

RESEARCH PAPER

Exploring natural genetic variation in photosynthesis-related traits of barley in the field

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Abstract

Optimizing photosynthesis is considered an important strategy for improving crop yields to ensure food security. To evaluate the potential of using photosynthesis-related parameters in crop breeding programs, we measured chlorophyll fluorescence along with growth-related and morphological traits of 23 barley inbred lines across different developmental stages in field conditions. The photosynthesis-related parameters were highly variable, changing with light intensity and developmental progression of plants. Yet, the variation in photosystem II quantum yield observed among the inbred lines in the field largely reflected the variation in CO₂ assimilation properties in controlled climate chamber conditions, confirming that the chlorophyll fluorescence-based technique can provide proxy parameters of photosynthesis to explore genetic variation under field conditions. Heritability (H^2) of the photosynthesis-related parameters in the field ranged from 0.16 for the quantum yield of non-photochemical quenching to 0.78 for the fraction of open photosystem II center. Two parameters, the maximum photosystem II efficiency in the light-adapted state ($H^2=0.58$) and the total non-photochemical quenching ($H^2=0.53$), showed significant positive and negative correlations, respectively, with yield-related traits (dry weight per plant and net straw weight) in the barley inbred lines. These results indicate the possibility of improving crop yield through optimizing photosynthetic light use efficiency by conventional breeding programs.

Keywords: Barley, chlorophyll fluorescence, crop yields, development, heritability, natural genetic variation, photosynthesis.

Abbreviations: A_{sat} , carbon assimilation at saturating light intensity; ASP, anthesis and senescence phase; DMP, dry mass per plant; F_v/F_m , maximum efficiency of PSII in light-adapted state; J_{max} , maximum rate of electron transport; LEF, linear electron flow; NPQ, non-photochemical quenching; NPQt, total non-photochemical quenching; PAR, photosynthetically active radiation; Φ_2 , quantum yield of PSII; Φ_{NO} , quantum yield of non-regulated dissipation processes; Φ_{NPQ} , quantum yield of non-photochemical quenching; PSII, photosystem II; qL, fraction of PSII open center; REP, rapid expansion phase; RGR, relative growth rate; SEP, slow expansion phase; SPAD, relative chlorophyll content; TPU, triose phosphate utilization; $V_{c,\text{max}}$, maximum rate of carboxylation.

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Introduction

To satisfy the increasing demand for agricultural products at constant crop production areas, crop yields need to be increased by the year 2050 by about 25–70% (Hunter *et al.*, 2017). The potential genetic yield under an optimal environment is the product of four main factors: incident solar radiation, light interception efficiency, conversion efficiency, and harvest index (Bonington, 1977). The green revolution led to considerable increases of light interception efficiency and harvest index by introducing dwarfing genes into cereal crops (Hedden, 2003). However, some studies suggest that these two parameters are close to their theoretical maximum in modern crop varieties (e.g. Zhu *et al.*, 2010). Accordingly, crop yield potential may be limited by the remaining bottleneck, the efficiency of light energy conversion by photosynthesis (source limitation) (Long *et al.*, 2006a; Alvarez Prado *et al.*, 2013; Kromdijk and Long, 2016). Thus, enhancing this conversion efficiency has become a breakthrough goal to improve crop yields (Zhu *et al.*, 2010).

Notably, selection of yields might have unintentionally improved the conversion efficiency, as indicated by a positive relationship between photosynthesis and crop yields (Kromdijk and Long, 2016; Theeuwens *et al.*, 2022). Still, the conversion efficiency has not reached the theoretical maximum in C_3 plants (Long *et al.*, 2006b; Zhu *et al.*, 2010; Prosekov and Ivanova, 2018) after decades of selection for crop yields. This suggests that the selection for yields is not sufficient to fully explore and make better use of natural genetic variation of photosynthesis. Direct phenotyping and selection for photosynthetic parameters are needed to identify variations in photosynthetic capacity and source limitation of crop yield (Theeuwens *et al.*, 2022).

Several studies have successfully increased yields through optimizing photosynthesis by genetic engineering (reviewed by Simkin *et al.*, 2019), such as manipulating the Calvin–Benson cycle in wheat (Driever *et al.*, 2017), carbon transport in rice (Gong *et al.*, 2015) and soybean (Hay *et al.*, 2017), and photo-protection in tobacco (Kromdijk *et al.*, 2016) and soybean (De Souza *et al.*, 2022). However, the use of genetically modified crops is restricted in some parts of the world (Turnbull *et al.*, 2021), and suggested yield improvements by genetic modification await rigorous testing in practical agricultural production conditions (Khaipho-burch *et al.*, 2023). Classical breeding can offer an alternative or additional approach. Indeed, natural variation of photosynthesis within (Wulfschleger, 1993) and across species (Flood *et al.*, 2011; van Bezouw *et al.*, 2019; Garcia *et al.*, 2022) can be exploited by classical breeding.

Natural genetic diversity of photosynthesis has been studied in cereals under field conditions. Driever *et al.* (2014) reported significant variations in photosynthetic capacity, biomass and yield in 64 wheat genotypes. Acevedo-Siaca *et al.* (2021a) observed high heritabilities for carbon assimilation-related parameters in 30 accessions of rice. However, the relationships between photosynthesis and yield observed in these studies

were not consistent. For example, Carmo-Silva *et al.* (2017) observed a positive correlation between carbon assimilation rate and grain yield in field-grown wheat at pre- and post-anthesis stages, while Driever *et al.* (2014) found no correlation between carbon assimilation-related parameters and grain yield in field-grown wheat in pre-anthesis stages. A possible explanation for such discrepancies may be the dependency of the photosynthetic traits on environmental conditions and/or developmental stages of the plants, although further research is needed to clarify this. Furthermore, in barley, one of the most important cereal crops as well as a model for other cereals because of its simpler genetics, natural variation of photosynthesis has not been investigated under field conditions.

High-throughput phenotyping techniques are essential for investigating the natural genetic variation in photosynthesis. Photosynthesis is divided into two main processes, the light reaction and CO_2 assimilation, which can be assessed by chlorophyll fluorescence- and gas exchange-based techniques, respectively (Long *et al.*, 1996; Baker, 2008). The analysis of chlorophyll fluorescence provides information on photosystem II (PSII) activity, such as the effective and the maximum quantum yields of PSII (Φ_{II} and F_v'/F_m' , respectively, for the light-adapted state) or non-photochemical quenching (NPQ) (Baker, 2008). Measurement of gas exchange allows estimation of carbon assimilation rate (A) and related parameters (Sharkey, 2016). Recently, the dynamic assimilation technique was introduced to enable gas exchange measurements in non-steady state, which substantially increased the throughput compared with steady-state measurements (Saathoff and Welles, 2021) albeit still slower than chlorophyll fluorescence-based methods. For application to crop breeding and selection, it is essential to check whether the genetic variation detected by these two techniques is comparable or not.

The objectives of this study were to (i) investigate genetic variation of photosynthesis-related parameters in barley across different developmental stages and evaluate the interaction between genotypes and environment in field conditions, (ii) compare gas exchange- and chlorophyll fluorescence-based assessments of photosynthetic traits, and (iii) assess correlation between photosynthesis-related and morphological or growth-related parameters. Based on the results obtained, we will consider the potential of using photosynthesis-related parameters in crop and particularly barley breeding programs.

Materials and methods

Field experimental design

Twenty-three spring barley (*Hordeum vulgare*) inbred lines (inbreds) were selected from a worldwide collection of 224 barley landraces and cultivars based on their genetic and phenotypic diversity (Weisweiler *et al.*, 2019). These 23 barley inbreds are the parents of the double round-robin population (Casale *et al.*, 2022). All 23 inbreds were grown at three

different locations [Bonn (50°37'31.82" N 6°59'18.508" E), Cologne (50°57'34.345" N 6°51'36.407" E), and Düsseldorf (51°10'42.599" N 6°48'8.268" E)] in Germany in 2021. In Bonn, the experimental design was an α -design with two complete replications, where the plants were sown in 10 m² plots on 31 March 2021. In Düsseldorf, the experimental design was an α -design with three complete replications. The experimental units were single rows with 33 kernels per row, and six rows together were considered as one plot (replicate). The plants in Düsseldorf were sown on 31 March 2021. In Cologne, two distinct trials were performed, which are named in the following as 'mini-big plot' and 'big plot' trials. Within each of these two trials, 23 inbreds were grown as replicated checks in an augmented design. In the mini-big plot trial, each plot had a size of 2.25 m². The entire mini-big plot trial had 320 plots, in which the 23 inbreds were grown as replicated checks twice. The big plot trial, in which each plot had a size of 10 m², comprised also 320 plots and the 23 inbreds were also grown as checks but only one time. Fertilization and crop protection followed local practices. Air temperature and precipitation were recorded during the field experiments at all three locations (Supplementary Fig. S1). In Bonn, the field site has chernozem-parabrown soil, and the field sites, in Cologne and Düsseldorf, have parabrown soil (Bundesanstalt für Geowissenschaften und Rohstoffe).

Climate chamber experimental conditions and design

Based on the results of the field experiments, six representative barley inbreds (HOR1842, IG128216, IG31424, ItuNative, K10877, and W23829/803911) were selected for a climate chamber experiment. The experimental design was a randomized complete block design with three replicates/blocks. A total of 32 plants were planted for each inbred in total. The gas exchange measurements were performed 21, 24, 26, 31, 36, 39, 46, 51, 57, 74, 87, 88, 100, and 102 days after sowing (DAS). At each measurement day, three measurements were taken from three different plants of an inbred, where always one plant from each of the blocks was studied. In addition, the Zadoks score for each evaluated plant was rated. In addition, we harvested three plants per inbred (i.e. one per block) and then measured dry weight of aboveground biomass per plant 26, 36, 46, 57, 74, 102, 113, and 142 DAS. The growth conditions in the climate chamber were as follows: 14 h/10 h light/dark photoperiod, 18 °C/16 °C temperature, and 55% relative humidity. The maximal light intensity measured at 15 cm from the light panel was 750 $\mu\text{mol m}^{-2} \text{s}^{-1}$.

Assessment of photosynthesis-related parameters

In the field experiments, the top fully expanded leaves of three representative plants from each plot were measured from seedling stage (ZS13; Zadoks et al., 1974) to dough development (ZS87) using a MultispeQ V2 device (Kuhlgert et al., 2016). We used the measurement protocol 'Photosynthesis RIDES', by which the intensity of actinic light was automatically set to the ambient light intensity measured by the built-in light sensor. The following parameters were used for the further analyses: linear electron flow (LEF), the fraction of open PSII centers (qL), the quantum yield of PSII (Phi2), the maximum efficiency of PSII in light-adapted state (F_v'/F_m'), the total NPQ (NPQt), the quantum yield of NPQ (PhiNPQ), the quantum yield of non-regulated dissipation processes (PhiNO), and relative chlorophyll content (SPAD). In addition, the MultispeQ also recorded environmental parameters, such as the intensity of photosynthetically active radiation (PAR), ambient temperature, ambient humidity, and ambient pressure.

In the climate chamber experiment, gas exchange parameters were measured multiple times from tillering stage (ZS21) to dough development (ZS89) alongside the MultispeQ measurements. The measurements were made on the top fully expanded leaves on the main stem. Three different light intensities (PAR=400, 800, 1500 $\mu\text{mol m}^{-2} \text{s}^{-1}$) were used as simulated low-light (LL), medium-light (ML) and high-light (HL)

conditions for the MultispeQ measurements. Leaf-level gas exchange measurements were performed by LI-6800 (LI-COR Biosciences Inc., Lincoln, NE, USA). Three replicates per genotype were measured from 1 h after the onset of the light period. The settings inside the LI-6800 chamber were as follows: PAR was kept at 1500 $\mu\text{mol m}^{-2} \text{s}^{-1}$ (as in the simulated HL) with 50% blue and 50% red light, 400 $\mu\text{mol m}^{-2} \text{s}^{-1}$ air flow rate, 10 000 rpm fan speed, 55% relative humidity, and 18 °C air temperature. The proportion of blue and red light was chosen to mimic the HL conditions in the field. The humidity and air temperature in the LI-6800 chamber were chosen to mimic the growth condition in the climate chamber and, thus, reduce the time needed for stabilization prior to the measurements. The CO₂ concentration inside the LI-6800 chamber was 400 ppm during pre-acclimation, which lasted between 10 and 15 min. After the pre-acclimation, photosynthetic CO₂ response ($A-C_i$) curves were measured according to the dynamic assimilation technique (Saathoff and Welles, 2021). CO₂ ramps were started from 1605 to 5 ppm with ramping rates of 200 ppm. The $A-C_i$ curves were then analysed using the 'plantecophys' package (Duursma, 2015) in R version 4.0.3 to estimate the maximum rate of carboxylation ($V_{c,\text{max}}$), the maximum rate of electron transport (J_{max}), and triose phosphate utilization (TPU).

Assessment of morphological and growth-related traits

To determine the relative growth rate (RGR) of the 23 barley inbreds, aboveground biomass data were collected in the field experiment in Düsseldorf at six different time points during the vegetative period: at 62, 69, 76, 83, 97, and 125 DAS. Plants of one row (initially 33 kernels were sown) per plot were harvested for the 23 genotypes with three replicate plots. Wild animals visited the trails, and therefore the number of damaged plants for each row was recorded.

The dry weight per row per plot was used to estimate the dry mass per plant (DMP), which was needed for the assessment of growth curve parameters, using the following equation:

$$\text{DMP} = \frac{\text{DM}}{(\text{TNP} - \text{NDP}) + 0.8 \times \text{NDP}} \quad (1)$$

where TNP was the total number of plants, NDP the number of damaged plants, 0.8 was the completeness of the damaged plants based on the observation during the harvest. DMP calculated as described above, was corrected separately for each time point for replicate and block effects. The corrected values were then used for further analyses.

In the climate chamber experiment, the total aboveground DMP was measured by weighing at eight different time points (26, 36, 46, 57, 74, 102, 113, and 142 DAS) except for the two inbreds IG31424 and HOR1842, for which only the initial and the final DMP were determined at 26 and 142 DAS. Three replicates per genotype were collected for each time point.

To assess the relationship between DMP and time, logistic (Verhulst, 1838), power-low (Paine et al., 2012), and quadratic regression (Lithourgidis and Dordas, 2010) models were fitted. The quadratic regression model was used:

$$y_t = a + bt - ct^2 \quad (2)$$

where a represents the initial biomass, b and c the growth rate parameters. This model had a high coefficient of determination (R^2) and the highest heritability across all 23 barley inbreds. Thus, the quadratic regression was used for estimation of RGR. RGR_a , RGR_b , RGR_c represent the parameters in quadratic regression a , b , and c , respectively.

Morphological parameters were collected in multi-year and multi-environment field experiments that took place in the years 2017–2021

at Düsseldorf, Cologne, Mechernich, and Quedlinburg (Shrestha *et al.*, 2022; Wu *et al.*, 2022). Not all locations were used in all years to assess all parameters. Flag leaf length (FL, cm) and width (FW, cm), plant height (PH, cm), flowering time (FT), awn length (AL, cm), spike length (EL, cm), and spikelet number in one row of the spike (SR), seed length (SL, mm), seed width (SW, mm), seed area (SA, mm²), and thousand grain weight (TGW, g), grain weight (GW, kg per 10 m²), and net straw weight (NSW, kg per 10 m²) were measured as morphological parameters. FL, FW, AL, EL were measured by ruler, SL, SW, and SA were measured by MARViN seed analyser (MARViNTECH GmbH, Germany), and TGW was measured by MARViN and a balance.

The same set of morphological parameters were also measured in the climate chamber experiment. FL and FW were collected at 74 and 102 DAS with three replicates, and spike-related traits (AL, EL, SR, SL, SW, SA, and TGW) were collected at 142 DAS with three replicates. Additionally, the total stem (without spike) weight per plant (SWP, g), total spike weight per plant (SKWP, g), total stem weight of main stem (TSWM, g), and spike weight of main stem (SKWM, g) were also collected in the climate chamber experiment. Harvest index (HI) was calculated using the following equation:

$$HI = \frac{SKWP}{DMP} \quad (3)$$

In addition, harvest index of main stem (MSHI) was calculated using the following equation:

$$MSHI = \frac{SKWM}{TSWM} \quad (4)$$

Statistical analyses

Field experiment

Due to the strong dependence of photosynthesis on light intensity (Ogren, 1993), we considered three light intensity clusters when analysing field measurements: LL, ML, and HL conditions. These light intensity clusters were identified by *K*-means clustering of PAR and LEF. In addition, we also compared three main developmental phases of barley, i.e. slow expansion phase (SEP) ($ZS < 30$), rapid expansion phase (REP) ($30 \leq ZS < 60$), and anthesis and senescence phase (ASP) ($ZS \geq 60$). These two factors, light intensity (*L*) and developmental phase (*S*), each with three levels, were considered when analysing the MultispeQ parameters from the field experiments based on the following linear model with the quantitative covariates light intensity (PAR) and developmental stage (ZS):

$$\begin{aligned} Y_{(p)ijklmnopqr} = & \mu + G_i + E_j + (G : E)_{ij} + ZS_k + L_l + S_m + (G : L)_{il} \\ & + (G : S)_{im} + M_n + D_o + PAR_{ijklmnopqr} + T_{ijklmnopqr} \\ & + (E : R)_{jp} + (E : R : B)_{jpq} + \epsilon_{(p)ijklmnopqr} \end{aligned} \quad (5)$$

where $Y_{(p)ijklmnopqr}$ was the observed MultispeQ parameter across all light conditions and all developmental stages, μ the general mean, G_i the effect of the *i*th inbred, E_j the effect of the *j*th environment, $(G : E)_{ij}$ the interaction between the *i*th inbred and the *j*th environment, ZS_k the effect of the *k*th Zadoks score of barley development, L_l the effect of the *l*th light intensity cluster, S_m the effect of the *m*th barley developmental phase, $(G : L)_{il}$ the interaction between the *i*th inbred and the *l*th light intensity cluster, $(G : S)_{im}$ the interaction between the *i*th inbred and the *m*th barley developmental phase, M_n the effect of the *n*th MultispeQ device, D_o the effect of measurement date, $(E : R)_{jp}$ the effect of the *p*th replicate

nested within the *j*th environment, $(E : R : B)_{jpq}$ the effect of the *q*th block nested within the *p*th replicate in the *j*th environment, $PAR_{ijklmnopqr}$ the light intensity of each measurement, $T_{ijklmnopqr}$ the ambient temperature of each measurement, and $\epsilon_{(p)ijklmnopqr}$ the random error.

To estimate adjusted entry means for MultispeQ parameters of all inbreds, G_i , E_j , $(G : E)_{ij}$, ZS_k , L_l , S_m , $(G : L)_{il}$, and $(G : S)_{im}$ were treated as fixed effects, and M_n , D_o , $(E : R)_{jp}$, $(E : R : B)_{jpq}$ as random effects, $PAR_{ijklmnopqr}$ and $T_{ijklmnopqr}$ were covariates. Furthermore, we calculated adjusted entry means for all inbreds for each light intensity cluster as well as each developmental phase.

In addition, to evaluate the effect of each fixed factor and covariate, analysis of variance (ANOVA) was conducted.

To assess the heritability of each photosynthesis-related parameter at each developmental stage, which was considerably shorter than the above-mentioned three developmental phases, data were separated into eight stages from Zadoks principal growth stages. The adjusted entry means were calculated based on the following model:

$$\begin{aligned} Y_{(pd)ijklmnopqr} = & \mu + G_i + E_j + M_n + D_o + PAR_{ijklmnopqr} + T_{ijklmnopqr} \\ & + (E : R)_{jp} + (E : R : B)_{jpq} + \epsilon_{(p)ijklmnopqr} \end{aligned} \quad (6)$$

where $Y_{(pd)ijklmnopqr}$ was the photosynthesis-related parameter for each developmental stage across all other factors. Due to convergence problems, the interaction between G_i and E_j was removed from this model.

To assess the similarities among the barley genotypes with respect to their photosynthesis parameters, we performed hierarchical clustering by Ward's minimum variance theory (Ward, 1963) using the adjusted entry means of PSII parameters and SPAD at three different developmental phases. Furthermore, principal component analysis (PCA) was conducted by using the adjusted entry means calculated for each inbred in each of the developmental phases described before. In addition, a PCA was conducted by using the environmental factors (temperature and precipitation) of the inbreds at the country of origin. The relationship between photosynthesis-related parameters and morphological or growth-related parameters of the inbreds was evaluated by Pearson's correlation coefficient among adjusted entry means.

Climate chamber experiment

The adjusted entry means of carbon assimilation-related parameters from the climate chamber experiment were calculated based on the following model:

$$\begin{aligned} Y_{(A)ijklmnr} = & \mu + G_i + ZS_j + D_k + (D : TW)_{kl} \\ & + S_m + (G : S)_{im} + \epsilon_{(A)ijklmnr} \end{aligned} \quad (7)$$

where $Y_{(A)ijklmnr}$ was the carbon assimilation-related parameter, $D : TW_{kl}$ the effect of the *l*th time window in the *k*th date of measurement, and $\epsilon_{(A)ijklmnr}$ the random error. To estimate adjusted entry means for carbon assimilation-related parameters of six barley inbreds, G_i , ZS_j , S_m and $(G : S)_{im}$ were treated as fixed effects, as well as D_k and $D : TW_{kl}$ as random effects.

The relationship between photosynthesis-related parameters and morphological or growth-related parameters of the inbreds was evaluated by Pearson's correlation coefficient between adjusted entry means.

Estimation of heritability

Broad-sense heritability (H^2) was estimated for both field and climate chamber experiments based on the following method:

$$H^2 = \sigma_G^2 / (\sigma_G^2 + \bar{v}_S^{\text{BLUE}} / 2) \quad (8)$$

where σ_G^2 was the genotypic variance calculated based on the above models with a random effect for G_i and \bar{v}_8^{BLUE} was the mean variance of the difference of two genotypic means (Holland *et al.*, 2003; Piepho and Möhring, 2007).

To avoid the effect of the varying number of replicates, the H^2 of photosynthesis-related parameters was estimated for each developmental stage based on the following equation:

$$H^2 = \sigma_G^2 / (\sigma_G^2 + \sigma_{G:E}^2/5 + \sigma_e^2/5) \quad (9)$$

where $\sigma_{G:E}^2$ was the variance of the interaction of barley inbreds and environments, and σ_e^2 was the residual variance.

We used the statistical software R to perform all statistical analyses.

Results

Factors affecting photosynthesis-related parameters in the field

Parameters of PSII and SPAD were collected under field conditions with a wide range of PAR from 67 to 2172 $\mu\text{mol m}^{-2} \text{s}^{-1}$. In general, LEF increased as PAR increased, with an increasing variability among the individual observations at higher PAR (Fig. 1A). An increase of PAR was associated with a decrease of Phi2 and an increase of PhiNPQ, while PhiNO remained relatively stable (Supplementary Fig. S2A–C). Note that the sum of Phi2, PhiNPQ, and PhiNO is equal to 1. The light-dependent changes in Phi2 were accompanied by the corresponding changes in F_v'/F_m' and qL (Supplementary Fig. S2D, E). The light response of NPQt was similar to that of PhiNPQ except that it often gave extreme values (Supplementary Fig. S2F). In contrast to these PSII parameters, SPAD values were not affected by momentary PAR (Supplementary Fig. S2G).

Given the strong influence of PAR on PSII parameters, K-means clustering was performed to separate the observations of LEF into three groups based on the light intensity: LL, ML, and HL conditions (Fig. 1B). As expected, significant ($P < 0.05$) differences in Phi2 and PhiNPQ, but not SPAD, were observed among the three light intensities (Fig. 2A; Supplementary Table S1). We then assessed the impact of developmental phase (SEP, REP, and ASP) on these parameters (Fig. 2B; Supplementary Table S2). All three parameters showed significant ($P < 0.05$) differences between SEP and REP; Phi2 and SPAD increased from SEP to REP while PhiNPQ decreased (Fig. 2B). Thus, both PAR and developmental phases seem to affect Phi2 and PhiNPQ, whereas SPAD changed with plant development.

Significant ($P < 0.05$) effects on PSII parameters and SPAD were observed for the interactions between genotype and environment ($\sigma_{G:E}^2$), genotype and light condition ($\sigma_{G:L}^2$) and genotype and developmental phase ($\sigma_{G:S}^2$), along with the effects of genetic variation (σ_G^2) or other variables such as the date of measurement (σ_D^2), the used MultispeQ device (σ_M^2), and the replicate ($\sigma_{E:R}^2$) (Table 1). Analysis of variance also confirmed significant ($P < 0.05$) effects of PAR, light condition, developmental phase, and developmental stage (rated on the Zadoks

scale) on the different PSII parameters and SPAD (Table 2). In addition, ambient temperature (T), which typically co-varies with light intensity in the field, also significantly ($P < 0.05$) affected the PSII parameters except PhiNPQ in barley.

Genetic variations in photosynthesis-related traits

When data from all light conditions and all developmental stages were combined together, H^2 of the examined parameters ranged between 0.16 (PhiNPQ) and 0.78 (qL) (Table 1). Notably, when the heritability was calculated separately at different developmental stages as defined by the Zadoks growth scale, the H^2 values of these parameters were considerably lower in the seedling growth stage and significantly ($P < 0.05$) higher in the dough developmental stage (Supplementary Fig. S3). In accordance, all PSII parameters and SPAD had low H^2 values in the SEP (Fig. 3). In the REP, SPAD and Phi2 had the highest H^2 while NPQt and F_v'/F_m' had the lowest. In the ASP, the H^2 of Phi2 decreased dramatically.

Hierarchical cluster analysis of the adjusted entry means of the PSII parameters and SPAD observed in each of the three developmental phases indicated the presence of four major clusters among the 23 barley inbred lines (Fig. 4A). In general, the four clusters differed in the PSII parameters but not in SPAD (Fig. 5A). All PSII parameters except NPQt showed significant ($P < 0.05$) differences among the four clusters in each of the three developmental phases (Fig. 5A).

We then asked whether the four clusters also represented differences in growth-related and morphological parameters among the 23 inbred lines. Relative growth rates (RGR) were calculated from the changes in DMP in the field experiment in Düsseldorf (Supplementary Fig. S4). Based on the growth parameters alone, the inbred lines could be divided into two clusters by hierarchical cluster analysis: DMP remained at the same level after 100 days after sowing, and DMP increased throughout the entire growth season (Supplementary Fig. S4). We observed no significant difference ($P = 0.3$) in flowering time between the two groups. When PCA was performed on a combination of the PSII parameters and SPAD data shown in Fig. 2 as well as the growth-related parameters derived from Supplementary Fig. S4 and morphological traits collected from multi-year and multi-environment field experiments, the analysis revealed four clusters (Fig. 4B) that were very similar to those identified based on the PSII parameters and SPAD alone (Fig. 4A). Comparing the four clusters, we found no significant difference in DMP and RGR (Fig. 5B) or the morphological traits (Supplementary Fig. S5). Moreover, no significant correlation was observed between the first two principal components and the environmental information of the country of origin of inbreds (Fig. 4C). Together, these results suggest that the clustering of the inbreds according to photosynthetic parameters primarily reflects genetic variations in photosynthetic traits among the 23 inbreds and is not confounded by differences in growth-related and morphological parameters.

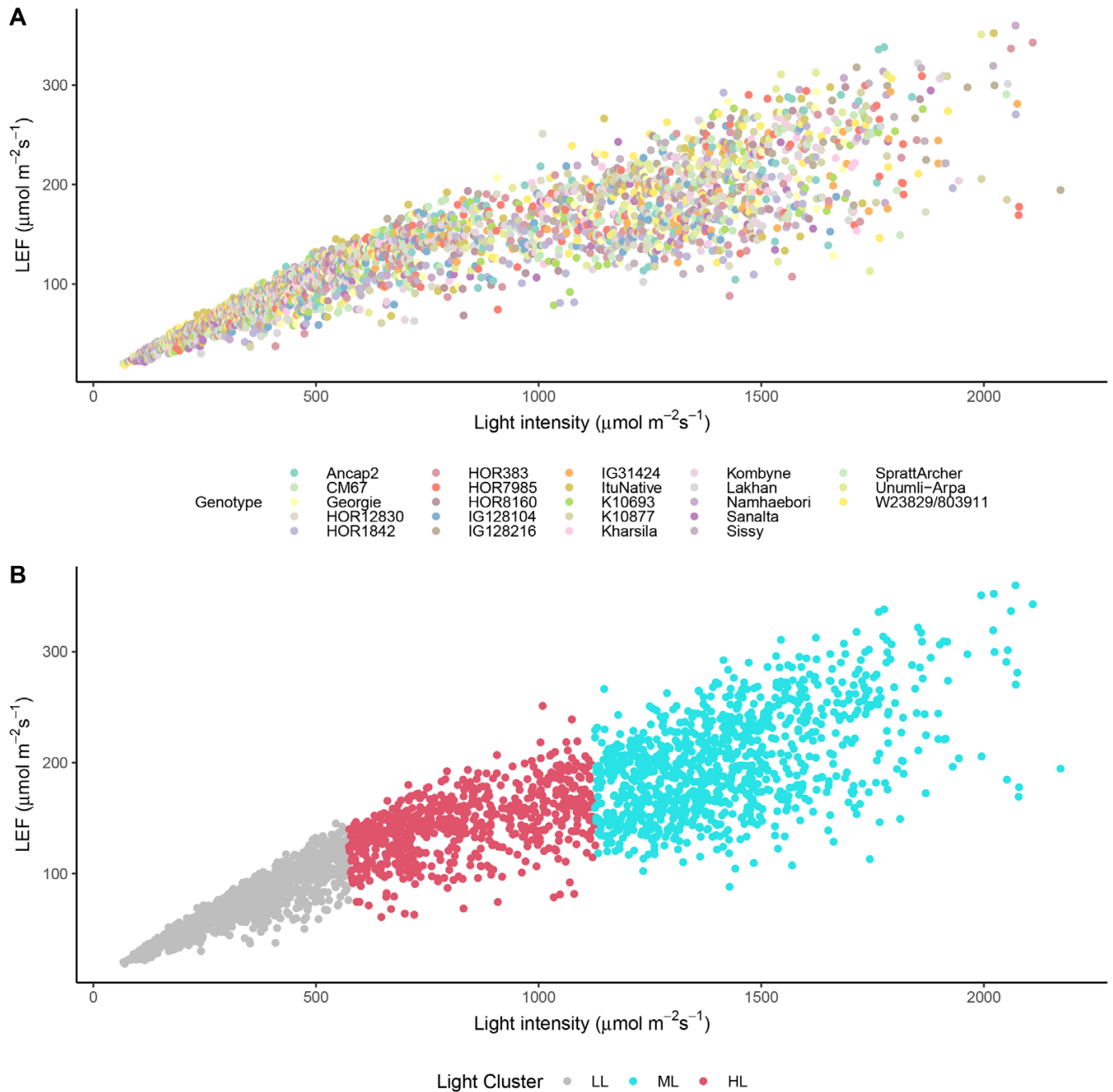


Fig. 1. Linear electron flow (LEF) for 23 barley inbred lines in the field experiment in response to changing light intensity across all environments. The different colors of the dots in (A) indicate 23 different barley inbred lines. Three different colors of the dots in (B) represent the clusters of low (LL), medium (ML), and high (HL) light condition.

Comparison of gas exchange-based parameters and PSII parameters

Of the 23 barley inbreds, six (HOR1842, IG128216, IG31424, ItuNative, K10877, and W23829/803911) were selected to assess carbon assimilation-related parameters in climate chamber conditions. These six inbreds differed in the PSII parameters

and SPAD assessed in the field. HOR1842 had the lowest adjusted entry means for Φ_i2 , q_L , and SPAD; IG128216 had the highest Φ_i2 and LEF. IG31424 had the highest $\Phi_i\text{NPQ}$ and the lowest SPAD. ItuNative had the lowest SPAD with relatively high Φ_i2 , whereas K10877 had the highest SPAD with average values of PSII parameters. W23829/803911 was characterized by the lowest $\Phi_i\text{NPQ}$ and NPQ_t .

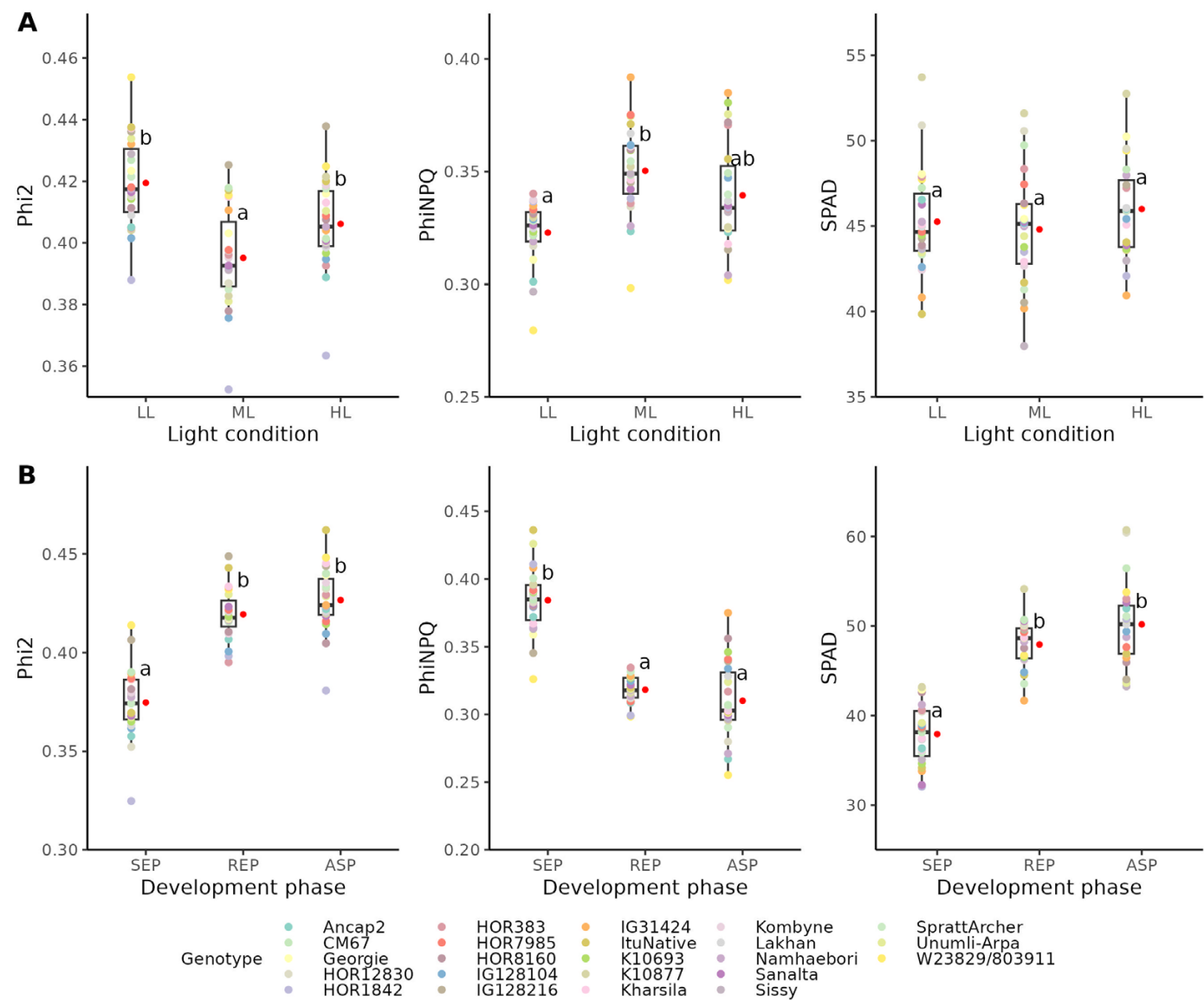


Fig. 2. Effects of light intensity and developmental phase on the quantum yield of PSII (Phi2), the quantum yield of non-photochemical quenching (PhiNPQ), and relative chlorophyll content (SPAD) of 23 barley inbred lines. (A) Comparison of three light conditions: LL (low light), ML (medium light), and HL (high light). (B) Comparison of three developmental phases: slow expansive phase [SEP; Zadoks score (ZS) from 10 to 29], rapid expansive phase (REP; ZS from 30 to 59), and anthesis and senescence phase (ASP; ZS from 60 to 87). The colored dots represent the adjusted entry means for 23 barley inbred lines. The red point next to each box plot indicates the average across all inbreds for each light condition (A) or developmental phase (B). The letters next to each box plot indicate statistical significance. Different letters denote significant differences based on Tukey's test ($P < 0.05$) between the means for each parameter in each condition.

The gas exchange measurements in the climate chamber resulted in high H^2 values for carbon assimilation-related parameters, ranging between 0.820 and 0.895 (Table 3). We observed a significant genetic variation ($P < 0.05$) for carbon assimilation at saturating light intensity (A_{sat}) among the six inbreds (Fig. 6A); the adjusted entry means of (A_{sat}) were ranging from 14.7 (IG31424) to 19.7 (K10877) $\mu\text{mol m}^{-2} \text{s}^{-1}$. The differences in the maximal carboxylation ($V_{c,max}$) and electron transport rates (J_{max}) as well as triose phosphate utilization capacity (TPU) were also significant ($P < 0.05$) among the six

inbreds (Fig. 6A). Similarly, Phi2 (measured at LL, ML and HL) and SPAD showed significant ($P < 0.05$) differences among the six inbreds (Fig. 6B). Carbon assimilation-related parameters underwent significant ($P < 0.05$) changes across the developmental phases, all peaking in REP together with Phi2 and SPAD (Fig. 6C, D). The H^2 values for the PSII parameters and SPAD were also generally high, including 0.92 for Phi2 and 0.96 for SPAD (Table 3).

We observed significant ($P < 0.05$) positive correlations between SPAD, Phi2, and LEF (both measured at HL) and all

Table 1. Summary statistics of adjusted entry means, variance components, and broad-sense heritability (H^2) for PSII parameters and SPAD measured in the field experiments

Trait	Mean	Min	Max	σ^2_G	$\sigma^2_{G,E}$	$\sigma^2_{G,L}$	$\sigma^2_{G,S}$	σ^2_D	σ^2_M	$\sigma^2_{E,R}$	$\sigma^2_{E,R,B}$	σ^2_ϵ	H^2
LEF	126.2	110.6	139	4.987	23.742***	8.307**	7.497*	151.189***	236.731***	0.325	2.935	469.69	0.42
Phi2	0.41	0.37	0.43	0.90***	0.84***	0.17	0.24	16.25***	12.54***	0.72**	0.1	21.29	0.74
F_v'/F_m'	0.67	0.64	0.7	0.5	0.54**	0.71***	0.87***	11.73***	2.34***	0.52**	0.03	25.52	0.58
PhiNO	0.26	0.22	0.3	1.36***	0.62**	0.65**	0.48*	6.99***	1.46***	1.29***	0.06	34.12	0.74
PhiNPQ	0.34	0.29	0.37	0.09	1.37***	0.84***	1.85***	32.62***	11.52***	0.29	0.17	32.57	0.16
NPQt	1.58	1.19	2.01	84.2	97.99***	168.23***	252.15***	1736.00***	372.24***	121.13***	7.58	5311.71	0.53
qL	0.35	0.28	0.42	4.25***	1.04*	0.96*	0	17.46***	5.51**	3.38***	0.29	83.11	0.78
SPAD	45.35	40.65	52.68	2.091	5.850***	0.544	5.309***	33.570***	31.471***	1.199*	0.983**	67.98	0.68

Note that the values of variance components of six photosynthesis-related parameters (Phi2, F_v'/F_m' , PhiNO, NPQt, qL) were multiplied by 10 000. Asterisks indicate the significance of a likelihood ratio test (* $P<0.05$, ** $P<0.01$, *** $P<0.001$). F_v'/F_m' , maximum efficiency of PSII in light-adapted state; NPQt, total non-photochemical quenching; Phi2, quantum yield of PSII; PhiNO, quantum yield of non-regulated dissipation processes; PhiNPQ, quantum yield of non-photochemical quenching; qL, fraction of PSII open center; SPAD, relative chlorophyll content; σ^2_G , genotypic variance component; $\sigma^2_{G,E}$, variance component of interaction between genotype and environment; $\sigma^2_{G,L}$, variance component of interaction between genotype and light conditions; $\sigma^2_{G,S}$, variance component of interaction between genotype and developmental phase; σ^2_D , variance component of date of measurement; σ^2_M , variance component of MultispeQ device; $\sigma^2_{E,R}$, variance component of replicate in environment; $\sigma^2_{E,R,B}$, variance component of block nested within the replicate in environment.

four carbon assimilation-related parameters (determined at HL) in the climate chamber (Fig. 7). As anticipated, PhiNPQ and NPQt were negatively correlated with the four carbon assimilation-related parameters.

The adjusted entry means of the six barley inbreds showed significant ($P<0.05$) positive correlations between Phi2 and carbon assimilation-related parameters in the climate chamber experiment (Fig. 8). In comparison, the correlations between these parameters assessed in the climate chamber experiment and Phi2 observed in the field were lower, with the highest correlation coefficient of 0.72 found for Phi2 at HL between these experiments.

Relationship between photosynthesis-related parameters and growth or morphological parameters

Morphological parameters and DMP were determined in the climate chamber experiment to assess the relationship between the photosynthesis-related parameters and morphological or growth-related parameters. As done for the field experiments (Supplementary Fig. S4), RGR was calculated for the six inbred lines by fitting a quadratic regression to the DMP data (Supplementary Fig. S6). No significant correlation was observed between the morphological traits, DMP-based RGR and photosynthesis-related parameters among the six barley inbreds (Fig. 7).

We then made the same analysis using the data from the 23 inbred lines in the field experiments (Fig. 9; Supplementary Table S3). As expected, we found significant ($P<0.05$) positive or negative correlations among the PSII parameters as well as among the growth-related parameters. No significant correlation was observed between SPAD and all PSII parameters when the adjusted entry means of all developmental stages and locations were considered (Fig. 9). Comparing the PSII parameters and the growth-related parameters, the final DMP was significantly ($P<0.05$) positively and negatively correlated with F_v'/F_m' and NPQt, respectively. RGR_c showed a significant ($P<0.05$) positive correlation with NPQt (Fig. 9). Looking at the PSII parameters and morphological traits collected from multiple environments and years, significant ($P<0.05$) positive correlations were observed between two PSII parameters (PhiNO and F_v'/F_m') and NSW (Fig. 10). In addition, significant negative correlations were observed between three PSII parameters (qL, NPQt, PhiNPQ) and NSW. Phi2, LEF and qL were significantly ($P<0.05$) negatively correlated with flag leaf morphology (FL and FW) (Fig. 10).

Discussion

Comparison of chlorophyll fluorescence- and gas exchange-based techniques

In order to assess the genetic variation of photosynthesis-related parameters in breeding programs, high-throughput methods

Table 2. Mean square values from analysis of variance for photosystem II parameters and SPAD measured in the field experiments

Trait	G	PAR	T	E	L	ZS	S
LEF	593.67	846205.72***	14345.49***	1751.45*	10979.05***	951.84	1453.20*
Phi2	0.48*	133.61***	6.99***	0.36	6.10***	0.35	1.06**
F_v'/F_m'	0.35	29.88***	2.85***	0.09	1.00*	4.74***	2.71***
PhiNO	0.73*	0.04	7.99***	0.56	0.03	9.78***	5.17***
PhiNPQ	0.31	136.65***	0.23	0.12	4.93***	6.33***	2.99***
NPQt	69.53	5967.81***	264.87*	10.22	86.6	686.60***	394.44***
qL	3.16***	74.74***	43.61***	0.91	4.01**	10.01***	10.02***
SPAD	94.54	0.19	216.02	45.77	80.4	4537.56***	932.87***

Asterisks indicate the significance of a likelihood ratio test (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$). G, genotype; PAR, light intensity; T, ambient temperature; E, environment; L, light condition; ZS, Zadoks score of barley development; S, developmental phases. Photosynthetic parameters: F_v'/F_m' , maximum efficiency of PSII in light-adapted state; LEF, linear electron flow; NPQt, total non-photochemical quenching; Phi2, quantum yield of PSII; PhiNO, quantum yield of non-regulated dissipation processes; PhiNPQ, quantum yield of non-photochemical quenching; qL, fraction of PSII open center; SPAD, relative chlorophyll content.

are needed. Chlorophyll fluorescence-based techniques and hyperspectral measurement techniques have the potential to serve as high-throughput methods to evaluate photosynthetic traits (for review see [van Bezouw et al., 2019](#)). Hyperspectral sensing techniques rely on indirect correlations between features of reflectance spectra and photosynthesis. Once such correlations have been characterized, they can be used to predict photosynthesis capacity at plot level ([Meacham-Hensold et al., 2019](#)) or leaf level ([Serbin et al., 2011](#); [Ainsworth et al., 2014](#); [Yendrek et al., 2016](#); [Silva-Perez et al., 2017](#)). However, compared with chlorophyll fluorescence- and gas exchange-based techniques, reflectance spectra are less sensitive to short-term changes in photosynthesis. Furthermore, correlation-based prediction models cannot be readily applied to new genetic materials, especially across different years and different environmental conditions ([Meacham-Hensold et al., 2019](#)). Hence, gas exchange- and chlorophyll fluorescence-based techniques, particularly the latter for high-throughput measurements, are considered more reliable and straightforward to explore genetic diversity of photosynthesis and related traits.

Positive correlations between PSII electron transport and carbon assimilation have been demonstrated under laboratory conditions, such as in *Phaseolus vulgaris* L. ([Farquhar et al., 1980](#)), red campion, barley, and maize ([Genty et al., 1989](#)) (for review see [Bellasio et al., 2016](#)). Our climate chamber experiment also confirmed the significant positive correlation between Phi2 and carbon assimilation-related parameters ([Fig. 7](#)) across diverse inbreds of barley. In addition, significant genetic effects with high heritability were estimated for both gas exchange- and chlorophyll fluorescence-based parameters in the climate chamber (ranging from 0.76 to 0.96) ([Table 3](#)). These results show the utility of chlorophyll fluorescence-based techniques to detect genetic variation in photosynthesis under controlled conditions ([Flood et al., 2016](#)).

Despite the increasing number of studies focusing on photosynthesis under dynamic conditions ([Keller et al., 2019](#); [Acevedo-Siaca et al., 2021c](#); [Fu and Walker, 2023](#); reviewed by

[Long et al., 2022](#)), few studies have demonstrated that chlorophyll fluorescence-based parameters can replace carbon assimilation parameters when investigating genetic diversity of photosynthesis parameters in the field ([Bucher et al., 2018](#)). Under field conditions, in which light intensity is changing dynamically, the relationship between the photosynthetic light reaction and carbon assimilation, as seen in a steady-state condition ([Farquhar et al., 1980](#); [Bellasio et al., 2016](#)), may be broken ([Rascher and Nedbal, 2006](#); [Eberhard et al., 2008](#); [Long et al., 2022](#)) due to competing processes such as photorespiration in C_3 species ([Pearcy, 1990](#); [Cornic and Fresneau, 2002](#); [Lawson et al., 2012](#)).

However, we observed a strong positive correlation of Phi2 between the dynamic conditions in the field and steady-state conditions in the climate chamber ([Fig. 8](#)). This correlation is based on the adjusted entry mean of Phi2, i.e. non-genetic variation was corrected for these means. Our results thus provide a strong support to the use of chlorophyll fluorescence-based high-throughput measurement techniques to study genetic diversity under dynamically changing, natural environmental conditions.

To use chlorophyll fluorescence-based techniques to assess highly variable photosynthesis parameters ([Figs 1, 2](#)) in breeding programs, however, it is important to consider the factors contributing to their variation.

Factors contributing to photosynthesis variability in the field

We observed a high variability in photosynthesis-related parameters among 23 barley inbreds in the field ([Table 1](#); [Fig. 2](#)). Four main factors are potentially contributing to the high variability of photosynthesis-related parameters: (i) environmental conditions, (ii) developmental stages, (iii) genetic diversity, and (iv) interaction among genotypes, environment conditions, and developmental stages. Below we will discuss these factors one by one.

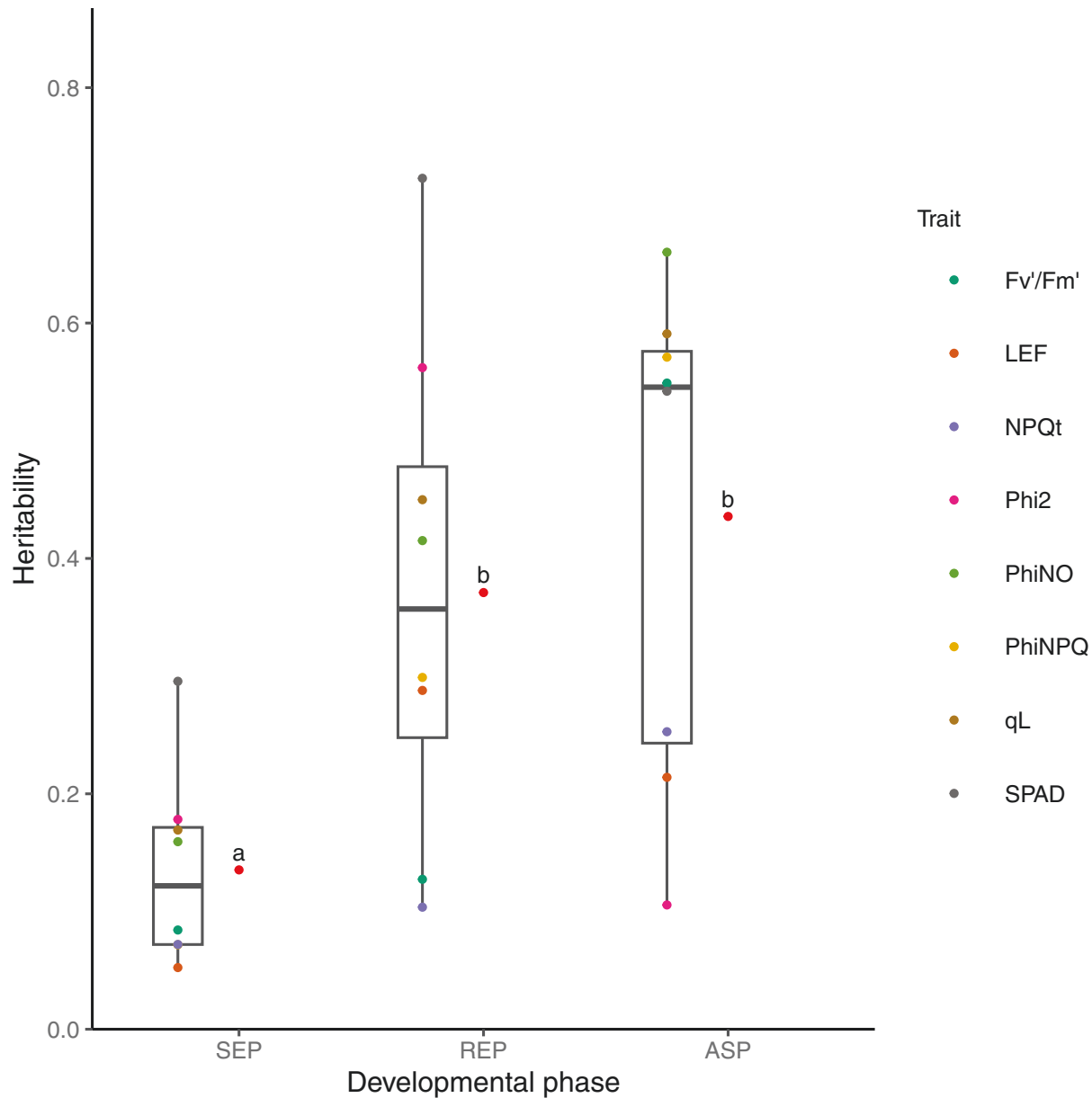


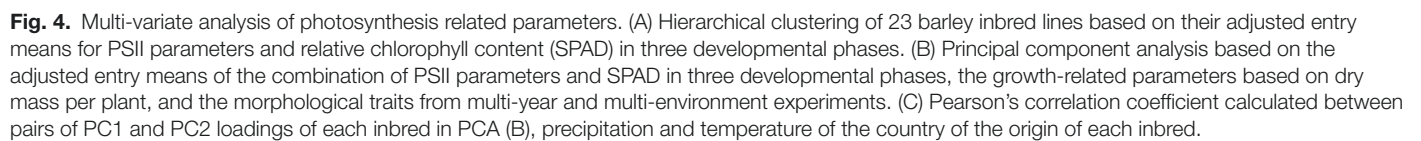
Fig. 3. Heritability of PSII parameters and SPAD in different developmental phases. SEP, slow expansive phase [Zadoks score (ZS) 10–29]; REP, rapid expansive phase (ZS 30–59); ASP, anthesis and senescence phase (ZS 60–87). The red point next to each box plot indicates the mean heritability across all traits for each developmental phase. Different letters next to each box plot indicate significant differences based on Tukey's test ($P < 0.05$) between the mean heritability. F_v'/F_m' , maximum efficiency of PSII in light-adapted state; LEF, linear electron flow; NPQt, total non-photochemical quenching; Phi2, quantum yield of PSII; PhiNO, quantum yield of non-regulated dissipation processes; PhiNPQ, quantum yield of non-photochemical quenching; qL, fraction of PSII open center; SPAD, relative chlorophyll content.

Growth environment of spring barley

We observed significant ($P < 0.05$) effects for the design variables, namely, location of the experiment, measurement date (Table 1), as well as replicate ($\sigma_{E;R}^2$). This can be explained by the dynamic environmental conditions during the growth season of spring barley, which was from late March to the beginning of August. Daily average temperature was fluctuating with an increasing trend (Supplementary Fig. S1). Also, fluctuations in light intensity occurring within and between days must have affected

photosynthesis. We observed a significant ($P < 0.05$) effect of light intensity (PAR) and ambient temperature (T) (Table 2), which were considered as co-variants because of the variability within a day and location of the measurement. In addition, lower temperature in May (Supplementary Fig. S1) might have suppressed Phi2 in the SEP compared with the other two developmental phases (Fig. 2B) (Bagley *et al.*, 2015; Moore *et al.*, 2021).

In parallel to the erratic changes of temperature and light intensity in the field, photosynthetic efficiency typically exhibits



The significant ($P < 0.05$) variance components observed in our study for environmental factors, namely date (D), PAR and ambient temperature (T), indicate that single time point measurements are not sufficient to draw conclusions on genetic variation in photosynthesis under field conditions.

Most previous studies exploring the genetic diversity of photosynthesis in cereals focused on carbon assimilation in the flag leaf, which is the most important leaf in pre- or post-anthesis (Driever *et al.*, 2014; Carmo-Silva *et al.*, 2017; Acevedo-Siaca *et al.*, 2021b). In our study, however, significant ($P < 0.05$)

Photosynthesis-related parameters are linked to plant development as well as leaf development (Wingler *et al.*, 2004; Bielschynski *et al.*, 2017). At the plant level, the sink tissues in

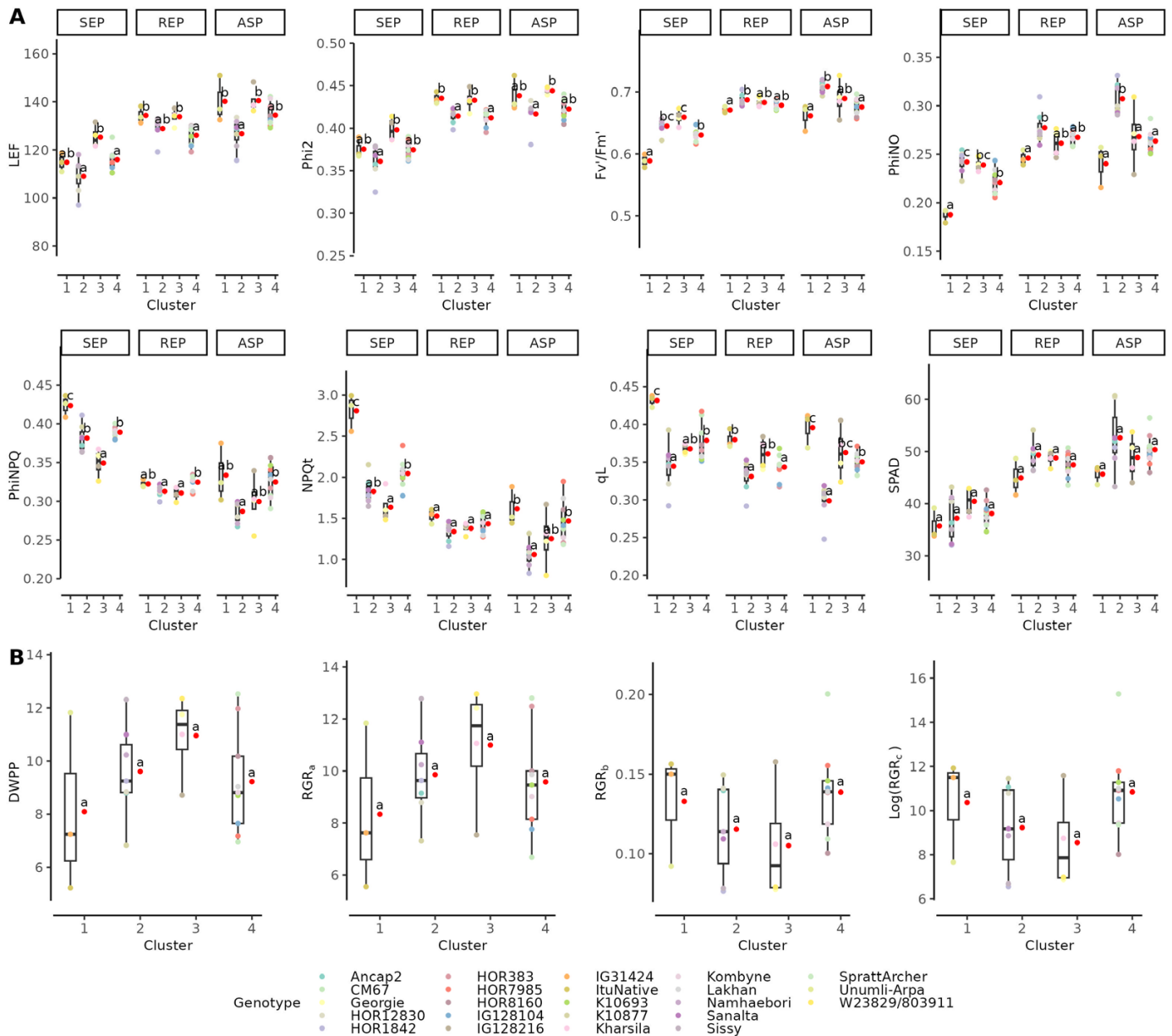


Fig. 5. Comparison of PSII parameters, relative chlorophyll content (SPAD) and growth-related parameters among the four clusters. (A) PSII parameters and SPAD in different developmental phases. (B) Dry mass per plant (DMP) and relative growth rates (RGR_a , RGR_b , RGR_c) calculated from DMP based on the quadratic regression ($y = a + bt - ct^2$). Due to the wide range of RGR_c , log-transformed data of RGR_c were used. The red point next to each box plot indicates the mean of the parameters in each cluster. Different letters next to each box show significant differences based on Tukey's test ($P < 0.05$) between the clusters. SEP, slow expansive phase [Zadoks score (ZS) 10–29]; REP, rapid expansive phase (ZS 30–59); ASP, anthesis and senescence phase (ZS 60–87); F_v/F_m' , maximum efficiency of PSII in light-adapted state; LEF, linear electron flow; NPQ, total non-photochemical quenching; Phi2, quantum yield of PSII; PhiNO, quantum yield of non-regulated dissipation processes; PhiNPQ, quantum yield of non-photochemical quenching; qL, fraction of PSII open center; SPAD, relative chlorophyll content.

SEP are mainly growing leaves and roots, while new sink tissues emerged in REP, such as larger root system and formation of inflorescence (Alqudah and Schnurbusch, 2017). The increased sink activity in REP coincided with the high Phi2 (Fig. 2B). In ASP, barley went from the anthesis stage to grain filling stage, which may further increase the sink strength. However, photosynthesis-related (source) parameters did not

show corresponding increases in ASP compared with REP (Fig. 2B). In fact, it has been proposed that spike photosynthesis may serve as the major photosynthate source for grain filling, as previously shown for wheat (Maydup *et al.*, 2010; Vicente *et al.*, 2018; Molero and Reynolds, 2020).

At the leaf level, photosynthetic efficiency typically increases with leaf development to reach the maximum during leaf

Table 3. Summary statistics of adjusted entry means, variance components and broad-sense heritability (H^2) for carbon assimilation-related parameters, SPAD and photosystem II parameters under 1500 $\mu\text{mol m}^{-2} \text{s}^{-1}$ assessed in the climate chamber experiment

Trait	Mean	Min	Max	σ^2_{G}	$\sigma^2_{\text{G:S}}$	σ^2_{D}	$\sigma^2_{\text{D:TW}}$	σ^2_{e}	H^2
$V_{\text{c,max}}$	43.3	37.5	49.8	14.9*	6.432*	21.331**	6.432*	50.886	0.848
J_{max}	111.6	94.8	132.4	141.76**	38.85	193.515***	38.85	324.241	0.895
TPU	7.61	6.37	9.13	0.717**	0.23*	0.688***	0.23	1.297	0.892
A_{sat}	17.2	14.7	19.7	2.169*	1.32*	2.544**	1.319	9.608	0.82
LEF_1500	185.18	73.39	278.13	132.69**	61.39***	197.73***	87.64***	707.85	0.92
Phi2_1500	0.27	0.11	0.41	0.03**	0.01***	0.04***	0.02***	0.16	0.92
$F_v'/F_m'_{1500}$	0.6	0.21	0.75	0.05**	0.02**	0.05**	0.02**	0.26	0.92
PhiNO_1500	0.23	0.04	0.45	0.03**	0.01	0.05***	0.02*	0.27	0.86
PhiNPQ_1500	0.49	0.24	0.79	0.08**	0.02**	0.08**	0.05***	0.39	0.93
NPQt_1500	2.33	0.64	17.89	11.70*	5.45**	11.51*	6.32**	80.99	0.9
qL_1500	0.26	0.1	0.74	0.02	0.02*	0.11***	0.02*	0.43	0.76
SPAD	44.19	6.28	75.47	36.22***	3.81*	10.45	28.91***	75.63	0.96

Note, the values of variance components of six PSII parameters (Phi2_1500, $F_v'/F_m'_{1500}$, PhiNO_1500, PhiNPQ_1500, NPQt_1500, qL_1500) were multiplied by 100. Asterisks indicate the significance of a likelihood ratio test (* $P<0.05$, ** $P<0.01$, *** $P<0.001$). A_{sat} , carbon assimilation at saturating light intensity; $F_v'/F_m'_{1500}$, maximum efficiency of PSII in light-adapted state; J_{max} , maximum rate of electron transport; LEF, linear electron flow; NPQt, total non-photochemical quenching; Phi2, quantum yield of PSII; PhiNO, quantum yield of non-regulated dissipation processes; PhiNPQ, quantum yield of non-photochemical quenching; qL, fraction of PSII open center; SPAD, relative chlorophyll content; TPU, triose phosphate utilization; $V_{\text{c,max}}$, maximum rate of carboxylation. σ^2_{G} variance component of inbred; $\sigma^2_{\text{G:S}}$ variance component of interaction between inbred and developmental phase; σ^2_{D} variance component of date of measurement, $\sigma^2_{\text{D:TW}}$ variance component of time window nested in date of measurement.

expansion (Bielczynski *et al.*, 2017). After anthesis, declining activity of photosynthesis has been reported in many studies (Wingler *et al.*, 2004; Liu *et al.*, 2017; Miao *et al.*, 2018; Yang *et al.*, 2018). This was not the case in the present study as no significant difference in Phi2 and SPAD was found between REP and ASP (Fig. 2B). By always choosing the top fully expanded leaves for measurements throughout all developmental stages of the plant, we minimized the effect of leaf development.

Genotypic effect

To evaluate the potential of classical breeding to optimize photosynthesis, the relative importance of genotypic effects versus non-genotypic effects on photosynthesis-related parameters (i.e. heritability) needs to be considered. The broad sense heritability varied between 0.16 and 0.78 (Table 1). As homozygous genotypes were evaluated in this study, dominance variance as well as additive×dominance and dominance×dominance epistasis will not contribute to the genotypic variation. Thus, broad sense heritability can be interpreted to evaluate the potential of selection.

The relatively high heritability together with the significant ($P<0.05$) genetic variances found for Phi2, PhiNO, and qL suggests that these parameters could be manipulated in barley by photosynthesis-oriented breeding programs, hence making them promising targets for quantitative genetic approaches. Notably, the heritability of photosynthesis-related parameters varied in the different developmental stages of barley plants, with the lowest values in the seedling stage (Supplementary Fig. S3). This dynamic heritability suggests that the relative contributions of environment and genetics are not stable during the plant growth and development (Yang *et al.*, 2015). Similar

dynamic heritability of photosynthetic traits has been observed in other species, such as in field-grown wheat, in which the heritability ranged from 0.267 to 0.764 in pre-anthesis stage and from 0.314 to 0.757 in post-anthesis stage (Carmo-Silva *et al.*, 2017). Even under controlled conditions, dynamic heritability of photosynthesis-related traits has been reported in Arabidopsis during long- and short-term response to light intensity (van Rooijen *et al.*, 2015; Flood *et al.*, 2016). Unlike in our study, however, the dynamic heritability found for short-term response of Arabidopsis under controlled conditions was mainly attributed to genetic variation and diurnal changes of photosynthesis (Flood *et al.*, 2016).

It is reasonable that the heritability of the photosynthesis-related parameters was lower in the field than that in the climate chamber (Tables 1, 3), due to variable environmental factors and interaction between genotypes and environments (Visscher *et al.*, 2008). Given the changing heritability, taking the photosynthetic measurements when the heritability is low may not be efficient to select genotypes (Visscher *et al.*, 2008). Better knowledge about the dynamic change of heritability during plant growth and development would help us identify the developmental stage(s) when genotype significantly contributes to variation of photosynthesis, thus facilitating more targeted and efficient plant breeding (Flood *et al.*, 2016).

From an evolutionary perspective, one could argue that historical (natural or artificial) selection has reduced genotypic variance of the traits, which are more tightly associated with fitness, thus leading to a lower heritability (Mousseau and Roff, 1987; Flood, 2019). In the context of variable heritability across developmental stages of barley found in this study (Fig. 3; Supplementary Fig. S3), this may imply stronger historical

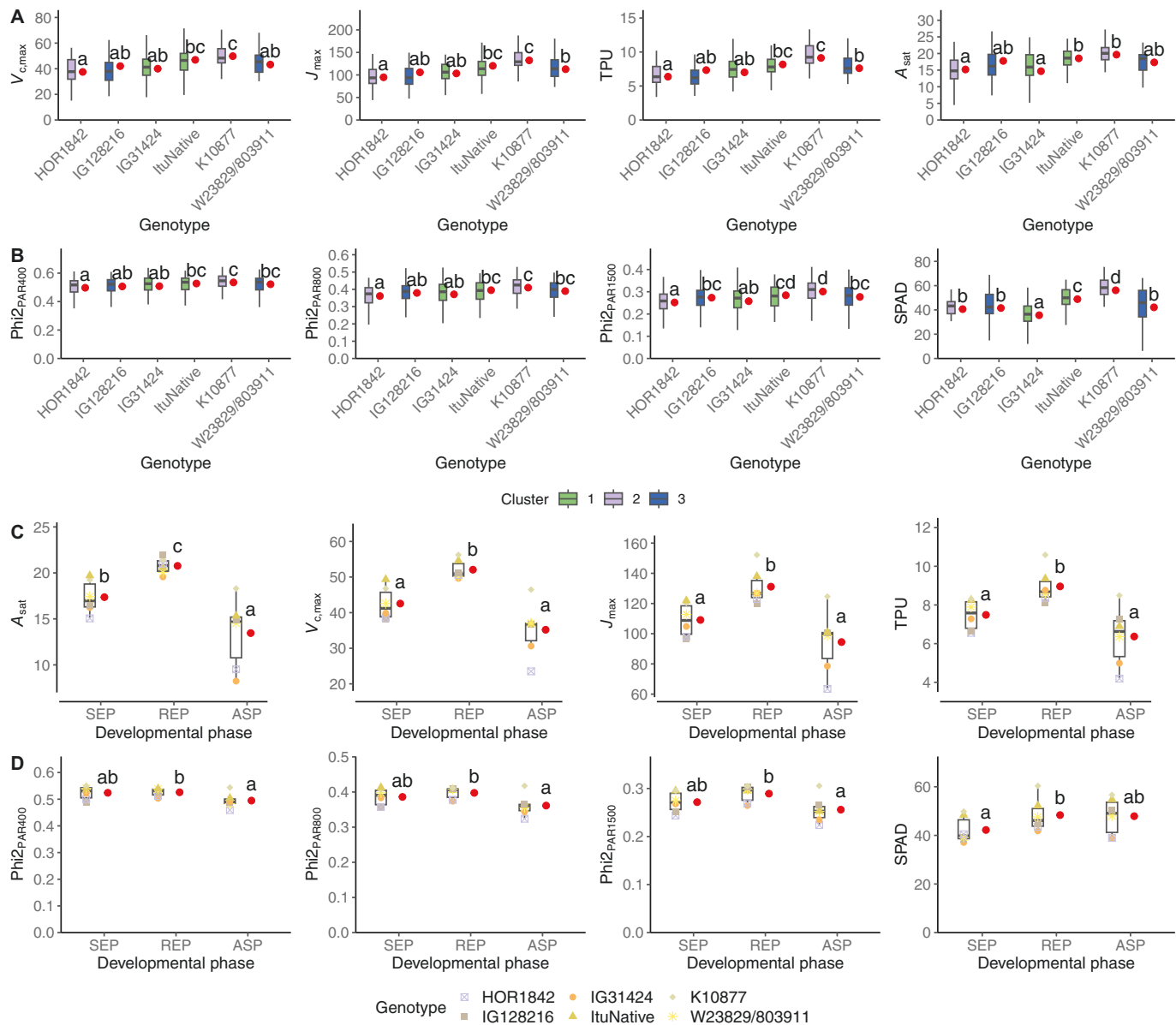


Fig. 6. Comparison of the six barley inbred lines in the climate chamber. (A) Carbon assimilation-related parameters (A_{sat} , $V_{\text{c,max}}$, J_{max} , TPU). (B) Φ_2 under simulated low light (LL; PAR 400 $\mu\text{mol m}^{-2} \text{s}^{-1}$), medium light (ML; 800 $\mu\text{mol m}^{-2} \text{s}^{-1}$), and high light (HL; 1500 $\mu\text{mol m}^{-2} \text{s}^{-1}$) conditions, and SPAD. For (A, B), the colors of boxes represent the clusters determined by the hierarchical clustering in Fig. 5A. (C) Adjusted entry means of A_{sat} , $V_{\text{c,max}}$, J_{max} , TPU of the six inbred lines in SEP, REP, and ASP. (D) Adjusted entry means of Φ_2 under the simulated LL, ML, and HL conditions, and SPAD of the six inbred lines in different developmental phases. The red dots next to boxes in (A, B) are the adjusted entry means of parameters of each genotype. The red dots next to boxes in (C, D) are the mean values of the six inbreds for each parameter in each developmental phase. Different letters next to each box denote significant difference based on Tukey's test ($P < 0.05$). A_{sat} , carbon assimilation at saturating light intensity; ASP, anthesis and senescence phase; J_{max} , maximum rate of electron transport; Φ_2 , quantum yield of PSII; REP, rapid expansion phase; SEP, slow expansion phase; SPAD, relative chlorophyll content; TPU, triose phosphate utilization; $V_{\text{c,max}}$, maximum rate of carboxylation.

selection of photosynthesis in SEP than in REP, reflecting presumably the importance of the adaptation of photosynthesis in SEP (Ackerly *et al.*, 2000). Accordingly, investigating the genetics of photosynthesis-related parameters in SEP in old and therefore less selected genetic material of barley might help to understand the evolutionary pressure on photosynthesis.

Interactions between genotype, environment, and developmental stage

As discussed above, photosynthesis is highly responsive to environmental conditions and subject to developmental influences. Except Φ_2 , $\Phi_2\text{NO}$, and q_L , no significant genetic variation was observed for the other parameters. However, we found

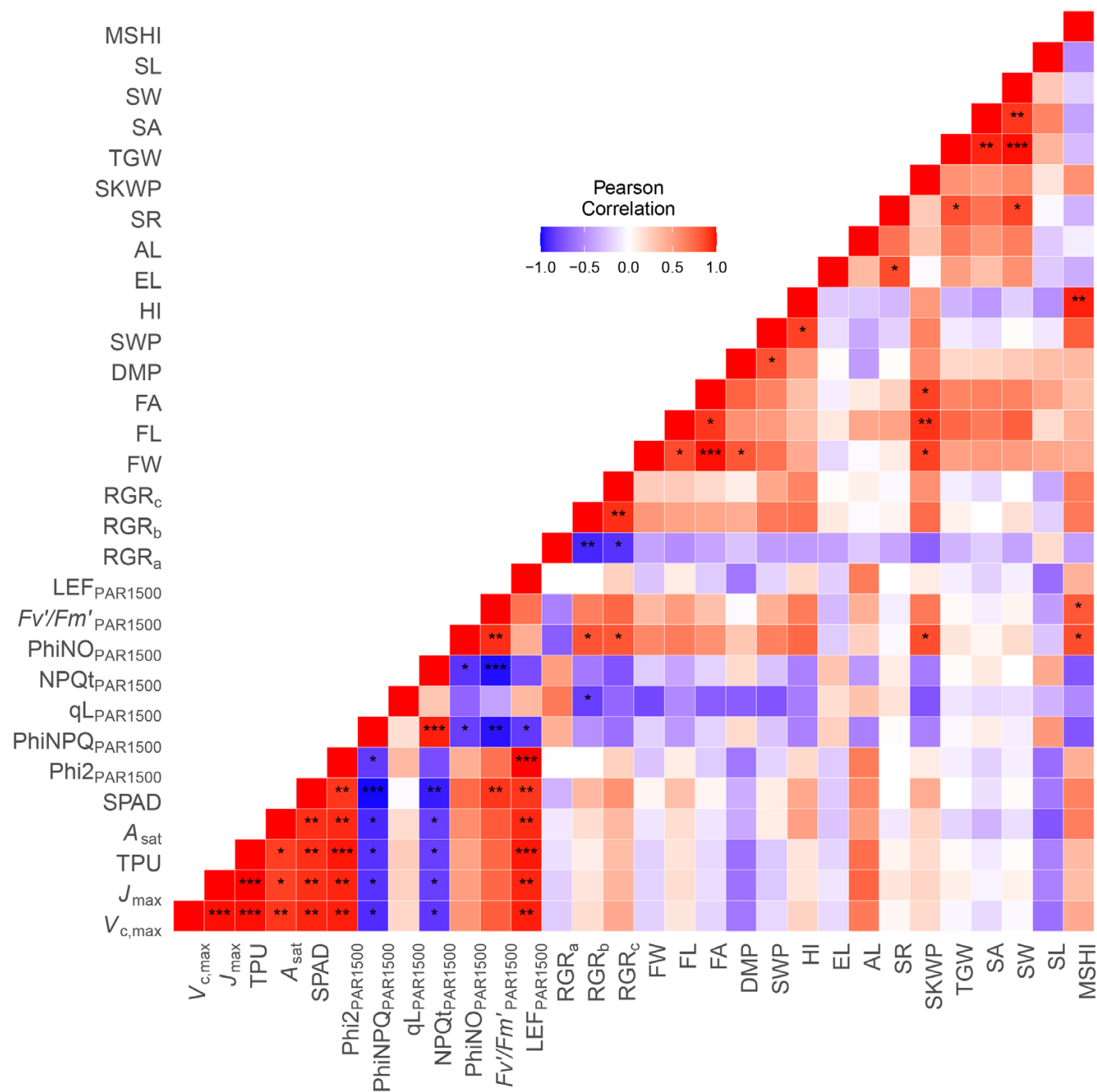


Fig. 7. Pearson's correlation coefficient calculated between pairs of adjusted entry means for six barley inbreds for photosynthesis-related parameters, dry mass per plant, flag leaf width (FW), flag leaf length (FL), flag leaf area (FA) and relative growth rate related parameters (RGR_a , RGR_b , RGR_c), awn length (AL), spike length (EL), spikelet number in one row of the spike (SR), seed length (SL), seed width (SW) seed area (SA), thousand grain weight (TGW), total aboveground dry mass (DMP), total stem weight without spike weight (SWP), harvest index (HI), spike weight per plant (SKWP), and main stem harvest index (MSHI), which were collected from the climate chamber experiments. Asterisks indicate the significance level (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$). A_{sat} , carbon assimilation at saturating light intensity; F_v'/F_m' , maximum efficiency of PSII in light-adapted state; J_{max} , maximum rate of electron transport; LEF, linear electron flow; NPQt, total non-photochemical quenching; Φ_{i2} , quantum yield of PSII; Φ_{iNO} , quantum yield of non-regulated dissipation processes; Φ_{iNPQ} , quantum yield of non-photochemical quenching; qL, fraction of PSII open center; SPAD, relative chlorophyll content; TPU, triose phosphate utilization; $V_{c,max}$, maximum rate of carboxylation.

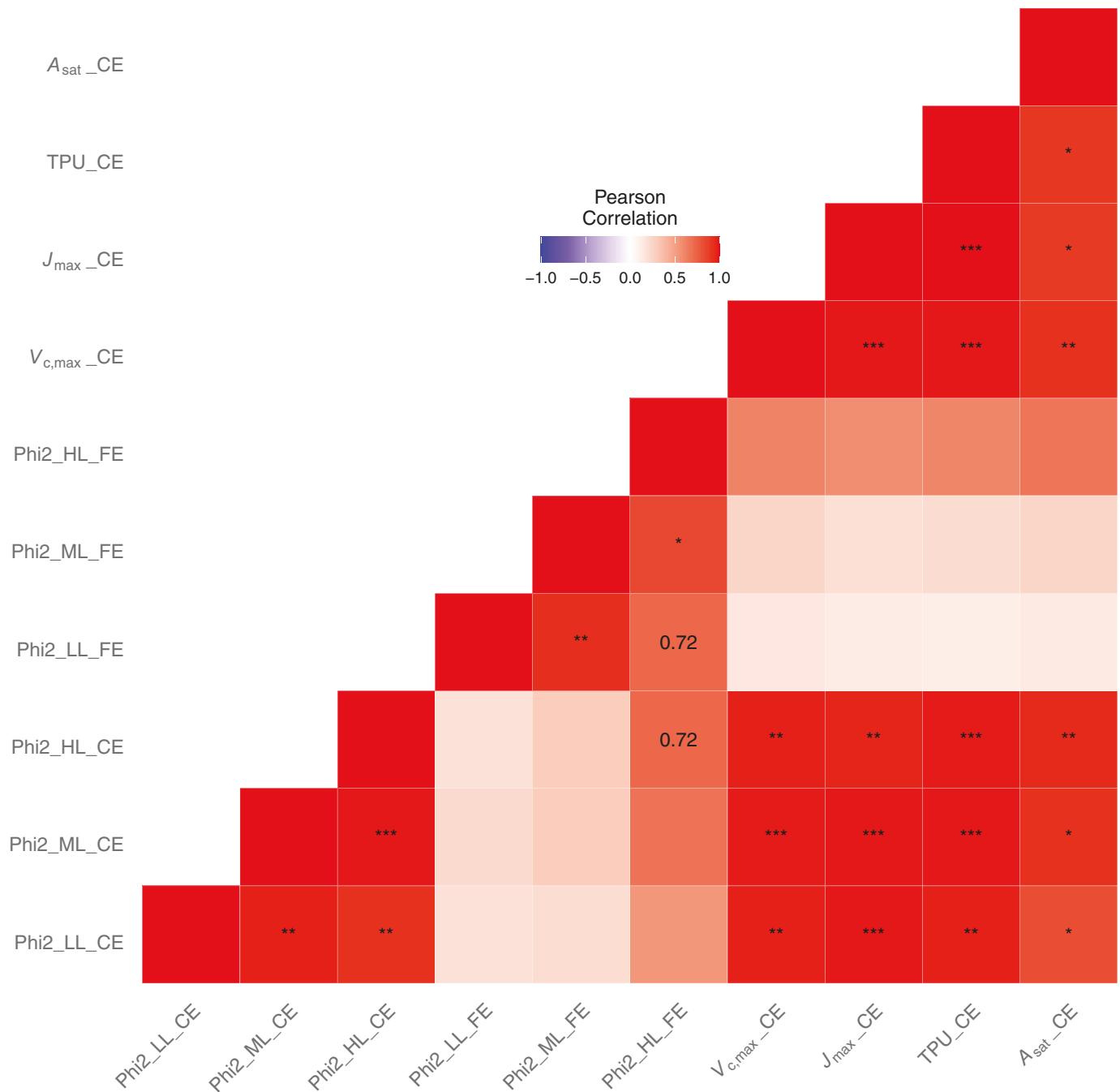


Fig. 8. Pearson's correlation coefficients calculated between pairs of adjusted entry means of six barley inbreds for Phi2 and carbon assimilation-related parameters measured in the climate chamber experiments (CE) and Phi2 measured in the field (FE). Phi2 was assessed separately for LL, ML and HL conditions. Caron assimilation was analysed at the light intensity of the HL condition. Asterisks indicate the significance level (* $P<0.05$, ** $P<0.01$, *** $P<0.001$). A_{sat}, carbon assimilation at saturating light intensity; J_{max}, maximum rate of electron transport; Phi2, quantum yield of PSII; TPU, triose phosphate utilization; V_{c,max}, maximum rate of carboxylation.

significant ($P<0.05$) interaction effects on all photosynthesis-related parameters between genotype and environment ($G : E$), genotype and light condition ($G : L$) except Phi2 and SPAD, and genotype and developmental phases ($G : S$) except Phi2 and qL (Table 1).

The significant ($G : S$) effect suggested that the 23 inbreds showed significant different responses across the different developmental phases. This might suggest changing importance of different genes across the development phases, highlighting again the necessity to assess the genetics of photosynthesis

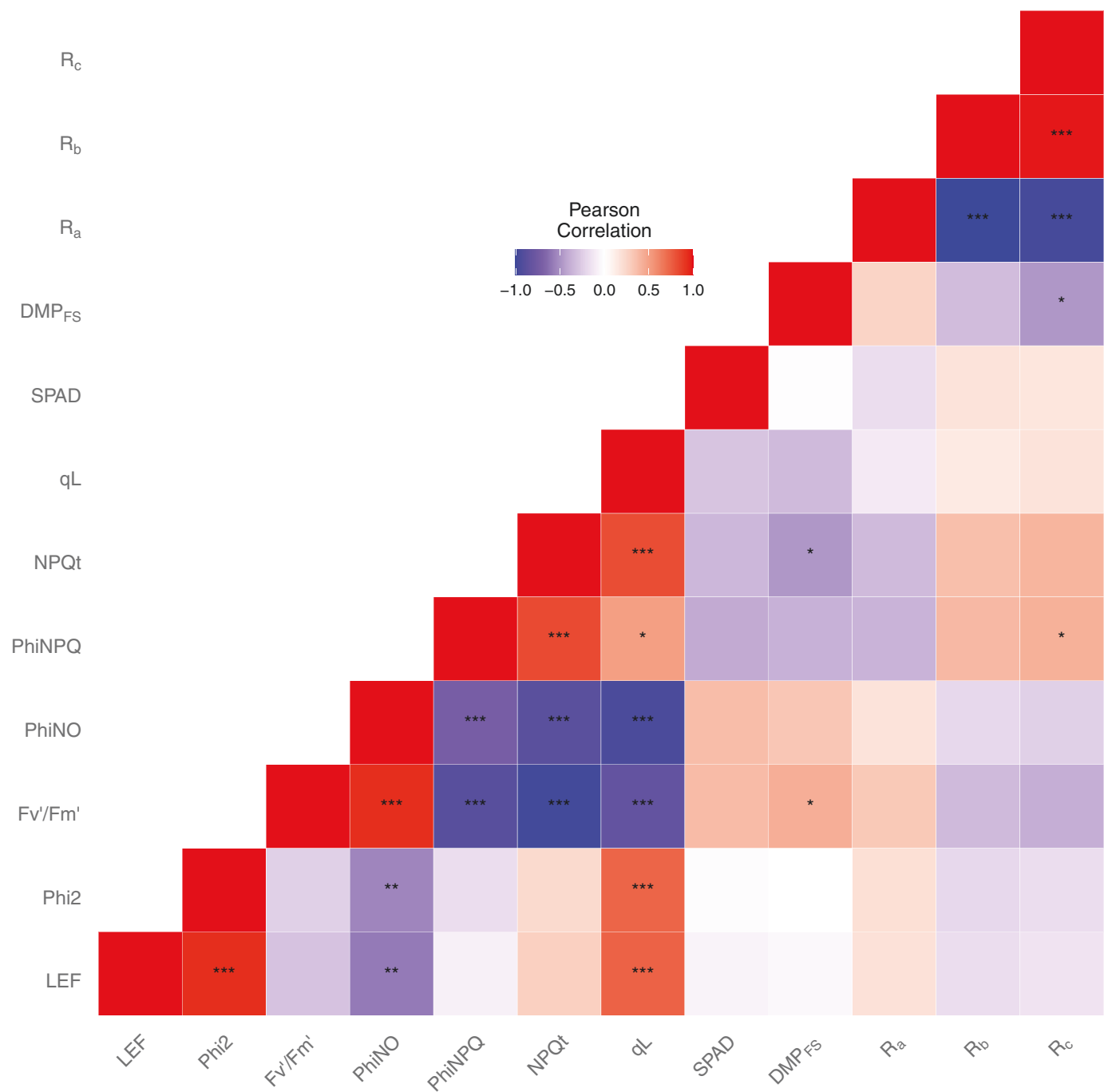


Fig. 9. Pearson's correlation coefficients calculated between pairs of adjusted entry means of 23 barley inbreds for photosynthesis- and growth-related parameters collected in the field. Asterisks indicate the significance level (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$). DMP, dry mass per plant; F_v'/F_m' , maximum efficiency of PSII in light-adapted state; LEF, linear electron flow; NPQt, total non-photochemical quenching; Phi2, quantum yield of PSII; PhiNO, quantum yield of non-regulated dissipation processes; PhiNPQ, quantum yield of non-photochemical quenching; qL, fraction of PSII open center; RGR, relative growth rates (RGR_a , RGR_b , RGR_c) calculated from DMP based on the quadratic regression ($y_r = a + bt - ct^2$); SPAD, relative chlorophyll content.

during plant growth and development (leaf-level and plant level). While it is still challenging to assess chlorophyll fluorescence-based parameters continuously, automatically, and in a high through-put fashion across plant developmental

stages under field conditions, several indoor facilities are able to do this (for review see [van Bezouw et al., 2019](#)). The significant ($G : L$) effect, on the other hand, indicates that different genes may gain importance in different

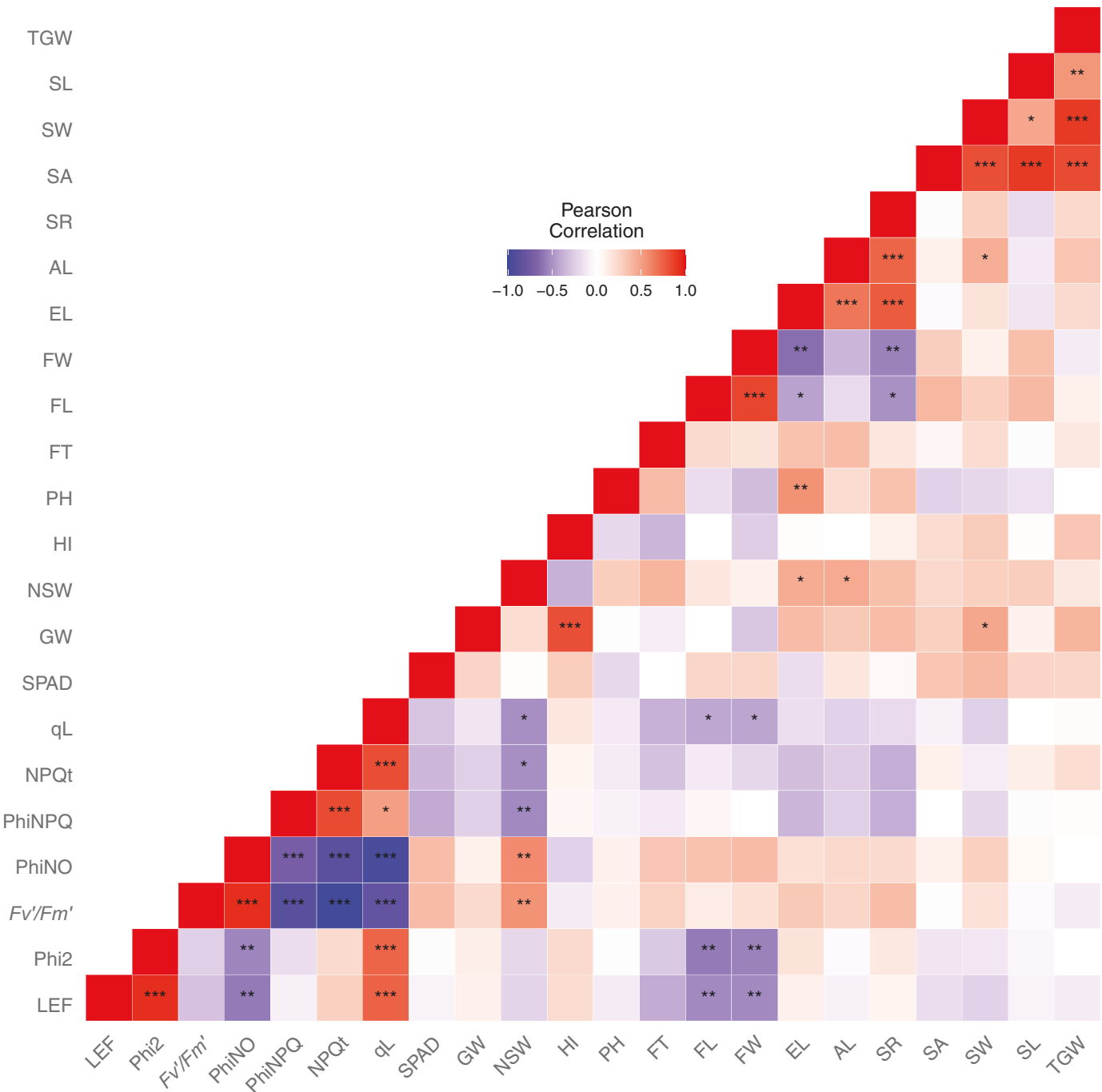


Fig. 10. Pearson's correlation coefficients calculated between pairs of adjusted entry means of 23 barley inbreds for PSII parameters, SPAD and morphological traits collected from multiple environments and years in the field conditions. Asterisks indicate the significance level (* $P<0.05$, ** $P<0.01$, *** $P<0.001$). Morphological parameters: AL, awn length; EL, spike length; FL, flag leaf length; FT, flowering time; FW, flag leaf width; GW, grain weight; HI, harvest index; NSW, net straw weight; PH, plant height; SA, seed area; SL, seed length; SR, spikelet number in one row of the spike; SW, seed width; TGW, thousand grain weight. Photosynthetic parameters: F_v/F_m' , maximum efficiency of PSII in light-adapted state; LEF, linear electron flow; NPQt, total non-photochemical quenching; Phi2, quantum yield of PSII; PhiNO, quantum yield of non-regulated dissipation processes; PhiNPQ, quantum yield of non-photochemical quenching; qL, fraction of PSII open center; SPAD, relative chlorophyll content.

light conditions. This is in line with previous observations in *Arabidopsis* under controlled conditions (van Rooijen *et al.*, 2015; Meyer *et al.*, 2023). The separation of three light intensity

levels (LL, ML, and HL) by *K*-means clustering (Fig. 1B), roughly corresponding to the three major phases of light response curve (Benedetti *et al.*, 2018), also underlines distinct

responses of photosynthesis to different light intensity levels. In our field experiments, we could only assess the parameters of instantaneous photosynthesis while the light condition was fluctuating. However, especially in fluctuating light environments, an increasing number of studies have shown the importance of the speed of photosynthetic reactions to respond to changing light for crop yields (Kromdijk *et al.*, 2016; De Souza *et al.*, 2022). The relevance of natural genetic variation for such kinetic traits of photosynthesis awaits investigations.

The factors (i)–(iv) are important not only in the context of photosynthesis breeding but also for fundamental understanding of how the genetics of photosynthesis interacts with environment (*E*), light condition (*L*) and plant developmental phase (*S*). Quantitative knowledge and understanding of these factors are essential for improving photosynthesis models and crop yield prediction (for review see Yin and Struik, 2010).

Covariation between photosynthesis and yield-related traits

Having confirmed genetic variation for photosynthesis-related parameters in the 23 spring barley inbreds, we also analysed the relationship between photosynthesis- and yield-related traits. The yield-related traits were collected in multi-environment and multi-year experiments, while photosynthesis-related parameters were collected in three different locations in one year. Our results indicated significant positive or negative correlations between some of the chlorophyll fluorescence parameters and NSW, but not for others (Fig. 10). The genotype×environment interactions, which are important not only for yield but also for photosynthesis, are most likely responsible for the non-significant correlations between photosynthesis-related parameters and yield-related traits in these experiments.

Several studies did not find a significant correlation between leaf-level photosynthesis and crop yields. For instance, Acevedo-Siaca *et al.* (2021a) reported no significant correlation between photosynthesis and agronomic traits of rice in field experiments. Likewise, Driever *et al.* (2014) observed no significant correlation between photosynthesis and yield in wheat. Plant growth may respond to environmental stress and perturbations more sensitively than photosynthesis does (Körner, 2015). In this case, increase in photosynthesis does not necessarily result in increased growth. Under controlled conditions or benign environments, however, targeted engineering of photosynthesis by transgenic approaches has led to increased biomass and/or yield in a number of plant species (reviewed by Simkin *et al.*, 2019). Clearly, we need to better understand the genotype×environment interactions of complex photosynthesis-related traits on one hand, and of similarly complex traits of growth and yield on the other hand to decipher the genetic relationship between photosynthesis and yield. Exploration of system biology (for review see Yin *et al.*, 2018) and gene regulatory networks (for review see Flood *et al.*, 2011; Theeuwes

et al., 2022) might facilitate understanding of photosynthetic regulation, and how it responds to the ambient environments, which ultimately improves crop yield.

Interestingly, Phi2 was significantly negatively correlated with flag leaf length and width across all three developmental phases (Fig. 10). This may imply that small size of flag leaf is compensated by increased photosynthetic efficiency (Poorter and Evans, 1998; Garnier *et al.*, 1999). Similar negative correlation was also observed between leaf area and CO₂ exchange rate in peanut, soybean, and sweet potato (Bhagsari and Brown, 1986). Future studies may explore natural genetic variation in trait-trait interactions.

Conclusions

The results of this study show that a chlorophyll fluorescence-based technique is able to detect genetic variation in PSII-related parameters in barley under climate chamber conditions, and Phi2, PhiNO, and qL could be suitable parameters to detect genetic variation also under field conditions. Due to the significant effects of environmental factors and significant interactions between the genotype and environments, single time point measurements are not sufficient to draw conclusions on genetic variation in photosynthesis under field conditions but elaborated experimental designs are required.

Significant correlations observed between photosynthesis-related traits (F_v'/F_m' and NPQt) and yield-related traits (NSW and DMP at final stage) in barley under field conditions suggest the possibility of improving crop yields via optimizing photosynthesis through conventional breeding approaches. Moreover, the difference in heritability of photosynthesis, across the plant development and growth stages, could be used to explore the selection pressure on photosynthesis an evolutionary timeline.

Supplementary data

The following supplementary data are available at [JXB online](#).

Fig. S1. Air temperature and precipitation recorded during the field experiments in Bonn, Cologne, Düsseldorf.

Fig. S2. Light response curves of PSII parameters and SPAD for the 23 barley inbred lines.

Fig. S3. Developmental changes in heritability.

Fig. S4. The growth trajectories for 23 barley inbred lines grown in the field.

Fig. S5. Boxplot of the adjusted entry means for 11 morphological traits of twenty-three barley inbred lines in multiple environments across multiple years experiments assigned to four clusters.

Fig. S6. The growth trajectory curves for six barley inbred lines grown in the climate chamber condition.

Table S1. The adjusted entry means of photosynthesis-related parameters of 23 barley inbreds for each light condition.

Table S2. The adjusted entry means of photosynthesis-related parameters of 23 barley inbreds for each developmental phase.

Table S3. The adjusted entry means of photosynthesis-related parameters of 23 barley inbreds across all developmental phases in the field experiment.

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Author contributions

BS and SM conceptualized the study, acquired funding and supervised the work; YG, SM, and BS designed the research. YG, MS, LO, and WZ performed experiments. YG analysed the data. YG, SM, and BS interpreted the results. YG, SM, and BS wrote the manuscript.

Conflict of interest

The authors declare no conflict of interest.

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Data availability

Data are publicly available in the manuscript and in the supplementary data.

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