

1 *Research Report in* BIOLOGICAL SCIENCES: Evolution

2 **Adaptive diversification of growth allometry in the plant**

3 *Arabidopsis thaliana*

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18 **Abstract**

19 Seed plants vary tremendously in size and morphology. However, variation and covariation
20 between plant traits may at least in part be governed by universal biophysical laws and biological
21 constants. Metabolic Scaling Theory (MST) posits that whole-organismal metabolism and
22 growth rate are under stabilizing selection that minimizes the scaling of hydrodynamic resistance
23 and maximizes the scaling of resource uptake. This constrains variation in physiological traits
24 and in the rate of biomass accumulation, so that they can be expressed as mathematical functions
25 of plant size with near constant allometric scaling exponents across species. However, observed
26 variation in scaling exponents questions the evolutionary drivers and the universality of
27 allometric equations. We have measured growth scaling and fitness traits of 451 *Arabidopsis*
28 *thaliana* accessions with sequenced genomes. Variation among accessions around the scaling
29 exponent predicted by MST correlated with relative growth rate, seed production and stress
30 resistance. Genomic analyses indicate that growth allometry is affected by many genes
31 associated with local climate and abiotic stress response. The gene with the strongest effect,
32 *PUB4*, has molecular signatures of balancing selection, suggesting that intraspecific variation in
33 growth scaling is maintained by opposing selection on the trade-off between seed production and
34 abiotic stress resistance. Our findings support a core MST prediction and suggest that variation
35 in allometry contributes to local adaptation to contrasting environments. Our results help
36 reconcile past debates on the origin of allometric scaling in biology, and begin to link adaptive
37 variation in allometric scaling to specific genes.

38 **Keywords:** Fitness trade-off, GWAS, metabolic theory of ecology, polygenic adaptation, scaling
39 exponent

40 **Significance statement**

41 Are there biological constants unifying phenotypic diversity across scales? Metabolic Scaling
42 Theory (MST) predicts mathematical regularity and constancy in the allometric scaling of
43 growth rate with body size across species. Here, we show that adaptation to climate in
44 *Arabidopsis thaliana* is associated with local strains that substantially deviate from the values
45 predicted by MST. This deviation can be linked to increased stress tolerance at the expense of

46 seed production, and it occurs through selection on genes that are involved in abiotic stress
47 response and that are geographically correlated with climatic conditions. This highlights the
48 evolutionary role of allometric diversification and helps establish the physiological bases of plant
49 adaptation to contrasting environments.

50 /body

51 **Introduction**

52 At the core of the quest for understanding and predicting biological diversity is the apparent
53 paradox that, despite the phenotypic changes that underlie divergent ecological strategies, there
54 seem to be constant or near-constant parameters across life forms (1). The latter is assumed to
55 result in part from biophysical constraints limiting the range of possible trait values (2), as well
56 as from strong stabilizing selection for optimal phenotypes (3, 4). Consistently, body size
57 variation in multicellular organisms is associated with many scaling regularities. Max Kleiber (5)
58 first reported that the consumption of energy (metabolic rate G) varies to the $3/4$ -power of
59 organism mass M , such that $G = G_0M^{3/4}$, implying that a 10-fold increase in M produces in
60 virtually all organisms a 5.6-fold increase in G . Several physiological models have been
61 proposed to explain this constancy. The most prominent is Metabolic Scaling Theory (MST) (6),
62 which predicts that scaling exponents of several traits tend to take on “quarter-power” values
63 (*e.g.*, $3/4$, $1/4$) as the outcome of an optimal balance between the scaling of hydraulic transport costs
64 and the scaling of exchange surface areas (*e.g.*, leaf area in plants) (7). According to MST, the
65 scaling of physiological rates matches the ability of exchange surfaces to obtain resources from
66 the environment and then distribute them to metabolizing cells through the vascular network.
67 Because the branching geometry of this network is highly constrained in space, it is predicted
68 that selection that minimizes the costs of resource transport and at the same time maximizes the
69 uptake of resources will lead to “allometrically ideal” organisms characterized by a common set
70 of quarter-power scaling relationships with body mass.

71 Empirical observations support MST predictions across land plants, where several traits,
72 including organismal growth rate, scale as body mass raised to the power of $3/4$ (8, 9). On the
73 other hand, the scaling exponent can vary across plants (10–12), or scaling can be constant but
74 deviate from $3/4$ (13). These seemingly contradictory observations have been proposed to reflect

75 (i) phenotypic, like life history, differences between species or populations (9, 10), (ii)
76 physiological changes along environmental gradients (14, 15), or (iii) non-linearity in
77 hydrodynamic resistance and metabolic scaling (16). Thus, important questions about the
78 evolution of allometry remain (4). For example, is the prevalence of ubiquitous scaling
79 relationships the result of stabilizing selection acting to remove unfit genetic allometric variants?
80 And does variation in the scaling exponent reflect adaptation and genetic diversification, or
81 developmental plasticity?

82 To address these and related questions, we examined how growth rate scales with body
83 size in a genetically diverse population of *Arabidopsis thaliana* accessions (Dataset S1), a
84 species that exhibits three orders of magnitude in plant dry mass (10) and occurs in a wide range
85 of contrasting environments (17). We provide evidences that scaling variation is maintained by
86 an adaptive trade-off between alternative environments. We show that this variation has a
87 polygenic basis, and that there is genetic correlation between allometry and local climate.

88 Results

89 **Variation of *A. thaliana* Growth Scaling with Climate.** The scaling exponent of growth is
90 conventionally quantified as the slope θ of the allometric function $y = \alpha + \theta x$, where x and y are
91 the logarithms of plant biomass and absolute growth rate, respectively. Fitting the allometry of
92 the mean absolute growth rate (GR, mg d^{-1}), estimated as the ratio of final plant dry mass (mg)
93 over total duration of the life cycle (days), across *A. thaliana* accessions returned a scaling
94 exponent θ that is not significantly different from the MST predicted value of $\frac{3}{4}$ ($y = -1.07 +$
95 $0.74x$; $r^2 = 0.97$; slope $\text{CI}_{95\%} = [0.725, 0.750]$; Fig. 1A). This value is the same as observed
96 across vascular plant species (box in Fig. 1A). However, the relationship is not a pure power
97 function, and instead was better explained by a non-linear quadratic function ($y = -1.93 + 1.43x -$
98 $0.14x^2$, $\Delta\text{AIC} = -192.4$; Fig. 1A). Our analyses indicate that this curvilinear scaling relationship
99 was due to differences in θ between accessions, which can be estimated as the first derivative of
100 the quadratic function ($\theta = 1.43 - 0.27x$), and which varied between accessions from 0.47 to 1.10
101 (Fig. 1B, Fig. S1C). The broad-sense heritability, H^2 , of θ was 0.95, which is higher than any
102 other trait measured in this study (Table S1), indicative of a high amount of variance explained
103 by genetic effects in our highly controlled growth conditions.

104 Modelling the dynamics of plant dry mass accumulation from imaging data (18) revealed
105 that the estimated relative growth rate (RGR) explains 18% of the variation in the scaling
106 exponent ($P < 0.001$), with both being negatively correlated with plant lifespan ($P < 0.001$, Fig.
107 1C; Dataset S2). Previous studies have shown that variation in *A. thaliana* growth allometry is
108 positively correlated with carbon assimilation rate and nutrient concentration, but negatively with
109 lifespan (10). Thus, variation of growth allometry in *A. thaliana* connects life-history variation to
110 the strategies for leaf resource-use. At the one end of the distribution are high scaling exponents,
111 representative of ‘live fast/die young’ strategies that maximize resource capture (high RGR and
112 carbon assimilation rate) at the expense of plant lifespan and final size. At the other end are low
113 scaling exponents, representative of ‘live slow/die old’ strategies that maximize the retention
114 (thick leaves with low nutrient concentration and long lifespan) rather than acquisition of
115 resources.

116 We then examined the correlations between the scaling exponent and 21 climatic
117 variables, which include 19 ‘Bioclim’ variables (<http://www.worldclim.org/bioclim>), as well as
118 the estimated mean annual Potential Evapo-Transpiration (PET, mm) and Aridity Index (19) at
119 the geographic origin of the accessions. Consistent with the idea that resource-acquisitive plants,
120 *i.e.* early-flowering/fast-growing ecotypes, are more adapted to hotter and drier regions, the
121 scaling exponent was positively correlated with the mean annual temperature measured at the
122 collection point of the accessions (Fig. 2A; Dataset S2). The strongest correlations were with
123 maximum temperature of the warmest month and mean temperature of the warmest quarter ($r =$
124 0.30 and 0.28, respectively, Fig. 2B; Dataset S2). Inversely, the scaling exponent was negatively
125 correlated with precipitation, specifically with precipitation during the driest quarter (Fig. 2C),
126 precipitation seasonality and the aridity index (Dataset S2). In contrast, it was not correlated with
127 the altitude at the collection point.

128 Using stepwise regression, we found that 13 climatic variables explain >27% of the
129 allometric variation. Four of these are related to summer and two to winter climate. The strongest
130 effects were estimated for annual mean temperature, isothermality and mean summer
131 temperature. Modeling the geographic distribution of scaling exponent with the 13 top-correlated
132 climatic variables as predictors showed that intermediate exponents are more common in
133 temperate regions (Fig. 2D), while extreme exponents are favored under more stressful

134 conditions (*e.g.* high altitude, high latitude).

135 **Fitness Costs and Benefits of Allometric Variation.** The scaling exponent was correlated with
136 resource-use traits including RGR and lifespan, as well as performance-related traits such as fruit
137 number, a proxy for lifetime fitness in annual species (fruit number varied from 18 to 336 per
138 plant, Table S1; *SI Appendix*). However, the relationship between fitness and the scaling
139 exponent under the non-limiting RAPA conditions was not linear (Fig. 3A). Instead, fruit number
140 was a bell-shaped function of the scaling exponent: it peaked for plants with an exponent around
141 $\frac{3}{4}$ and declined towards higher or lower exponents. Thus, genetic deviations from the $\frac{3}{4}$ scaling
142 exponent are associated in *A. thaliana* with extreme resource-use strategies, and a general
143 decline in fruit number ($r = -0.62$, $P < 0.001$; Dataset S2). A polynomial regression of relative
144 fitness - using fruit number standardized by the population mean - over the scaling exponent
145 returned a significant, negative second-order coefficient ($y = 1.00 + 4.23x - 4.06x^2$, $P < 0.001$ for
146 all coefficients), *i.e.* an estimate of quadratic selection gradient $|y|$ that might be indicative of
147 stabilizing selection for the allometric exponent under benign conditions (20).

148 Conversely, deviation from $\frac{3}{4}$ scaling was positively correlated with survival under
149 severe drought ($r = 0.16$, $P < 0.05$; measured in (21) across 210 common accessions; Dataset
150 S2), and negatively correlated with growth reduction under moderate drought ($r = -0.26$, $P <$
151 0.05 ; measured in (22) across 60 common accessions, Dataset S2). However, neither stress-
152 resistance trait was correlated with the scaling exponent itself. This suggests that deviation of
153 allometric exponents from $\frac{3}{4}$ in either direction is associated with increased resistance to
154 stressful conditions at the expense of reduced reproductive fitness under benign conditions.
155 Consistently, a re-analysis of an experimental population phenotyped for tolerance to combined
156 high temperature and water deficit (23) pointed to higher stress sensitivity of accessions with
157 scaling exponents close to $\frac{3}{4}$ (Fig. 3B). In contrast, allometric exponents at both the low and high
158 end of the distribution were correlated with improved stress tolerance, specifically under high
159 temperature (Fig. 3B). A possible explanation of this result could be that a ‘fast’ strategy with
160 high scaling exponents allows stress escape by maximizing resource acquisition and completion
161 of the life cycle before a short window of non-stressful conditions closes (23). Alternatively, the
162 ‘slow’ strategy might support stress tolerance by reducing metabolic activities and thus, the
163 resource demand associated with a fast growth (10).

164 **The Genetic and Evolutionary Bases of Allometric Variation.** Because we suspected that
165 allometric variation might result from adaptation to the diverse environments at the places of
166 origin of accessions, we looked for genetic evidence of local adaptation and of genetic
167 diversification with climate. Principal component analysis (PCA) performed after eigen
168 decomposition of the relatedness matrix revealed that the scaling exponent was correlated with
169 population structure, notably with the second PCA axis ($r = 0.37$, $P < 0.001$), which explains
170 28% of total genetic variation and mainly differentiates accessions from Relicts, N. Sweden and
171 Spain groups (17) (Fig. S2). By contrast, flowering time was correlated with the first PCA axis,
172 which explains 42% of genetic variation and is associated with longitudinal divergence among
173 accessions (Fig. S2). Compared to the ancestral ('Relict') genetic group (17), scaling exponent
174 differed significantly ($P < 0.001$) for two groups: N. Sweden and S. Sweden, while the eight
175 other groups were not different ($P > 0.3$). Q_{st} of scaling exponent - measured as the ratio of
176 between-group phenotypic variance over total variance - was above 0.9 quantile of genome-wide
177 F_{st} (Q_{st}/F_{st} ratio = 2.14, $P < 0.001$; Table S1, Fig. S3), which is potentially indicative of
178 polygenic selection acting on the scaling of plant growth (24).

179 We ran GWA models on the scaling exponent θ and the 21 climatic variables using the
180 EMMAX procedure to correct for population structure (25). In total, 8,250 single nucleotide
181 polymorphisms (SNPs) out of 1,793,606 tested were significantly associated with at least one
182 phenotypic trait or climatic variable (Dataset S3) after multiple-testing correction (26). Only six
183 SNPs were significantly associated with the scaling exponent ($FDR < 0.05$). Five of these six
184 SNPs were located in the same region on chromosome 2 (Fig. 4A), and were associated with
185 maximum temperature of the warmest month (Fig. 4B). Three SNPs were also significantly
186 associated with the mean annual temperature and the mean temperature of the coldest month
187 (Dataset S4). The same genomic region showed strong association with precipitation during the
188 driest month (Fig. 4C), although the six SNPs that were associated with scaling variation did not
189 reach the significance threshold for this climatic variable ($FDR > 0.05$). In contrast, no
190 significant SNPs were shared between RGR, lifespan, fruit number or rosette dry mass and the
191 climatic variables (Dataset S4), suggesting that genetic association between traits and climate is
192 relatively rare.

193 One SNP among the five associated with both the scaling exponent and the maximum

194 temperature of the warmest month was located in the U-box protein gene *PUB4* (At2g23140;
195 MAF = 6.1%; Fig. 4A). As E3 ubiquitin ligases, U-box proteins are involved in protein turnover,
196 a key regulatory component of plant responses to abiotic stresses (27). *PUB4* plays notably a role
197 in a quality-control pathway that removes damaged chloroplasts (28). Two other SNPs were
198 located in the nearby cytochrome P450 gene *CYP81D6* (At2g23220), 40 kb from *PUB4* ($r^2 =$
199 0.63). CYP450s catalyze the production of diverse secondary metabolites that are involved in
200 biotic and abiotic stress response (29). The remaining two SNPs were also linked to *PUB4* and
201 *CYP81D6*, but affected non-coding sequences. We note that the *PUB4* polymorphisms only
202 account for about 1% of the genetic variance in the scaling exponent. Because broad-sense
203 heritability was $H^2 > 95\%$, many other loci are expected to contribute to allometric variation,
204 potentially reducing the power of classical GWA to detect SNPs significantly associated with the
205 scaling exponent. For instance, we expected that, given the strong correlation between the
206 scaling exponent and plant lifespan (Dataset S2), many flowering time genes would be
207 significantly associated with allometry. However, no SNP reached the significance threshold for
208 lifespan in our analysis (FDR > 0.05), and we therefore do not have evidence for flowering time
209 genes being predictors of allometric variation. This might be due to over-correcting for
210 population structure, or to the high number of SNPs involved in phenotypic variation between
211 accessions. Indeed, a strong correction for population structure might be inappropriate if many
212 genes across the entire genome contribute to the phenotype in question.

213 To account for the potentially complex genetic architecture of traits, we ran Bayesian
214 Sparse Linear Mixed Models (BSLMM) implemented in GEMMA (30). BSLMM models two
215 hyperparameters, a basal effect α_i that captures the fact that many SNPs contribute to the
216 phenotype, and an extra effect β_i that captures the fact that not all SNPs contribute equally. SNP
217 effects, which can be estimated as the sum of α_i and β_i (30), were strongly correlated between the
218 scaling exponent and all climatic variables except temperature annual range (Dataset S5). As
219 expected, correlations between SNP effects on scaling exponent and climate were strongest for
220 mean annual temperature, and temperature and precipitation during summer (Dataset S5).
221 Consistent with the measurement of broad-sense heritability (H^2), ‘chip’ heritability - a proxy for
222 narrow-sense heritability (h^2) measured with GWA - was very high for the scaling exponent (h^2
223 = 0.87 versus $H^2 = 0.95$; Table S1), suggesting that most of the phenotypic variance can be
224 explained by the additive effects of SNPs controlling allometric variation.

225 Gene ontology (GO) analysis (31) of the 1% top-genes affecting the scaling exponent
226 revealed enrichment in genes with catalytic activity and ones related to carbohydrate
227 metabolism, post-embryonic development, post-translational protein modification, and response
228 to abiotic stimulus (Fig. S4A, B). A large fraction of the proteins encoded by these genes are
229 predicted to localize to plasma membranes or the chloroplast (Fig. S4C). F_{st} values across the
230 100 top-genes were significantly higher than genome-wide F_{st} values ($F_{st [100 \text{ top-genes}]} = 0.23$
231 versus $F_{st [\text{Genome-wide}]} = 0.17$, $P < 0.001$; Fig. S3), which is consistent with Q_{st} analysis and
232 indicative of polygenic selection on the genes controlling growth allometry. As expected, *PUB4*
233 is among the 100 top-genes associated with plant allometry, showing strong effects on both the
234 scaling exponent and climatic variables (Fig. 4D, E). We estimated that *PUB4* alone favors plant
235 adaptation to warmer and drier summers by up to +1.4 °C and -3mm (Fig. 4D, E) through an
236 increase of the scaling exponent by up to +0.03.

237 A scan for genomic signatures of selection in the 50 kb region around *PUB4* revealed
238 increased Tajima's D (Fig. 5A) and SNP-level F_{st} (Fig. 5B), but we did not observe signatures of
239 recent selection sweeps. As an index of allelic diversity that quantifies departures from the
240 standard neutral model (32), high Tajima's D values indicate an excess of intermediate-
241 frequency alleles, a potential sign for balancing selection, specifically in *A. thaliana* where
242 Tajima's D is commonly negative due to recent population expansion and selfing (33, 34). This
243 is consistent with molecular signatures of climate selection previously observed in *A. thaliana*
244 (35, 36). Moreover, climate-envelope modelling of *PUB4* allelic distribution revealed strong
245 geographic structure associated with summer conditions; the major *PUB4* allele is mostly found
246 in temperate and cold northern parts of Europe (Fig. 5C), while the minor allele is mostly
247 Mediterranean (Fig. 5D). This supports the role of *PUB4* in evolutionary adaptation to warmer
248 and drier regions around the Mediterranean through variation in growth scaling.

249 Discussion

250 Metabolic allometry links physiology, ecology and evolution at different levels of organization
251 (4, 6, 37, 38). The study of scaling relationships in both plants and animals is grounded on the
252 importance of universal metabolic properties that allow the measurement and prediction of
253 critical rates of energy flow from individuals to the biosphere (6, 39). However, explanations for

254 the origin of allometric variation between species remain elusive, despite a recognized role of
255 evolutionary processes in animals (40). Changes in scaling intercept in response to selection are
256 well documented (41), but evidence for the evolution of allometric slopes is scarce (but see (42)),
257 in particular in plants where the focus has been on the specific value that the allometric slope
258 should take (*e.g.* $\frac{2}{3}$ versus $\frac{3}{4}$ versus 1) (9, 13, 43).

259 Our results reconcile recent debates on the origin of biological allometry. On the one
260 hand, our results support the idea that growth allometry varies significantly and that genetic
261 variation in allometry is maintained within species. On the other hand, the canonical $\frac{3}{4}$ scaling
262 exponent reported within and across plant and animal species was found to be associated with a
263 phenotypic optimum that maximizes fitness under benign conditions, consistent with a role of
264 stabilizing selection (4). Nonetheless, depending on the local environment, deviations in both
265 directions from the $\frac{3}{4}$ scaling exponent might be advantageous for stress resistance despite their
266 cost on seed production. Thus, stabilizing selection on metabolic allometry could be disruptive
267 under unfavorable environments, as we have found for *A. thaliana*. Allometric adaptation may be
268 due to, for instance, selection for fast growth and short lifespan to escape drought, or selection
269 for resistance to hydraulic cavitation associated with reduced stomatal conductance and carbon
270 assimilation in late flowering ecotypes (23, 44).

271 Specifically, these findings shed light on the important role of allometry for local
272 adaptation to various climates in *A. thaliana*. Moreover, our results inform our understanding of
273 the evolutionary basis of the tenets of MST. The maintenance of high intermediate-frequency
274 nucleotide diversity in genes affecting allometry could result from long-term, geographically
275 heterogeneous selection to optimize growth and survival in contrasting environments. This
276 appears to have resulted in the genetic diversification of the scaling exponent around the intra-
277 and interspecific mean of $\frac{3}{4}$, potentially reconciling the original MST prediction of an optimal
278 scaling $\frac{3}{4}$ value with observed departures from it that have generated past debates (45). An
279 intriguing question is whether the observed variation in scaling exponents across species (46) is
280 associated with a similar climate adaptation as we observed for *A. thaliana*. Inter- and
281 intraspecific variation in the vascular network and its impact on hydrodynamic resistance,
282 resource distribution and plant allometry is already being explored (47, 48). If genetic variability
283 in growth allometry is confirmed in other species and associated with climate, this would have

284 important implications for our understanding of the physiological bases of plant adaptation.
285 Moreover, it would connect macroevolutionary patterns of trait covariation observed across
286 species to microevolutionary processes occurring within species.

287

288 **Materials and Methods**

289 **Published data.** For stress resistance analysis, we used published data from two studies on the
290 response of *A. thaliana* natural accessions to drought: one where 210 accessions shared with our
291 study were subjected to severe, lethal drought and survival was estimated for all accessions (21),
292 and one where 60 shared accessions were subjected to 7 d non-lethal drought and fresh weight
293 measured (22). We also re-analyzed phenotypic data previously published (10, 23) from a
294 population of 120 *Ler-2* x *Cvi* recombinant inbred lines (49), and grown under water deficit and
295 high temperature (10, 23).

296 Climatic data consisted of 19 bioclimatic variables (<http://www.worldclim.org/bioclim>)
297 with a 2.5 arc-minutes resolution for the 1950 to 2000 CE period, plus mean annual Potential
298 Evapo-Transpiration (PET, mm) and annual Aridity Index downloaded from [http://www.cgiar-](http://www.cgiar-csi.org/data/global-aridity-and-pet-database)
299 [csi.org/data/global-aridity-and-pet-database](http://www.cgiar-csi.org/data/global-aridity-and-pet-database) (19). Monthly averages were calculated with 30 arc-
300 seconds (ca. 1 km). Additional details in SI.

301 **Plant Material and Growth.** We selected 451 natural accessions of *Arabidopsis thaliana* from
302 the 1001 Genomes project (17) (<http://1001genomes.org/>; Dataset S1). Seeds were from parents
303 propagated under similar conditions in the greenhouse. Four replicates of each accession were
304 grown, with one replicate each sown on four consecutive days. Two replicates per accession
305 were harvested as 16 day-old seedlings for dissection, imaging and weighing, and two were
306 cultivated until the end of the life cycle (until fruit ripening) for trait measurement. Plants were
307 cultivated in hydroponics culture on rockwool. Seedlings were vernalized for 4°C (8 h light) for
308 41 days. Plants were then transferred to 16 °C (12 h light). Additional details in SI.

309 **Plant Measurements.** The Raspberry Pi Automated Plant Analysis (RAPA) system was used for
310 continuous imaging using 192 micro-cameras (OmniVision OV5647), which simultaneously
311 acquired 6 daily top-view 5 Megapixel images for each tray of 30 plants during the first 25 days

312 after vernalization. Recording and storage of images were managed through embedded
313 computers (Raspberry Pi rev. 1.2, Raspberry Pi Foundation, UK). Inflorescences and rosettes of
314 mature plants were separated and photographed (Canon EOS-1, Canon Inc., Japan). The rosette
315 was dried for at least three days at 65 °C, and weighed with a microbalance (XA52/2X, A. Rauch
316 GmbH, Graz, Austria).

317 Fruits (siliques) were counted by eye on inflorescence images of 352 plants harvested at
318 maturity. We analyzed the inflorescence pictures of all harvested plants with ImageJ (50) to
319 estimate the number of fruits through image 2D skeletonization (18). The inferred variables were
320 used to predict fruit number with linear regression (*glm*) performed on the 352 plants for which
321 we had both measurements (18).

322 Drought survival index were from published data, measured as the quadratic coefficient
323 of the polynomial regression between green leaves and time after the end of watering; more
324 negative values mean lower survival (21). Measurements of growth reduction under moderate
325 drought were also from published data, measured as the percentage of rosette fresh weight after
326 seven days of water deficit compared to control (22). In the re-analysis of the population of 120
327 RILs previously phenotyped for growth scaling exponent (10), and trait plasticity in response to
328 water deficit and high temperature (23), we measured resistance to combined stresses through the
329 log ratio of dry mass under stress or no stress. Additional details in SI.

330 **Modeling Growth and RGR.** Absolute growth rate (mg d^{-1}) was estimated as the ratio of final
331 rosette dry mass and plant lifespan. Using rosette dry mass estimated from image analysis (18),
332 we fitted a sigmoid curve as a three-parameter logistic equation (51) with the function *nls* in R.
333 From the parameters of the fitted function of each individual, we measured RGR (rosette growth
334 rate divided by rosette dry mass, $\text{mg d}^{-1} \text{g}^{-1}$) at the inflection point of the growth trajectory (18).

335 **Statistical Analyses.** Statistical analyses except genomic analyses were performed in R (52).
336 The coefficients of correlation (and their associated *P*-values) reported between phenotypic traits
337 and climatic variables were the Pearson's product moment coefficients obtained with the
338 function *cor.test* in R. Effect of population structure on the scaling exponent was tested with
339 ANOVA, using the nine genetic groups identified in the 1001 genomes dataset
340 (<http://1001genomes.github.io/admixture-map/>) after removing admixed accessions (17). Broad-
341 sense heritability (H^2) was measured as the proportion of variance explained by genotype (Vg)

342 over total variance ($V_g + V_e$) in a linear mixed model fitted with the ‘lme4’ R package, such as:
343 $H^2 = V_g/(V_g + V_e)$. Similarly, Q_{st} was measured as the amount of variance in phenotypes
344 explained by genetic group membership. As for H^2 , we used linear mixed model in the package
345 ‘lme4’ in R to fit traits against genetic groups (nine genetic groups after removing ‘admixed’
346 accessions).

347 **Genetic Analyses.** Conventional genome-wide association (GWA) studies were performed with
348 easyGWAS (25) (<https://easygwas.ethz.ch/>). We used 1,793,606 SNPs with a minor allele
349 frequency (MAF) above 0.05 to compute the realized relationship kernel from the full sequence
350 of the accessions (<http://1001genomes.org/>). Association analyses were performed with
351 EMMAX (53). For polygenic GWA, we used the Bayesian Sparse Linear Mixed model
352 (BSLMM) implemented in GEMMA (30). Gene Ontology (GO) analysis was performed online
353 using AgriGO (<http://bioinfo.cau.edu.cn/agriGO/>) (31) and REVIGO (<http://revigo.irb.hr/>) (54).

354 Prior to F_{st} calculation, genetic groups in the 1001 Genomes collection had been defined
355 by ADMIXTURE clustering (55) (<http://1001genomes.github.io/admixture-map/>) (17). Genome-
356 wide estimates of Weir and Cockerham F_{st} (56) were obtained with PLINK v1.9 (57). Local
357 selection scans (Tajima’s D and F_{st}) were obtained in 1 kb sliding windows in the 50 kb region
358 around *PUB4* using PLINK. Selection sweep scans were carried out using SweeD software (58).
359 Additional details in SI.

360 **Modeling Geographic Distribution.** We performed stepwise regression to identify the set of
361 climatic variables that best explain the variation of the scaling exponent between 36°N and 64°N,
362 and 10.5°W and 27.5°E. We then used linear regression of the scaling exponent with the 13 best
363 climatic variables to predict the exponent at every location across Europe. Geographic
364 representation was obtained with the package ‘raster’ in R. We performed climate-envelope
365 modelling of allelic frequency at *PUB4* with *maxent* modelling (59), using the package ‘dismo’
366 and ‘raster’ in R. We used the 19 Bioclim variables downloaded from Worldclim database at the
367 origin of accessions with a 2.5 arc-minutes resolution. Additional details in SI.

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375 **Author Contributions**

376 FV, CV and DW designed the study. FV performed the experiments and extracted the data. FV,
377 OJAG, DV, GW and MEA performed statistical analyses. All authors interpreted the results and
378 wrote the paper.

379 **Competing interests**

380 The authors declare no conflict of interest.

381 **Data Availability**

382 Phenotypic data are available in SI and on Dryad repository (<http://datadryad.org/>). R codes and
383 ImageJ macro for data analysis are available on Github (<https://github.com/fvasseur>). GWAS
384 results are available in easyGWAS (<https://easygwas.ethz.ch/>).

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Figure Legends

Figure 1. Variation of growth scaling in *A. thaliana*. (A) Linear (dashed line) and quadratic (solid line) fits of mean growth rate versus final dry mass in 451 *A. thaliana* accessions. Box: linear fit (black line) of growth rate versus plant dry mass in 333 vascular plant species from Niklas and Enquist (8). (B) Distribution of the scaling exponent derived from the quadratic fit in the 451 *A. thaliana* accessions. (C) Relationship between relative growth rate (RGR) at growth maximum, plant lifespan and scaling exponent in the 451 accessions. Black curve is Loess fit \pm 95% CI (grey area). In all panels, dots and triangles represent genotypic and species means, respectively, colored by the value of the scaling exponent reported in panel (B).

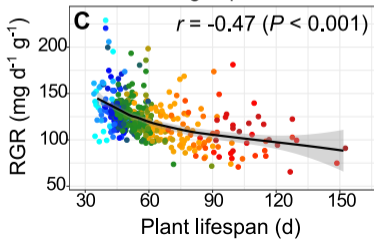
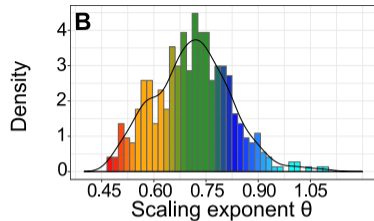
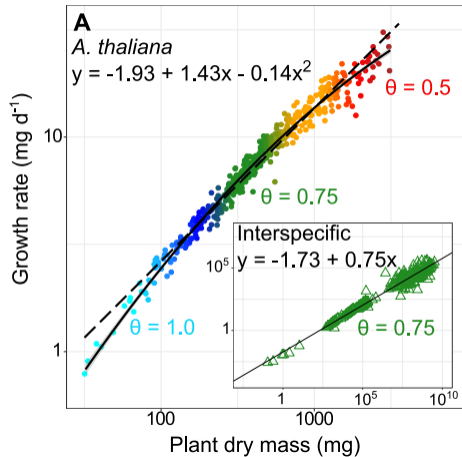
Figure 2. Relationships between scaling exponent and climate. (A-C) Correlations between the scaling exponent measured across the 451 accessions and local mean annual temperature (A), maximum temperature of the warmest month (B), and precipitation of the driest month (C). Dots represent genotypic mean. Fitted lines are SMA regressions. r is the Pearson's coefficient of correlation with associated P -value. (D) Geographic distribution of the scaling exponent across Europe in *A. thaliana*, modelled as a function of 13 Bioclim variables. Colors indicate the predicted value of the scaling exponent. Black dots represent geographic origins of the accessions phenotyped.

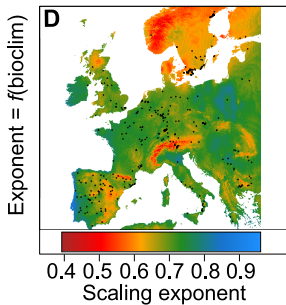
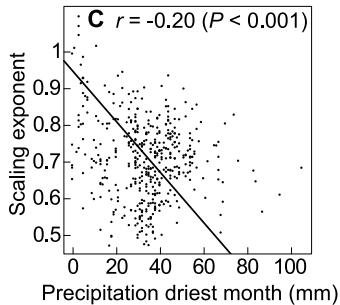
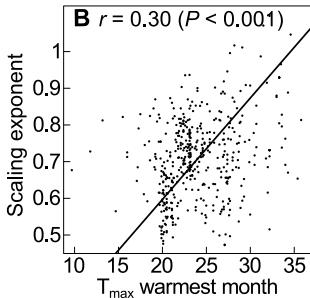
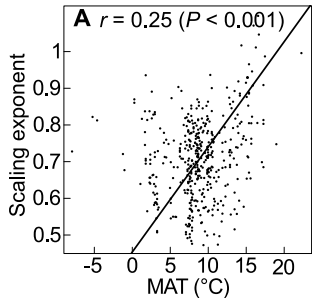
Figure 3. Relationships between scaling exponent, fitness and resistance to abiotic stress. (A) Relationship between fruit production and scaling exponent in the 451 accessions. Black curve is Loess fit \pm 95% CI (dashed lines). (B) Stress resistance expressed as the \log_{10} of the ratio of final rosette dry mass under water deficit, high temperature, and both compared to control conditions, across 120 *A. thaliana* recombinant inbred lines. Data have been published (10, 23). Dots indicate genotypic means ($n = 4$). Colored curves are Loess fit \pm 95% CI (dashed lines).

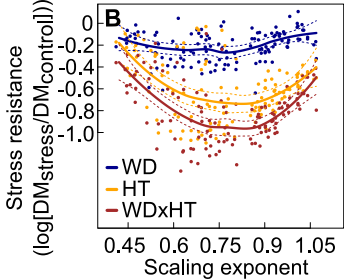
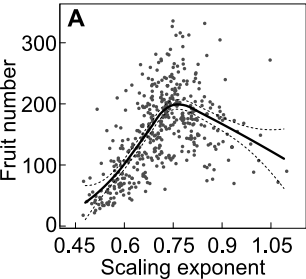
Figure 4. GWA mapping of allometric variation in *A. thaliana*. (A-C) Test statistics for SNP associations (EMMAX) with (A) scaling exponent, (B) maximum temperature during the warmest month, and (C) precipitation during the driest month. Dots are 1% top-associated SNPs along the five chromosomes (alternate grey and black dots represent chromosomes). Orange lines represent genome-wide significance threshold with Bonferroni correction at $\alpha = 0.05$ (solid line) and $\alpha = 0.1$ (dashed line). Red triangle is *PUB4* (FDR < 0.05) (D, E) Correlation between

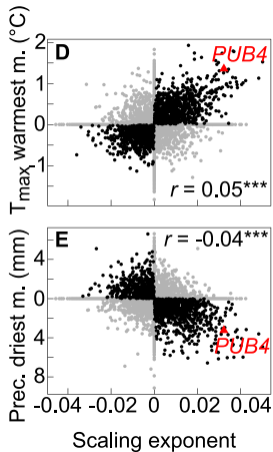
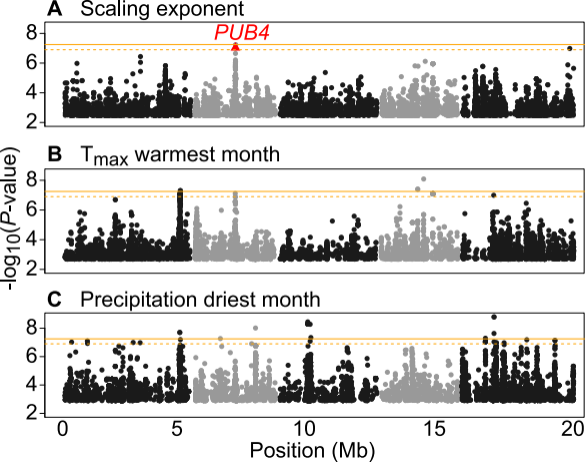
SNP effects (BSLMM) for scaling exponent and maximum temperature of the warmest month (**D**), and precipitation of the driest month (**E**). Black dots represent similar SNP effect for x and y variables (both positive or both negative). r is Pearson's coefficient of correlation (***: $P < 0.001$).

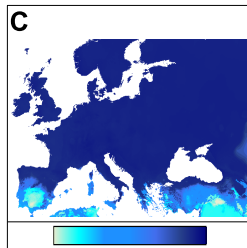
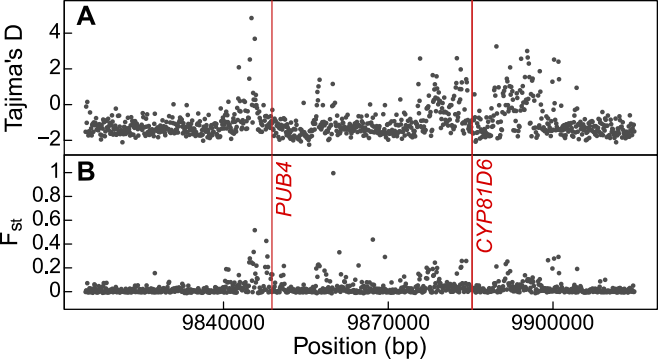
Figure 5. Genomic signatures of adaptation to climatic conditions at genes controlling the scaling exponent. (A, B) Tajima's D (A) and F_{st} (B) in a 50 kb region around *PUB4* and *CYP81D6*. Grey dots are mean values in 1 kb-bins, red lines indicate positions of significant SNPs. (C, D) Predicted geographic frequency of the major (C) and minor (D) alleles at *PUB4* following climate-envelope modelling with 19 Bioclim variables. Color gradient indicates predicted allele frequency.



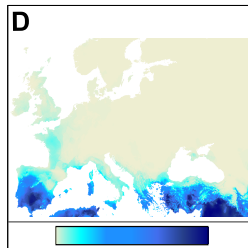








Major allele frequency



Minor allele frequency