

Supplementary methods

1. Colchicine treatment

We exposed 50-100 plants of each strain to a polyploidisation mixture consisting of Hoagland's E medium (Cross 2002) supplemented with 0.7% colchicine and 0.5% DMSO under a 16-8 light-dark light regime at $40-45 \mu\text{mol m}^{-2} \text{s}^{-1}$ PPFD and 24 °C. After 24 hours, all fronds were washed in ddH₂O to remove the colchicine before transferring them to regular medium for recovery. The ploidy of the strains was determined using flow cytometry, three to five weeks following colchicine treatment.

2. Growth rate

Half of the twelve samples for growth rate assessment were transferred to a new box containing 100 ml of fresh medium to start each of our six replicates. The other half were used for dry and fresh weight measurements (see below). All boxes were photographed at a fixed height, using bottom illumination and a Canon (Tokyo, Japan) EOS 550D combined with a Canon 24mm F/2.8 EF objective (gradient 1 and 2) or a Canon EOS 850D combined with a Canon 24mm F/2.8 EF-S objective (gradient 3). After 7 days of growth, all boxes were photographed again, the material was spread over an absorbent paper towel to remove excess medium before assessing fresh weight and transferring it to a paper bag for drying at 60 °C. After 72 hours the bags were emptied, and the dry weight was determined. Frond number, and percentage coverage were extracted from the pictures using the LemnaTec (Aachen, Germany) LemnaGrid software. Subsequently, fresh weight (fw), dry weight (dw), frond number (fn), and covered surface area (sa), were used to calculate the relative growth rate (RGR) assuming exponential growth i.e., $\text{RGR} = (\ln P_1 - \ln P_0)/(t_1 - t_0)$, where P₁ and P₀ represent the population size and t₁ and t₀ the corresponding points in time.

3. Photosynthetic parameters

All boxes were dark-adapted for approximately 20 minutes, placed under a measuring light to assess their minimum fluorescence yield with all PS II centres open (F_0) and exposed to a saturating light pulse to measure the maximum fluorescence yield of the dark-adapted samples with all PS II centres closed (F_m). This allowed us to calculate the maximum quantum efficiency of PSII photochemistry ($F_v/F_m = (F_m - F_0)/F_m$). After approximately 30 minutes of light adaptation, we measured the fluorescence yield of the light adapted samples before (F) and after exposure to another saturating pulse closing all PS II reaction centres (F'_m), allowing to estimate the amount of non-photochemical quenching ($NPQ = (F_m - F'_m)/F'_m$) and the PS II operating efficiency ($Y_{II} = (F'_m - F)/F'_m$) (Murchie and Lawson 2013).

4. Microscopy

For each line, four plants were immersed in 70 % ethanol solution, heated for five minutes at 80 °C, washed for two minutes in fresh 70% ethanol solution, transferred to 10% bleach solution to remove any remaining pigmentation, and washed twice in demineralised water to remove all remaining ethanol and bleach. Stomatal features were examined and photographed using an Olympus (Tokyo, Japan) BX51 microscope equipped with an Olympus UplanFLN 40x/0.75na and UplanFLN 20x/0.50na objective. Stomatal density was determined by counting the number of stomata in twelve different fields (for each of the four plants) at a magnification of 20x, captured using a Toupcam (TouTek, Hangzhou, China) camera. The length and width of at least 25 stomata were measured on microphotographs taken with the same camera at 40X magnification using ImageJ.

5. Pigment quantification

100 mg of fresh duckweed tissue was washed and immersed in 90% (v/v) MeOH and stored for 48 hours in the dark at 4°C. Subsequently, plant material was removed by 10 minutes of centrifugation at 3000 rpm. The supernatant's absorbance at 663nm, 647nm, and 470nm was determined using a Thermo Fisher (Waltham, US), Genesys 10S UV-VIS spectrophotometer to estimate chlorophyll a (chl a), chlorophyll b (chl b), and carotenoid (car) content using the formulas of Lichtenthaler (1987). Anthocyanin (AC) content was assessed using the method of Mancinelli (1975). 100 mg of fresh plant material was grinded using a bead beater, immersed in 1.5 ml acidified methanol (99 ml methanol: 1 ml HCl) and shaken for 15 mins. The plant material was removed by centrifugation (15 min at 14000 rpm and 4 °C) and the absorbance was measured at 530 and 657 nm using the same spectrophotometer as above. All results were normalised for fresh weight.

6. Statistics

As root number is a Poisson distributed discrete variable with group averages lower than 10, we modelled it using a generalised linear model using a log link function. The stomatal measures for each strain were derived from 4 different individual fronds; consequently, we opted to use a linear mixed model with frond as a random effect with a compound symmetry covariance matrix and Satterthwaite degree of freedom approximation using the proc mixed procedure in SAS 9.4. Specific contrasts were post hoc determined using least squares means estimation with MaxT adjustments for multiplicity as implemented in the Isestimate statement of the SAS 9.4 proc plm procedure.

Supplementary results

1. Pigments

The pigmentation changes with increasing Cd concentration in a ploidy specific way that differs for the four strains (significant three-way interaction see Table 1). Nevertheless, there are some consistent patterns. When adding 0.3 mg/L CdCl₂, the ploidy-induced difference in pigment content remains stable for most of the strains. Only the average difference between diploid and tetraploid lines of strain 9242 for chl a, chl b, and car and strain 9346 for car decreases slightly (see Table S3 and Figures 2A and S2). If the Cd concentration increases to 0.5 mg/L CdCl₂, the average chl a, chl b and car concentrations for each line drop below the benign level. Although the strength of the decrease depends on the specific strain and ploidy combination, this difference is significant at the 5% level for all lines except strain 0013 tetraploid (car, chl a, chl b), strain 9242 tetraploid, and strain 9316 diploid (car) (see Table S3, Figures 2A and S2). Despite this decrease, the ploidy-induced difference in pigment content is maintained for strains 9316 and 9346 but decreases further for strain 9242 and ceases to be significant for strain 0013 (chl a and chl b) (see Table S3, Figures 2A and S2). When comparing the chl a-, chl b- and car-pigmentation along the salinity gradient, the effect of 2.5 g/L NaCl on the pigmentation of both diploids and tetraploids of all four strains is rather limited. The direction of the change is ploidy and strain-specific. At the 5% significance level, there is no significant effect on diploids of strain 0013, and tetraploids of strains 9242 and 9316, and a small but significant increase in tetraploids of strain 0013 and the diploids of strains 9316 and 9346. The remaining lines, i.e., the diploids of strain 9242 and the tetraploids of strain 9346, show a slight but significant increase in pigmentation (see Figures 2C and S3 and Table S4). Due to the opposing change in the pigmentation of diploids and tetraploids of strain 9346, the tetraploids end up with a higher pigmentation than the diploids in the low salt environment, but this difference is only significant for carotenoids (see p= 0.0194) (see Table S4). When increasing the salt concentration to 3 g/L, all lines show a strong and highly significant (p adj < 0.0005) reduction in pigmentation (see Table S4).

2. Growth rate

With increasing NaCl concentration in the second gradient, the relative growth rate decreases for diploids of strain 9242 (Fig. 3B), and although the average RGR of the isogenic tetraploids at 2.5 g/L is reduced for all proxies, this reduction is not significant (Table S4). The significant difference between the two ploidies is however, maintained for the RGR measured using frond numbers (Table S4). None of the RGR estimates of tetraploids of strain 9242 at 3g/L differs significantly from the corresponding estimate in the benign condition or at 2.5 g/L (Table S4). For the tetraploids of strain 9346, the RGR initially (2.5 g/L) decreases and although it subsequently (3g/L) increases a bit for fw and dw, the difference between both stress concentrations is non-significant, and the RGR at 3 g/L NaCl remains significantly different and lower than that in the benign condition (Table S4). The RGRs of diploids of the same line are not significantly affected by salt stress but are on average higher than those in the benign conditions for both sa and fn (Table S4). For the four proxies, the stressed diploids outperform the tetraploids significantly in both concentrations of NaCl (Fig. 3B, Table S4). Over the entire second gradient, the tetraploids of strain 0013 have on average a lower relative growth rate than their isogenic diploids for each of the four proxies assessed (Fig. 3B), but this difference is only significant at 2.5 g/L (fn, fw, sa) and 3g/L (fn) (Table S4). The relative growth rate of the stressed tetraploids of this strain is reduced significantly compared to the benign conditions when looking at fresh and dry weight (Table S4). The RGR of the diploid and tetraploid lines of strain 9316 seems to be quite robust against salt stress, only the RGR dw for the tetraploids at 3g/L is significantly reduced compared to the benign condition (Table S4). In general, the diploids of strain 9316 outperform their isogenic tetraploids, but the difference between both ploidies is only significant for the fresh weight at 2.5g/L and frond number at 3g/L (Table S4).

Supplementary tables

Landolt accession	Continent	Country	Province/City	sample ID (Xu)	population genetic cluster (Xu)
0013	Asia	Vietnam	Hanoi	Sp063	SE Asia
9346	Europe	Switzerland	Zurich	Sp093	Europe
9316	Asia	India	Rajasthan, Ajmer Lake	Sp051	India
9242	South America	Ecuador	Guayas, Yaguachi Nuevo	Sp011	America

Table S1: Origin of the strains used and link to the population genetic clusters in Xu et al. 2019

parameter	categorical AIC	continuous AIC	Gradient	Delta AIC
RGR_sa	-1070.9222	-1061.6642	gradient1	-9.25799
RGR_fn	-1132.2667	-1130.8941	gradient1	-1.37259
RGR_fw	-1000.1439	-996.79235	gradient1	-3.35152
RGR_dw	-1032.7918	-1026.8903	gradient1	-5.90148
NPQ	-571.51225	-532.06547	gradient1	-39.44678
FvFm	-1450.9095	-1453.7382	gradient1	2.82863
FqFm	-1076.2944	-1063.0514	gradient1	-13.24304
chl_a	-843.22239	-589.04502	gradient1	-254.17737
chl_b	-1149.051	-966.01616	gradient1	-183.03483
car	-1267.2704	-1066.5864	gradient1	-200.68403
anthocyanin	955.76318	1029.9108	gradient1	-74.14766
thickness	-1912.0848	-1859.3152	gradient1	-52.76962
size	5556.8731	5765.7961	gradient1	-208.92298
RGR_sa	-987.85851	-999.88556	gradient2	12.02705
RGR_fn	-1094.2018	-1083.9846	gradient2	-10.21718
RGR_fw	-956.76249	-962.89613	gradient2	6.13364
RGR_dw	-975.15061	-951.11471	gradient2	-24.0359
NPQ	-523.40377	-514.53641	gradient2	-8.86736
FvFm	-1415.5255	-1418.496	gradient2	2.97046
FqFm	-1023.0277	-1011.5497	gradient2	-11.47804
chl_a	-942.60819	-338.30373	gradient2	-604.30446
chl_b	-1159.2949	-673.88526	gradient2	-485.40965
car	-1265.6342	-1015.366	gradient2	-250.26816
anthocyanin	977.86926	1004.4272	gradient2	-26.55794
thickness	-2086.2039	-2062.6043	gradient2	-23.59967
size	5316.9938	5347.5803	gradient2	-30.58656
RGR_sa	-1965.7419	-1720.8937	gradient3	-244.84821
RGR_fn	-1849.2632	-1729.9994	gradient3	-119.26377

Table S2: Differences in the AIC values between models with stress as a categorical and as a continuous factor

Table S3: Post-hoc analysis (t-test) of gradient 1 (CdCl_2), estimated differences and MaxT adjusted P values

gradient2	size	LSM			Chia			Car			AC			NPQ			Fv/Fm			VII			RGRsa			RGRfwi			RGRdw		
		Estimate	Adj P	Estimate	Adj P	Estimate	Adj P	Estimate	Adj P	Estimate	Adj P	Estimate	Adj P	Estimate	Adj P	Estimate	Adj P	Estimate	Adj P	Estimate	Adj P	Estimate	Adj P								
constr.33.contr.33.dip_0_vs_2.5	14.4521	-0.0057	0.3327	-0.02586	0.4407	-0.0114	0.575	0.00964	0.187	-91.0627	<0.001	0.0364	1	-0.00577	0.3895	0.01469	0.9457	-0.00807	1	0.01051	0.9757	0.007704	1	0.023686	1	0.0338	0.0697	0.0338	0.0697	0.0338	0.0697
constr.33.contr.33.dip_0_vs_3	20.8602	<0.001	-0.0003	1	0.4288	<0.001	0.1255	<0.001	0.03982	<0.001	-0.01386	<0.001	0.06046	0.9986	-0.00204	1	-0.003401	0.0136	0.002278	1	0.00096	0.6564	0.002349	0.6564	-0.00191	0.00338	0.0697	-0.00191	0.00338	0.0697	
constr.33.contr.33.dip_3_vs_2.5	-6.4048	<0.001	-0.00054	0.4246	-0.4547	<0.001	-0.1367	<0.001	-0.04947	<0.001	-0.3044	0.0536	-0.02405	1	-0.00373	0.053	0.01933	0.6451	-0.01034	0.0998	0.00102	0.9848	-0.01759	0.9884	-0.0344	0.1298	-0.0344	0.1298	-0.0345	0.1298	
constr.33.contr.33.dip_3_vs_3	24.3631	<0.001	-0.00059	0.7743	-0.0544	<0.0002	-0.02071	0.0029	-0.01568	0.0006	-0.0544	<0.0001	0.05050	0.9984	-0.00676	0.0161	-0.00767	0.0162	-0.04556	<0.0001	0.01782	0.902	0.001526	0.6218	0.004464	0.0079	0.002494	0.0079	0.002494	0.0079	
constr.33.contr.33.dip_3_vs_2.5	23.6549	<0.001	-0.00116	0.160	0.2607	<0.001	0.07464	<0.001	-0.01683	0.0004	-53.3123	<0.001	0.02816	1	-0.00797	0.0162	-0.04556	<0.0001	-0.00728	1	0.00065	0.158	1	-0.00105	1	-0.016504	0.9714	-0.016504	0.9714	-0.016504	0.9714
constr.33.contr.33.dip_3_vs_2.5	0.7082	1	0.0005	0.63	0.3611	-0.3148	<0.001	-0.095535	<0.0001	-0.03271	<0.001	-0.024242	0.0079	1	0.2506	<0.0001	0.01941	0.0079	-0.00436	0.7891	0.0013492	0.0248	0.00657	0.0248	0.005852	<0.0001	0.005852	<0.0001	0.005852	<0.0001	
constr.33.contr.33.dip_0_vs_2.5	8.5765	<0.001	-0.00064	0.0786	0.9947	-0.00767	0.0001	0.1748	<0.001	0.03629	<0.0001	-0.7291	1	0.1011	0.7477	-0.00456	0.028	-0.06192	<0.0001	0.04611	0.00756	0.0001	0.07215	<0.0001	0.07215	<0.0001	0.07215	<0.0001			
constr.33.contr.33.dip_0_vs_2.5	9.9242	dip_0_vs_2.5	0.9242	dip_0_vs_2.5	0.9242	dip_0_vs_2.5	0.9242	dip_0_vs_2.5	0.9242	dip_0_vs_2.5	0.9242	dip_0_vs_2.5	0.9242	dip_0_vs_2.5	0.9242	dip_0_vs_2.5	0.9242	dip_0_vs_2.5	0.9242	dip_0_vs_2.5	0.9242	dip_0_vs_2.5	0.9242	dip_0_vs_2.5	0.9242	dip_0_vs_2.5	0.9242	dip_0_vs_2.5	0.9242	dip_0_vs_2.5	
constr.33.contr.33.dip_3_vs_2.5	0.7957	0.000166	1	-0.5409	<0.0001	-0.1554	<0.0001	-0.02387	<0.0001	7.7317	1	0.1494	0.1385	-0.00063	1	0.004594	0.0001	-0.01119	0.9994	-0.01274	0.8889	-0.02408	0.6564	-0.04539	0.00018	-0.04539	0.00018	-0.04539	0.00018		
constr.33.contr.33.dip_0_vs_2.5	13.7511	<0.001	-0.0003	0.99245	0.0001	0.1987	0.8578	0.00638	0.9928	0.000985	0.1	-0.1942	0.0108	-0.00672	0.1111	-0.08585	0.0001	0.008454	0.0106	0.5545	0.02256	0.7599	0.003937	0.1651	0.01542	0.1	0.01542	0.1	0.01542	0.1	
constr.33.contr.33.dip_0_vs_2.5	13.0541	<0.001	-0.00045	0.7465	0.4205	0.0001	0.01875	0.0001	0.01202	0.0001	-0.01136	<0.0001	-0.01776	<0.0001	-0.01861	0.014	-0.01105	0.0056	-0.00582	0.0001	0.01062	0.9997	0.009346	0.99931	-0.01248	0.9996	-0.023883	0.2315			
constr.33.contr.33.dip_3_vs_2.5	5.2729	<0.003	0.00015	1	-0.4006	<0.0001	-0.1136	<0.0001	-0.023588	<0.0001	-0.1259	<0.0001	-0.023538	<0.0001	-0.023538	<0.0001	-0.023538	<0.0001	-0.023538	<0.0001	-0.023538	<0.0001	-0.023538	<0.0001	-0.023538	<0.0001	-0.023538	<0.0001			
constr.33.contr.33.dip_3_vs_2.5	14.2514	<0.001	-0.00066	0.3619	0.1	-0.3619	<0.0013	-0.01861	0.014	-0.0117	0.0056	-0.00456	0.0009	-0.05874	0.0009	-0.00464	0.00709	-0.00589	0.0001	-0.01186	0.9987	-0.000335	1	-0.001142	0.9998	-0.002068	0.7887				
constr.33.contr.33.dip_0_vs_2.5	13.6461	<0.001	0.00008	1	0.4441	<0.0001	0.1259	<0.0001	-0.01741	0.0001	-0.05108	<0.0001	-0.01741	0.0001	-0.05108	<0.0001	-0.01741	0.0001	-0.01741	0.0001	-0.01741	0.0001	-0.01741	0.0001	-0.01741	0.0001	-0.01741	0.0001			
constr.33.contr.33.dip_3_vs_2.5	0.6104	1	-0.00064	0.1684	-0.4924	<0.0001	-0.1445	<0.0001	-0.0373	<0.0001	-0.1494	1	-0.018	1	-0.00004	1	-0.01178	0.9949	-0.00994	1	0.009999	0.9849	-0.01446	0.9957	-0.02928	0.2102					
constr.33.contr.33.dip_0_vs_2.5	20.1286	<0.001	-0.00035	0.00859	-0.00021	1	-0.00402	1	0.00175	0.0001	-0.01895	0.0001	-0.02883	0.0001	-0.017362	0.0001	-0.017362	0.0001	-0.06434	<0.0001	-0.01588	0.9932	-0.00699	0.9999	0.01794	0.9988	-0.01794	0.9988	-0.01794	0.9988	
constr.33.contr.33.dip_0_vs_2.5	20.7042	<0.001	0.000571	0.3386	0.314	<0.0001	0.02089	0.0001	-0.01914	<0.0001	-0.09397	<0.0001	-0.147789	0.9981	-0.00564	0.9985	-0.006704	0.0001	-0.01127	0.9994	-0.009365	0.99804	-0.01127	0.9994	-0.01127	0.9994	-0.01127	0.9994			
constr.33.contr.33.dip_3_vs_2.5	-5.5757	1	0.000129	1	-0.3142	<0.0001	-0.0174	<0.0001	0.026	<0.0001	0.101780	<0.0001	0.08111	0.9501	-0.000531	0.4528	-0.00420	0.0006	-0.01652	0.9879	-0.001223	0.0041	-0.000338	1	-0.02623	0.9961	-0.03252	0.9961	-0.03252	0.9961	
constr.33.contr.33.dip_0_vs_2.5	8.3596	<0.001	0.001308	0.00001	0.101780	<0.0001	0.05179	<0.0001	0.01741	<0.0001	-0.05108	<0.0001	-0.01741	0.0001	-0.05108	<0.0001	-0.01741	0.0001	-0.01741	0.0001	-0.01741	0.0001	-0.01741	0.0001	-0.01741	0.0001	-0.01741	0.0001			
constr.33.contr.33.dip_3_vs_2.5	3.8657	<0.001	0.00051	0.0539	-0.0539	<0.0001	0.09234	<0.0001	0.03044	<0.0001	-0.01751	<0.0001	-0.01751	0.0001	-0.01751	0.0001	-0.01751	0.0001	-0.01751	0.0001	-0.01751	0.0001	-0.01751	0.0001	-0.01751	0.0001					
constr.33.contr.33.dip_0_vs_2.5	2.8039	1	0.000677	0.1146	-0.4742	<0.0001	-0.1481	<0.0001	-0.0343	<0.0001	-0.1486	1	0.007935	1	-0.000174	0.9984	-0.003478	0.0001	-0.00588	0.0001	-0.0178	0.00083	-0.01266	0.00026	-0.06873	0.00026	-0.06873	0.00026			
constr.33.contr.33.dip_3_vs_2.5	13.7709	<0.001	-0.00335	0.00001	-0.06496	<0.0001	-0.01833	0.0177	-0.01872	<0.0001	-0.01834	0.0001	-0.0265	0.9986	-0.002236	0.00026	-0.06873	<0.0001	-0.00588	0.0001	-0.00239	0.3827	-0.00533	<0.0001	-0.00292	0.0032	-0.00292	0.0032			
constr.33.contr.33.dip_0_vs_2.5	16.6564	<0.001	0.00459	-0.00001	0.3826	0.000126	-0.0474	<0.0001	-0.12021	<0.0001	-0.13844	<0.0001	-0.05377	0.0001	-0.02409	<0.0001	-0.12047	<0.0001	-0.05952	0.9987	-0.00662	0.9993	-0.006704	0.0001	-0.00588	0.0024	-0.00588	0.0024			
constr.33.contr.33.dip_3_vs_2.5	-13.7776	<0.001	-0.00148	<0.0001	0.04	<0.0001	0.1212	<0.0001	0.03044	<0.0001	-0.01759	<0.0001	-0.01759	0.0001	-0.01759	0.0001	-0.01759	0.0001	-0.01759	0.0001	-0.01759	0.0001	-0.01759	0.0001	-0.01759	0.0001					
constr.33.contr.33.dip_0_vs_2.5	-3.8657	1	-0.00151	0.00001	0.09234	<0.0001	-0.01751	<0.0001	-0.01751	0.0001	-0.01751	0.0001	-0.01751	0.0001	-0.01751	0.0001	-0.01751	0.0001	-0.01751	0.0001	-0.01751	0.0001	-0.01751	0.0001	-0.01751	0.0001					
constr.33.contr.33.dip_3_vs_2.5	-10.9709	<0.001	-0.00261	<0.0001	-0.04692	<0.0001	-0.06724	<0.0001	-0.04733	<0.0001	-0.01872	<0.0001	-0.01872	0.0001	-0.01872	<0.0001	-0.01872	<0.0001	-0.01872	0.0001	-0.01872	0.0001	-0.01872	0.0001	-0.01872	0.0001					
constr.33.contr.33.dip_0_vs_2.5	-14.2457	<0.001	-0.00115	<0.0001	-0.04549	<0.0001	-0.01836	<0.0001	-0.01836	<0.0001	-0.01836	<0.0001	-0.01836	<0.0001	-0.01836	<0.0001	-0.01836	<0.0001	-0.01836	<0.0001	-0.01836	<0.0001	-0.01836	<0.0001	-0.01836	<0.0001					
constr.33.contr.33.dip_3_vs_2.5	-9.9242	dip_0_vs_set_3	-9.9242	dip_0_vs_set_3	-9.9242	dip_0_vs_set_3	-9.9242	dip_0_vs_set_3	-9.9242	dip_0_vs_set_3	-9.9242	dip_0_vs_set_3	-9.9242	dip_0_vs_set_3	-9.9242	dip_0_vs_set_3	-9.9242	dip_0_vs_set_3	-9.9242	dip_0_vs_set_3	-9.9242	dip_0_vs_set_3	-9.9242	dip_0_vs_set_3	-9.9242	dip_0_vs_set_3	-9.9242	dip_0_vs_set_3			
constr.33.contr.33.dip_0_vs_2.5	-14.5044	<0.001	-0.00052	0.5062	0.1355	<0.0001	-0.04399	<0.0001	-0.04399	<0.0001	-0.04399	<0.0001	-0.04399	<0.0001	-0.04399	<0.0001	-0.04399	<0.0001	-0.04399	<0.0001	-0.04399	<0.0001	-0.04399	<0.0001	-0.04399	<0.0001	-0.04399	<0.0001			
constr.33.contr.33.dip_3_vs_2.5	-18.3363	<0.001	-0.00017	0.0001	-0.04347	<0.0001	-0.0175	<0.0001	-0.0175	<0.0001	-0.0175	<0.0001	-0.0175	<0.0001	-0.0175	<0.0001	-0.0175	<0.0001	-0.0175	<0.0001	-0.0175	<0.0001	-0.0175	<0.0001	-0.0175	<0.0001	-0.0175	<0.0001			
constr.33.contr.33.dip_0_vs_2.5	-14.5044	<0.001	-0.00052	0.5062	0.1355	<0.0001	-0.04399	<0.0001	-0.04399	<0.0001	-0.04399	<0.0001	-0.04399	<0.0001	-0.04399	<0.0001	-0.04399	<0.0001	-0.04399	<0.0001	-0.04399	<0.0001	-0.04399	<0.0001	-0.04399	<0.0001	-0.04399	<0.0001			
constr.33.contr.33.dip_3_vs_2.5	-5.9038	<0.003	-0.00017	0.0001	-0.04347	<0.0001	-0.0175	<0.0001	-0.0175	<0.0001	-0.0175	<0.0001	-0.0175	<0																	

Table S4: Post-hoc (t-test) analysis of gradient 2 (NaCl), estimated differences and MaxT adjusted P values

gradient3	RGR sa		RGR fn	
Label	Estimate	Adj P	Estimate	Adj P
13_dipl_0_vs_2	-0.00844	1	-0.01676	1
13_dipl_0_vs_2.5	0.02795	0.4829	0.02687	0.9205
13_dipl_0_vs_3	0.03656	0.0616	0.02956	0.8
13_dipl_0_vs_4	0.07313	<.0001	0.06503	<.0001
13_dipl_0_vs_6	0.1557	<.0001	0.1098	<.0001
13_dipl_2_vs_2.5	0.03639	0.0642	0.04362	0.079
13_dipl_2.5_vs_3	0.008613	1	0.002693	1
13_dipl_3_vs_4	0.03657	0.0616	0.03547	0.4037
13_dipl_4_vs_6	0.08256	<.0001	0.04476	0.0599
13_tet_0_vs_2	0.01135	1	-0.0021	1
13_tet_0_vs_2.5	0.01171	1	0.005237	1
13_tet_0_vs_3	0.05035	0.0003	0.04753	0.0278
13_tet_0_vs_4	0.07917	<.0001	0.06131	0.0002
13_tet_0_vs_6	0.1101	<.0001	0.06448	<.0001
13_tet_2_vs_2.5	0.000361	1	0.007334	1
13_tet_2.5_vs_3	0.03863	0.0323	0.04229	0.109
13_tet_3_vs_4	0.02882	0.4119	0.01378	1
13_tet_4_vs_6	0.03093	0.2704	0.003167	1
9242_dipl_0_vs_2	0.01112	1	0.006255	1
9242_dipl_0_vs_2.5	0.02244	0.8967	0.02256	0.9922
9242_dipl_0_vs_3	0.05193	0.0002	0.02803	0.8776
9242_dipl_0_vs_4	0.1019	<.0001	0.07101	<.0001
9242_dipl_0_vs_6	0.1711	<.0001	0.1459	<.0001
9242_dipl_2_vs_2.5	0.01132	1	0.0163	1
9242_dipl_2.5_vs_3	0.02949	0.3626	0.005471	1
9242_dipl_3_vs_4	0.04993	0.0003	0.04298	0.0913
9242_dipl_4_vs_6	0.06929	<.0001	0.07494	<.0001
9242_tet_0_vs_2	0.000322	1	0.01123	1
9242_tet_0_vs_2.5	-0.01864	0.9921	-0.0028	1
9242_tet_0_vs_3	-0.01053	1	-0.0038	1
9242_tet_0_vs_4	0.02359	0.833	0.02549	0.9564
9242_tet_0_vs_6	0.09173	<.0001	0.08378	<.0001
9242_tet_2_vs_2.5	-0.01896	0.989	-0.01403	1
9242_tet_2.5_vs_3	0.008112	1	-0.00101	1
9242_tet_3_vs_4	0.03412	0.1249	0.0293	0.816
9242_tet_4_vs_6	0.06814	<.0001	0.05829	0.0011
9316_dipl_0_vs_2	-0.01109	1	-0.00452	1
9316_dipl_0_vs_2.5	0.009104	1	0.0148	1
9316_dipl_0_vs_3	-0.00582	1	0.01404	1
9316_dipl_0_vs_4	0.02614	0.642	0.02477	0.9704
9316_dipl_0_vs_6	0.118	<.0001	0.1056	<.0001
9316_dipl_2_vs_2.5	0.02019	0.9729	0.01932	0.9996
9316_dipl_2.5_vs_3	-0.01492	0.9999	-0.00076	1
9316_dipl_3_vs_4	0.03196	0.2147	0.01073	1
9316_dipl_4_vs_6	0.09186	<.0001	0.08082	<.0001
9316_tet_0_vs_2	-0.00648	1	-0.00801	1
9316_tet_0_vs_2.5	0.002913	1	-0.00975	1
9316_tet_0_vs_3	-0.00374	1	-0.01305	1

	RGR sa		RGR fn	
Label	Estimate	Adj P	Estimate	Adj P
9316_tet_0	0.01451	0.9999	-0.02178	0.9961
9316_tet_0	0.08272	<.0001	0.0462	0.0403
9316_tet_2	0.009397	1	-0.00175	1
9316_tet_2	-0.00665	1	-0.0033	1
9316_tet_3	0.01825	0.9945	-0.00872	1
9316_tet_4	0.06821	<.0001	0.06798	<.0001
9346_dipl_0	-0.0497	0.0003	-0.03803	0.2599
9346_dipl_0	-0.04088	0.0161	-0.03855	0.2345
9346_dipl_0	-0.01447	0.9999	-0.01247	1
9346_dipl_0	0.02083	0.9578	0.0155	1
9346_dipl_0	0.09613	<.0001	0.07473	<.0001
9346_dipl_2	0.008826	1	-0.00051	1
9346_dipl_2	0.0264	0.6202	0.02608	0.9432
9346_dipl_3	0.0353	0.0878	0.02796	0.8804
9346_dipl_4	0.0753	<.0001	0.05924	0.0007
9346_tet_0	-0.03825	0.037	-0.027	0.9173
9346_tet_0	-0.01948	0.9833	-0.00044	1
9346_tet_0	-0.01384	1	0.002144	1
9346_tet_0	0.02312	0.8588	0.04605	0.0421
9346_tet_0	0.07716	<.0001	0.06385	<.0001
9346_tet_2	0.01877	0.991	0.02655	0.93
9346_tet_2	0.005635	1	0.002587	1
9346_tet_3	0.03696	0.0544	0.0439	0.0747
9346_tet_4	0.05404	<.0001	0.0178	1
13_dip_vs_te	0.02181	0.9256	0.01786	1
13_dip_vs_te	0.04161	0.0124	0.03252	0.6105
13_dip_vs_te	0.00558	1	-0.00377	1
13_dip_vs_te	0.0356	0.0808	0.03583	0.3836
13_dip_vs_te	0.02785	0.4905	0.01414	1
13_dip_vs_te	-0.02379	0.8203	-0.02746	0.9022
9242_dip_vs	0.03737	0.0475	0.02407	0.9804
9242_dip_vs	0.02657	0.6066	0.02904	0.8309
9242_dip_vs	-0.00371	1	-0.00129	1
9242_dip_vs	-0.02509	0.7281	-0.00777	1
9242_dip_vs	-0.04089	0.016	-0.02144	0.9968
9242_dip_vs	-0.04205	0.0107	-0.0381	0.2562
9316_dip_vs	0.01458	0.9999	0.03004	0.7722
9316_dip_vs	0.01918	0.9867	0.02655	0.9299
9316_dip_vs	0.008388	1	0.005485	1
9316_dip_vs	0.01666	0.999	0.002946	1
9316_dip_vs	0.002958	1	-0.0165	1
9316_dip_vs	-0.02069	0.9616	-0.02934	0.8133
9346_dip_vs	0.03529	0.0881	0.01494	1
9346_dip_vs	0.04674	0.0015	0.02598	0.9461
9346_dip_vs	0.05669	<.0001	0.05304	0.0057
9346_dip_vs	0.03592	0.0735	0.02955	0.8006
9346_dip_vs	0.03758	0.0453	0.04549	0.0493
9346_dip_vs	0.01632	0.9994	0.004051	1

Table S5: Post-hoc analysis (t-test) of gradient 3 (NaCl), estimated differences and MaxT adjusted P values

	root number		root length		stomatal density	
contrast	Estimate	AdjP	Estimate	AdjP	Estimate	AdjP
0013_dip_vs_tet	0.3329	<.0001	-2.1	0.0002	6.2683	<.0001
9242_dip_vs_tet	0.1955	0.0709	-1.5	0.0101	11.6075	<.0001
9316_dip_vs_tet	0.3396	<.0001	-2.85	<.0001	8.5902	<.0001
9346_dip_vs_tet	0.02432	0.9963	-0.1	0.9995	11.5435	<.0001
					-5.9948	<.0001
					-4.7435	<.0001
					-4.3497	<.0001
					-5.3941	<.0001
					-2.078	<.0001

Table S6: Post-hoc analysis of traits measured uniquely in Hoagland E medium, estimated differences and MaxT adjusted P values (t-test except for rootnr z-test)

Supplementary figures

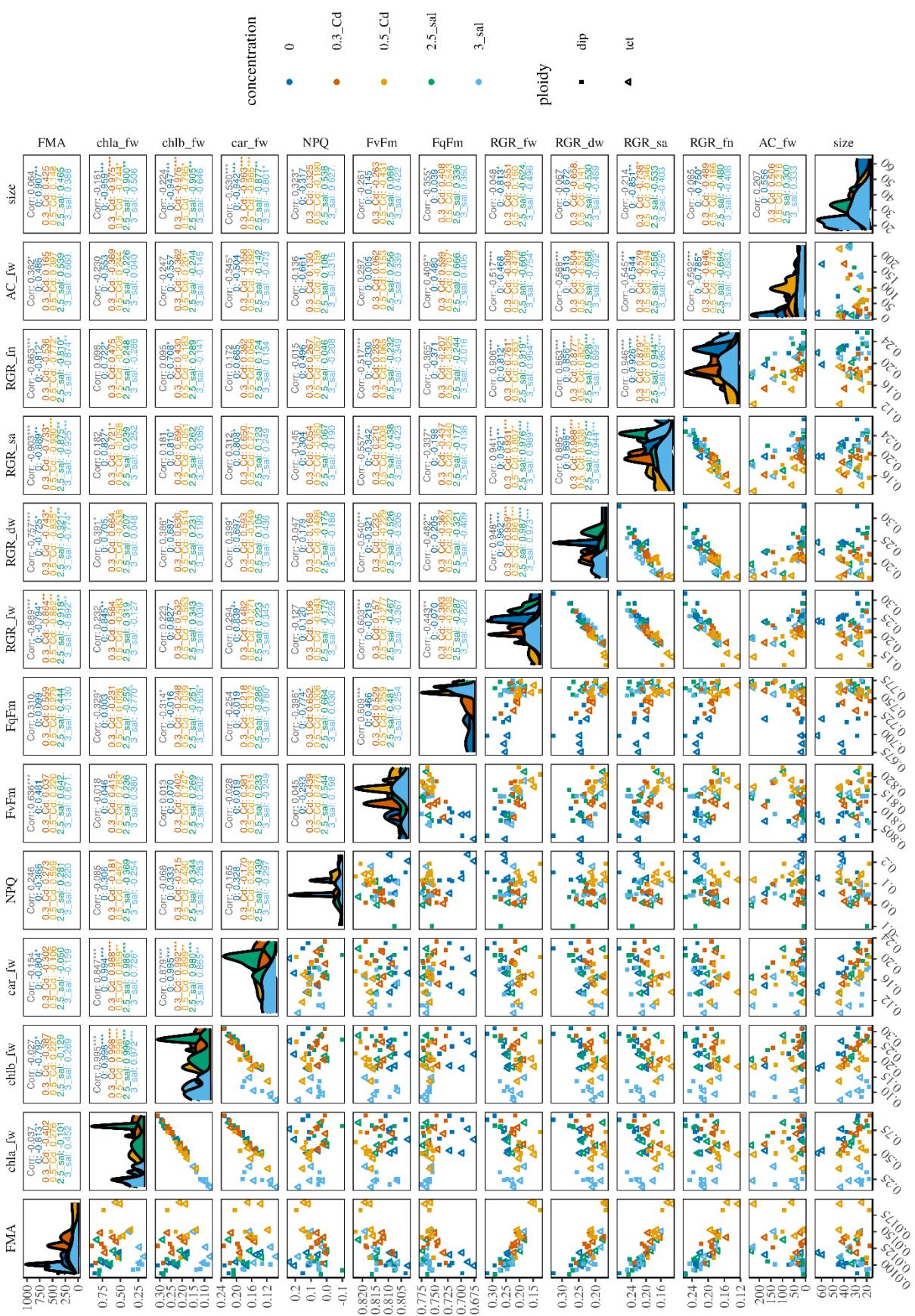


Fig. S1: Global (in grey) and within environment (in colour) Pearson correlations between all measured phenotypical traits for gradient 1 and 2.

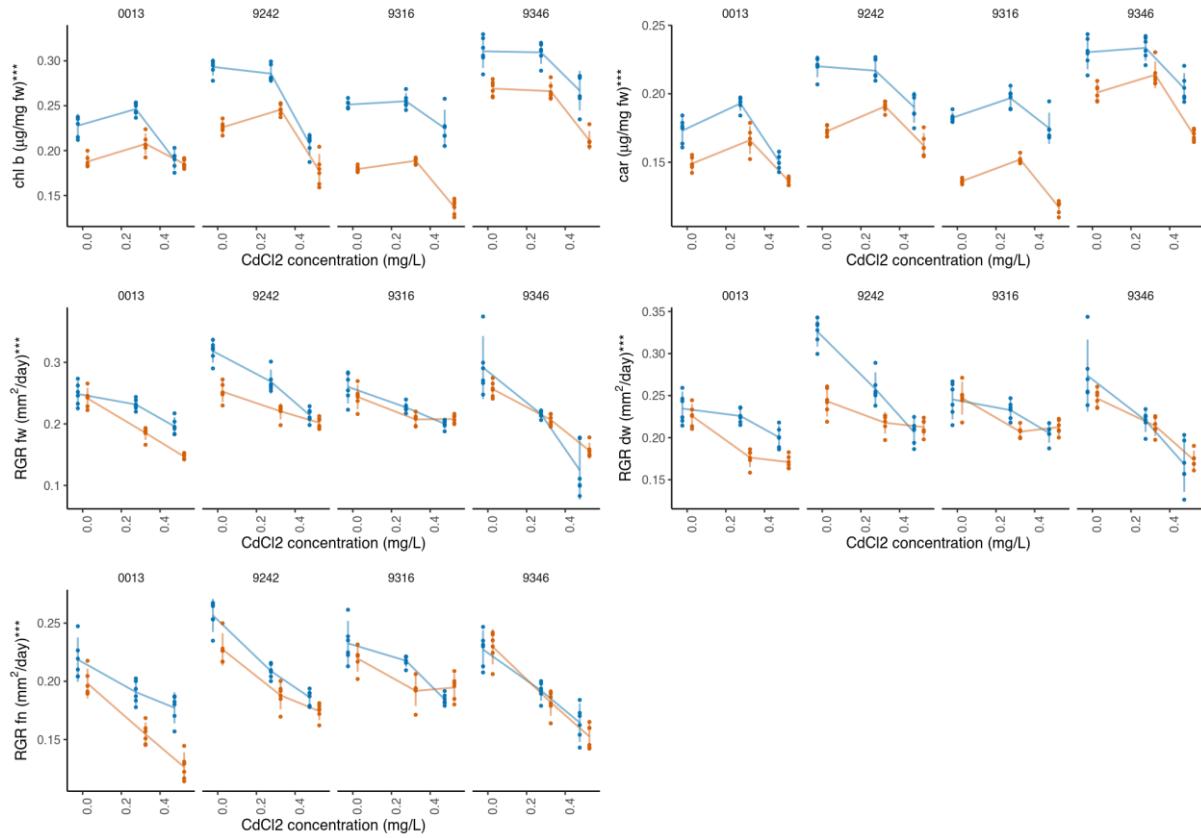


Fig. S2: The effects of WGD on chlorophyll b (A) and carotenoid (B) concentration per unit fresh weight and on the relative growth rate measured using fresh weight (C), dry weight (D) and frond number (E) along gradient 1. Error bars represent 95% confidence intervals, diploids in blue and tetraploids in orange. The asterisks next to the dependant variables refer to the significance of the ploidy*strain*condition effect.

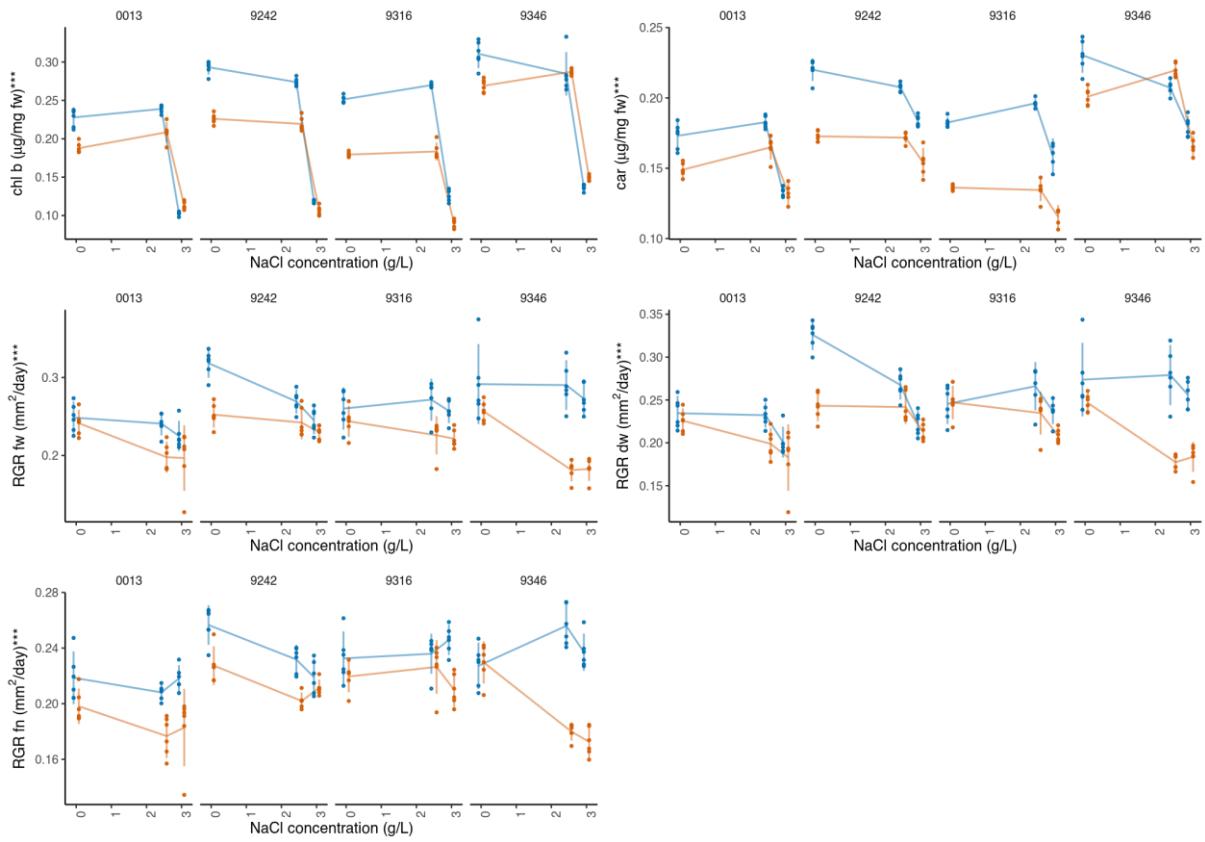


Fig. S3: The effects of WGD on chlorophyll b (A) and carotenoid (B) concentration per unit fresh weight and on the relative growth rate measured using fresh weight (C), dry weight (D) and frond number (E) along gradient 2. Error bars represent 95% confidence intervals, diploids in blue and tetraploids in orange. The asterisks next to the dependant variables refer to the significance of the ploidy*strain*condition effect.

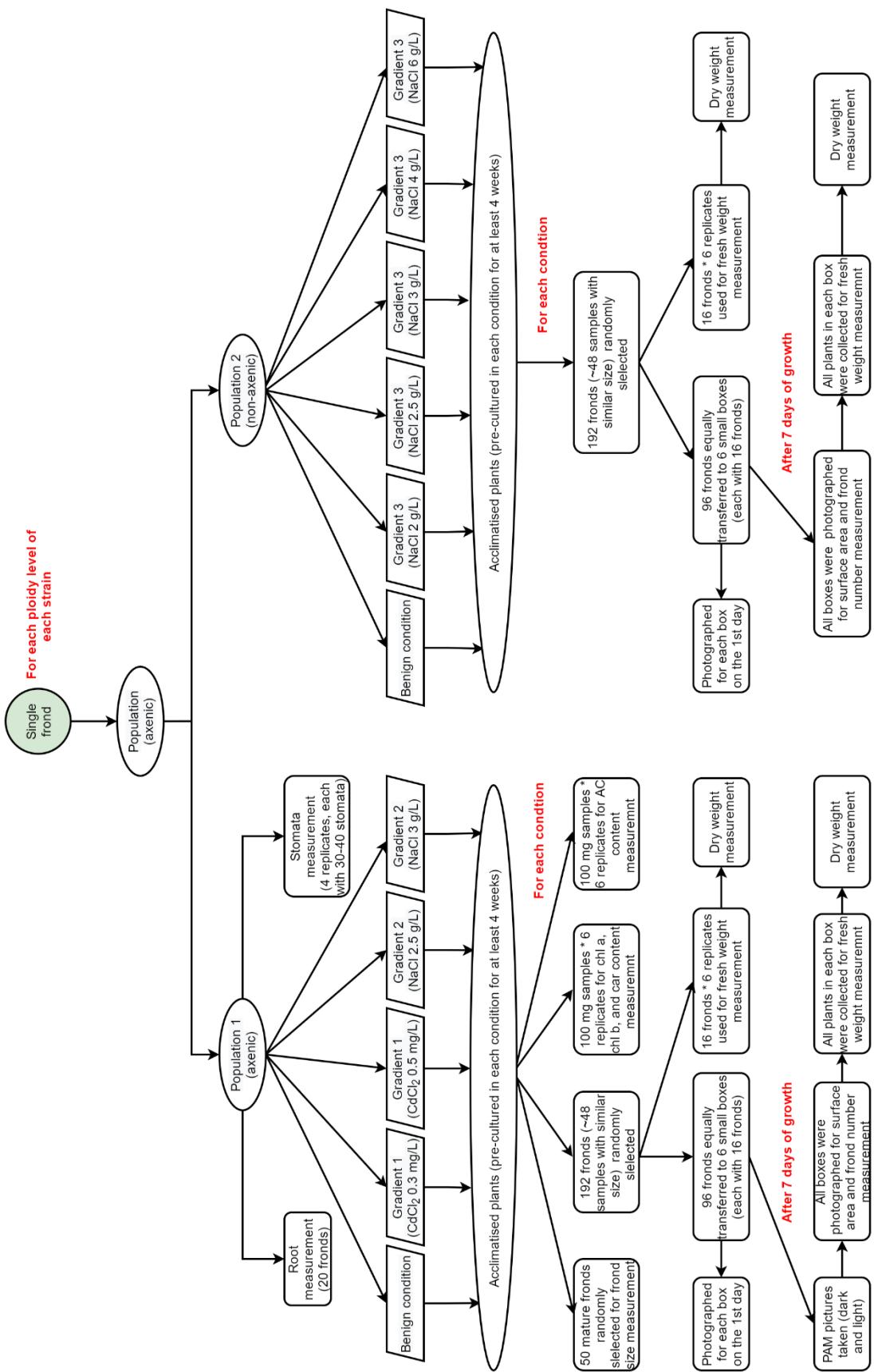


Fig S4: Graphical representation of the methods