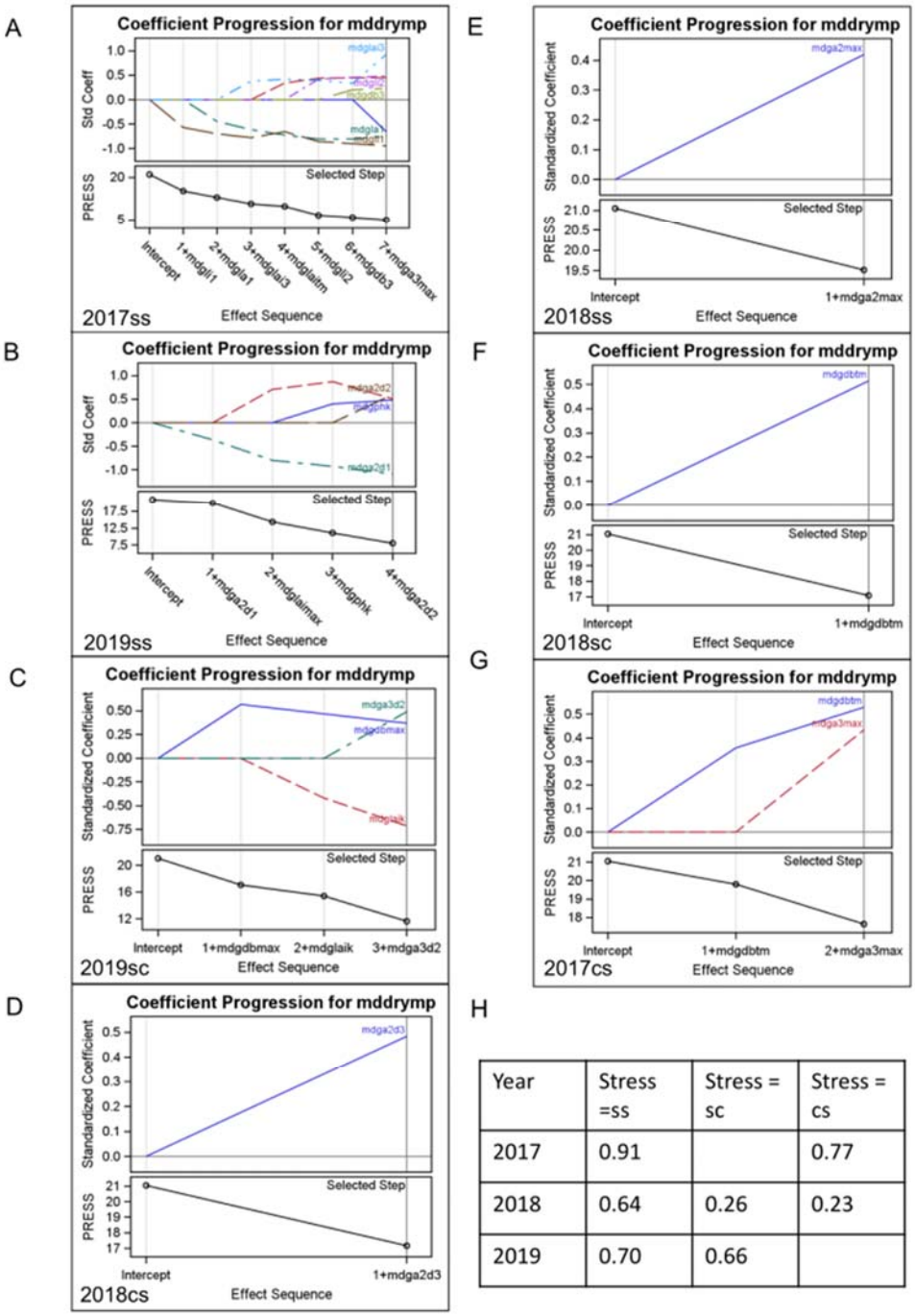


Figure S5. Correlation between leaf position parameters measured before (left) and after (right) flowering and drought tolerance index for late (DRYMpcs), early (DRYMpsc) and long-term stress (DRYMpss). The tolerance index was determined from all three experiments. The number below the DRYMp value indicates the year, in which the phenotyping was performed. Only those variables are shown, for which at least one correlation was significant.



Year	Stress =ss	Stress = sc	Stress = cs
2017	0.91		0.77
2018	0.64	0.26	0.23
2019	0.70	0.66	

Figure S6. Fixed model prediction of drought tolerance from regression parameters and phenotypes measured on fixed single day. Tolerance and phenotype measured under the same stress scenario. Long-term stress tolerance (A, B, E), early stress (C, F), late stress (D, G). R^2 values in section (H).

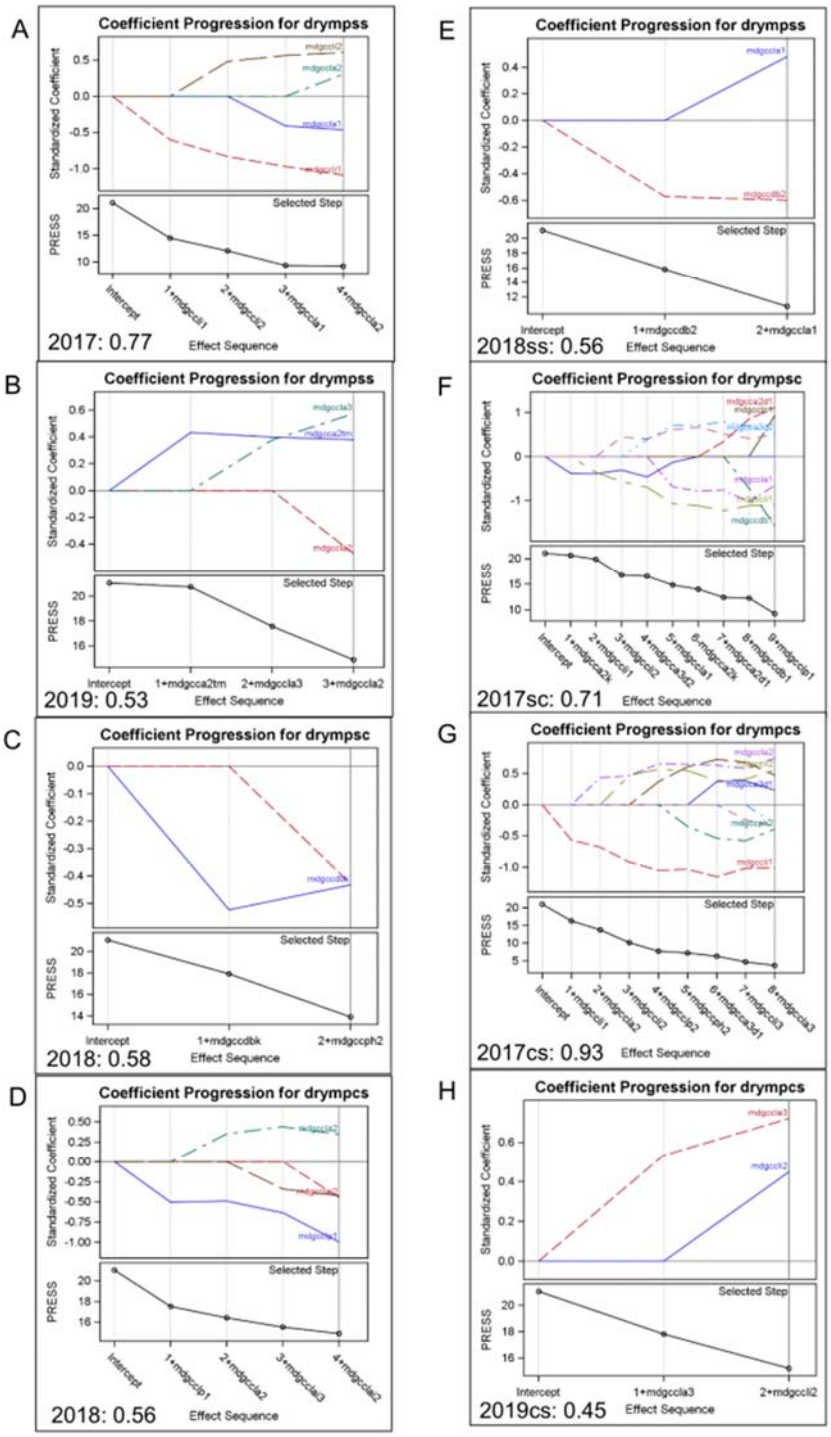


Figure S7. Fixed model prediction of drought tolerance from regression parameters and phenotypes measured on fixed single day. Phenotypes were measured under optimal water supply. Inset legend: First four digits indicate year of phenotyping, decimal number indicates R^2. No significant model was found for the prediction of early stress tolerance from 2019 data.