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1 **CropQuant: An automated and scalable field phenotyping platform for crop**  
2 **monitoring and trait measurements to facilitate breeding and digital agriculture**

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13  
14 **Abstract**

15 Automated field phenotyping provides continuous and precise measures of adaptation  
16 and performance traits that are key to today's breeding and agricultural practices.  
17 Besides monitoring morphological changes of crop growth and development, high-  
18 resolution and high-frequency of phenotypic measures can empower an accurate  
19 delineation of the genotype to phenotype pathway enabling the assessment of genes  
20 controlling yield potential and environmental adaptation. Here, we present CropQuant,  
21 a cost-effective Internet of Things (IoT) powered phenotyping platform, designed to  
22 be easily used and widely deployed in any environment. To manage and process data  
23 generated by the platform, we developed an automatic in-field control system, high-  
24 throughput trait analysis algorithms, and machine-learning based modelling to explore  
25 the dynamics between genotypes, phenotypes and environment. We used the platform  
26 in a 95-day field experiment to generate dynamic developmental profiles of five  
27 wheat genotypes within the single genetic background of *Paragon* (a UK spring  
28 wheat variety) and demonstrated a successful example of how this technology could  
29 be applied to breeding, crop research and digital agriculture.

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31 *NOTE: The final version of this manuscript provides much more detailed explanation*  
32 *of the CropQuant technology and novel biological discoveries through applying the*  
33 *field crop phenotyping technology in two-year wheat field experiments.*

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### 34 **Background**

35 The great American wheat breeder and Agri-Tech innovator Orville Vogel once  
36 stated that the plant you are looking for is in your plots, but you have to be there when  
37 it is. Four decades after temporary success in ensuring global food security, we are  
38 now facing an even bigger challenge to feed generations to come<sup>1</sup>. Due to a narrowing  
39 range of available genetic diversity of modern crop germplasm and increasing  
40 fluctuations in weather caused by global climate change<sup>2</sup>, we rely on exploiting new  
41 sources of variation such as landraces and wild relatives to seek traits with greater  
42 yield potential as well as environmental adaptation<sup>3</sup>. This process requires robust  
43 measures of adaptive traits from many experimental plots throughout the growing  
44 season. Our work aims to address this challenge through a cost-effective IoT-powered  
45 phenotyping platform, **CropQuant**, which facilitates continuous monitoring and  
46 accurate measures of crop growth and development in different environments.

47  
48 To increase yield and improve crop adaptation to diverse environments sustainably,  
49 modern genetic and genomics technologies have been employed to enable an efficient  
50 selection of valuable lines with high yield, biotic and abiotic stress tolerance, and  
51 disease resistance<sup>3,4</sup>. For example, QTL analysis and genome-wide association studies  
52 (GWAS) to examine genetic architecture<sup>5</sup>, genome sequencing to reveal gene content  
53 and diversity<sup>6</sup> and marker-assisted selection (MAS) or genomic selection (GS) to  
54 accumulate favourable alleles<sup>7</sup>. However, these technical advances are limited by  
55 low-throughput, laborious and inaccurate in-field phenotyping approaches<sup>8</sup>. This is  
56 why phenotyping is widely recognised as the bottleneck that prevents us from linking  
57 the richness of genomic and genotypic information to important traits, so that they can  
58 be effectively deployed for agriculture.

59  
60 To date, along with the development of remote sensing technologies<sup>7</sup> and open  
61 analytics software libraries<sup>9</sup>, agricultural practitioners such as breeders, growers,  
62 farmers and crop scientists have been employing new approaches to relieve the  
63 bottleneck<sup>10</sup>. For instance, non-invasive remote sensors and aerial imaging devices  
64 such as unmanned aerial vehicles (UAV) and blimps are being used to study crop  
65 performance and field variability<sup>11</sup>. Satellite imaging<sup>12</sup> and tailored portable devices<sup>13</sup>  
66 are applied to the prediction of crop growth and yield potential based on canopy  
67 photosynthesis and normalised difference vegetation indices (NDVI). Large-scale  
68 imaging systems equipped with 3D laser scanners and multispectral sensors have been  
69 established to automate plant monitoring for a fixed number of pots or plots either in  
70 greenhouse (e.g. Scanalyzer HTS/3D HT, LemnaTec) or in the field (e.g. LeasyScan,  
71 Phenospex; Field Scanalyzer, LemnaTec)<sup>14-16</sup>. However, the challenges associated  
72 with these technologies are high costs, small scale, low frequency of measures and  
73 inadequate software analytical tools that can be used by agricultural practitioners to  
74 make sense of complicated phenotypic datasets<sup>14,17</sup>. From this perspective, our ability  
75 to measure crop growth dynamically and key adaptive traits in large numbers of  
76 experimental plots in different regions is still limited. Hence, there is a pressing need  
77 to develop an affordable and reliable phenotyping platform that can be easily used and  
78 widely adopted in breeding pipelines and by crop research communities worldwide.

### 80 **The IoT-powered phenotyping platform**

81 Here we describe the CropQuant platform designed to automatically monitor crop  
82 growth and development through low cost in-field terminal workstations. The current

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83 design of the platform is driven by a number of IoT technologies<sup>18</sup>, together with our  
84 vision for how to implement advanced Agri-Tech innovations in breeding, agriculture  
85 and crop research.  
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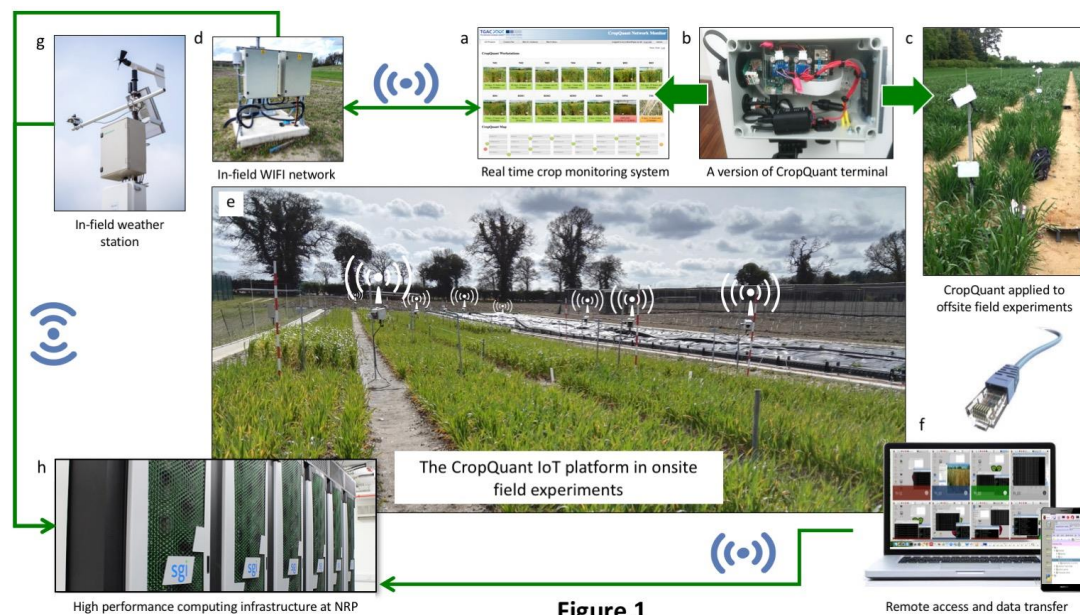


Figure 1

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**Figure 1. The CropQuant IoT platform in onsite and offsite field trials.**

(a) CropMonitor, a centralised control system, administers CropQuant terminals and records online (green) or offline (red) status, operational mode (amber if imaging halts), daily images, micro-environment (e.g. temperature and humidity), and computational resource. (b) The hardware design of CropQuant terminals. (c) CropQuant used in offsite field trials, which was powered by batteries and solar panels. (d) An in-field WIFI system installed for onsite field trials. (e) The automated IoT platform established for onsite field trials. (f) Real-time crop monitoring through connecting CropQuant with a mobile device in the field or a computer in an office. (g) A comprehensive in-field weather station. (h) HPC is used for durable data storage and in-depth trait analysis.

100

101 **Figure 1** shows an experimental scale CropQuant platform used in wheat in-field  
102 assessment plots, incorporating networked remote sensors, single-board computers,  
103 in-field wireless communication, and open data exchange solutions. There are 14  
104 terminal workstations jointly operating on the platform, all of which are administered  
105 by a centralised control system called **CropMonitor** (**Fig. 1a** and **Supplementary**  
106 **Methods**). Using the platform, a number of tasks essential for next generation  
107 phenotyping<sup>19</sup> have been accomplished. They are *continuous monitoring* through high  
108 resolution time-lapse photography, *in-field evaluation* using dedicated hardware and  
109 software, and *efficient data transfer* via real-time file sharing and data exchange  
110 servers. To complete these tasks with low-cost hardware and minimal energy  
111 requirement, we have tested a range of single-board computers to conduct the above  
112 in-field computing tasks and chose to use *Raspberry Pi 2*, Pi camera modules (e.g.  
113 RGB, red/green/blue colour model), and remote sensor boards as the internal  
114 hardware (see **Final Publication**) due to the scalability and accessibility of the *Pi*  
115 computer. For the peripheral hardware, we have applied a weatherproof design to  
116 ensure environmental endurance, easy installation and outdoor maintenance (**Fig. 1b**

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117 and **Final Publication**). A hardware list and a construction manual for CropQuant can  
118 be seen in **Final Publication**.

119

120 As onsite and offsite field experiments are conducted using diverse infrastructures,  
121 we produced two versions of CropQuant terminal. For offsite field experiments, a  
122 workstation is powered by a replaceable battery with trickle charging from a solar  
123 panel (**Fig. 1c**). It is self-operating during the growing season. We have implemented  
124 a headless access mode to enable high-speed data transfer and systems control via an  
125 Ethernet connection. For onsite field trials, CropQuant devices are powered by 5V/2A  
126 power supplies and connected to an in-field WIFI network acting as nodes in a mesh  
127 network (**Figs. 1d&e, Final Publication**). For both versions, we developed an open  
128 software package running on the Linux *Debian* operating system to enable image  
129 acquisition, image quality control, regular humidity/temperature recording, and  
130 systems interactions (**Supplementary Methods and Final Publication**).

131

132 The CropQuant platform facilitates automatic crop phenotyping. Scientists and  
133 agricultural practitioners can access every terminal workstation remotely for real-time  
134 monitoring, either using a mobile device (e.g. a tablet/smartphone) in the field or an  
135 office computer (**Fig. 1f and Final Publication**). They can inspect not only the whole  
136 field in different regions via CropQuant terminals, but also take control of any  
137 operational workstation to review the performance of crops, initiate new monitoring  
138 sessions, or transfer on-board phenotypic and sensor datasets to external computing  
139 storage. If users are granted administrative access to the platform, they can oversee  
140 the whole platform through CropMonitor, where the status of every terminal node is  
141 constantly updated by the control system, including information such as online and  
142 offline status, operational mode, representative daily images, micro-environment (e.g.  
143 temperature/humidity in a plot region), and computational resource such as CPU and  
144 memory (**Supplementary Methods and Final Publication**). The architecture of the  
145 control system supports the collation of phenotypic and sensor data for storage,  
146 visualisation, GUI-based systems interactions, and processing on high-performance  
147 computing (HPC) infrastructure (**Final Publication**).

148

149 As our long-term research interests lie in efficient gene discovery, crop adaptation,  
150 agronomic characterisation and crop management, we have installed a comprehensive  
151 in-field weather station for our onsite field trials. The station records a range of  
152 meteorological datasets including photosynthetically active solar radiation, rainfall,  
153 temperature, relative humidity and wind speed (**Fig. 1g**). Phenotypic and climate  
154 datasets are managed and saved in HPC (SGI UV 2000 system equipped with Intel  
155 Xeon cores) for durable data storage and centralised trait analysis (**Fig. 1h**).

156

### 157 **The high-throughput analysis pipeline**

158 We configured CropQuant terminals to carry out high-frequency (three times per  
159 hour) and high-resolution (2592x1944 pixels) of measurement to capture phenotypic  
160 plasticity, early expression of traits, and crop-environment interactions (**Final  
161 Publication**). For example, over 200 GB data have been generated by ten offsite  
162 CropQuant terminals in the 2015 field season, during a 95-day period. To extract  
163 meaningful results from the growth and developmental data effectively, we exploited  
164 some latest open-source analytic libraries such as OpenCV<sup>20</sup>, Scikit-learn<sup>21</sup> and

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165 Scikit-image<sup>22</sup> and developed automated bioimage informatics algorithms that are  
166 embedded in a high-throughput trait analysis pipeline.  
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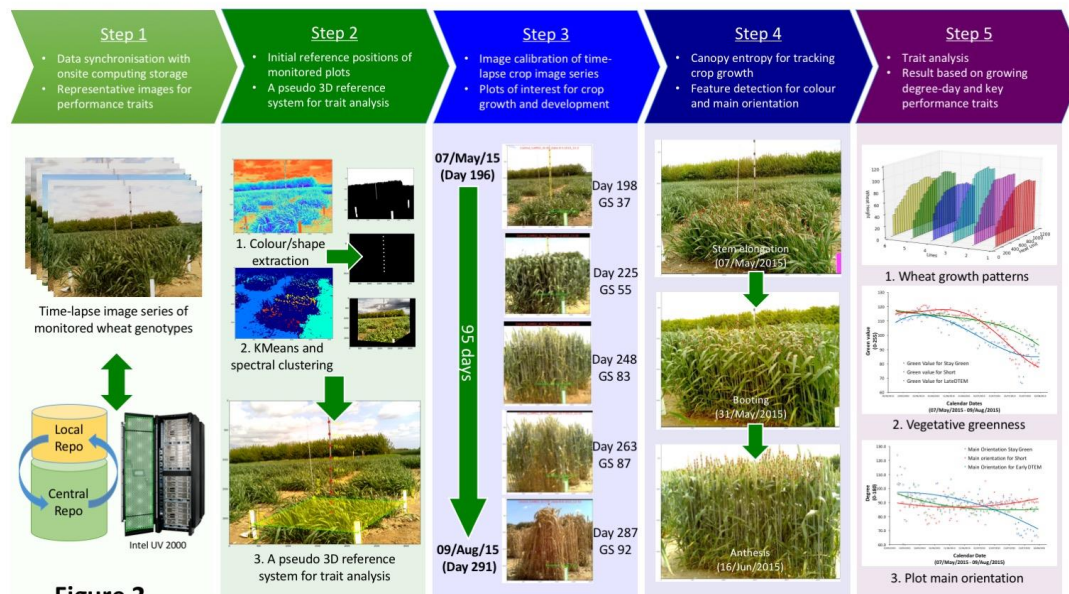


Figure 2

168 **Figure 2. The high-throughput analysis pipeline for processing and quantifying crop growth**  
169 **patterns and adaptive traits.**

170 In *step 1*, high-quality crop images are chosen by the selection algorithm and stored in both local  
171 and central Git repositories. In *step 2*, initial reference positions of five monitored plots are  
172 detected by the plot detection algorithm, which also calculates the pixel-metric conversion. In *step*  
173 *3* and *4* of the pipeline, the CropMeasurer algorithm is used for tracking plots of interest based on  
174 the initial reference positions and then conducts in-depth traits analysis to measure the canopy  
175 region and key adaptive traits. In *step 5*, crop growth patterns in relation to thermal time (degree  
176 day), continuous vegetative greenness (0-255) and the change of the main orientation of given  
177 plots (0°-180°) are quantified and illustrated.  
178

179  
180 **Figure 2** illustrates the analysis pipeline designed for both workstation computers  
181 and HPC. First, to arrange the collected crop images, we have developed a crop image  
182 selection algorithm to choose representative images according to their size, clarity,  
183 imaging dates and genotypes (**Fig. 2, Step 1**). Only high-quality images were retained  
184 for trait analysis (**Final Publication**). All datasets, including those low quality images,  
185 were stored in a central repository. Source code of the analysis pipeline was arranged  
186 into source trees and saved in both local and central Git repositories (**Supplementary**  
187 **Methods** and **Final Publication**).  
188

189  
190 Secondly, we have designed a detection algorithm to define reference positions of  
191 plots monitored during the experiment (**Fig. 2, Step 2**). In the real agricultural and  
192 breeding situations for which CropQuant was designed, strong wind, heavy rainfall,  
193 irrigation and chemical spraying will result some modest camera movements, which  
194 can cause issues when cross-referencing trait measures in a time-lapse image series.  
195 To resolve this issue, the algorithm identifies the initial reference position of a given  
196 plot and then geometrically transforms every image in the series to the same position  
197 for comparison. For instance, the algorithm detects coordinates of white reference  
198 canes (the plot region) and dark markers on a ranging pole (for crop height) using  
199 colour feature selection. Then, it classifies pixels into different groups such as crop

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200 canopy, wheel tracks, and plot regions based on the machine-learning methods (e.g.  
201 k-means and spectral clustering). Finally, the algorithm establishes a pseudo reference  
202 system that records the plot area, the canopy space, height markers and the pixel-  
203 metric conversion (**Supplementary Methods** and **Final Publication**).

204

205 Following Step 2, we incorporated initial reference positions of monitored plots into  
206 the third algorithm called **CropMeasurer** for in-depth trait analysis. For a given  
207 genotype, CropMeasurer employs an adaptive intensity and gamma equalisation to  
208 adjust colour and contrast to minimise colour distortion caused by variable in-field  
209 lighting (**Supplementary Methods**). Then, the algorithm tracks geometric differences  
210 between the plot on a given image and the initial plot position. If different, a  
211 geometric transformation method is applied to recalibrate the image, which removes  
212 areas outside the plot area and could generate different sizes of black bars to the top  
213 of the given image (**Fig. 2, Step 3**). Within a given plot, CropMeasurer calculates the  
214 crop height by detecting the visible part of the ranging pole as well as the canopy  
215 region (**Final Publication**). Finally, the algorithm locates corner-featured points  
216 within the canopy region (**Fig. 2, Step 4**), which generates red pseudo points  
217 (**Supplementary Methods** and **Final Publication**) to represent the tips of erect  
218 leaves at stem elongation or jointing (the Zadoks scale<sup>23</sup>, growth stages, GS 32-39),  
219 reflective surfaces of curving leaves and heads between booting and anthesis (GS 41-  
220 69), and corner-featured points on wheat spikes during senescence (GS 71-95).

221

222 In addition to crop growth patterns in relation to thermal time (degree day, °Cd), we  
223 have also included other dynamic measures of a number of traits in the pipeline (**Fig.**  
224 **2, Step 5**). For example, vegetative greenness is calculated through separating the  
225 green channel in RGB images within plots of interest (**Supplementary Methods**).  
226 The output (0-255) has been used to assess green biomass and stay-green (prolonged  
227 green leaf area duration through delayed leaf senescence). Morphological traits such  
228 as the main orientation of a given plot (0°-180°) are quantified based on an optimised  
229 edge detection method, which computes the alignment of crop stems for assessing  
230 stem rigidity and lodging risk (**Supplementary Methods** and **Final Publication**).

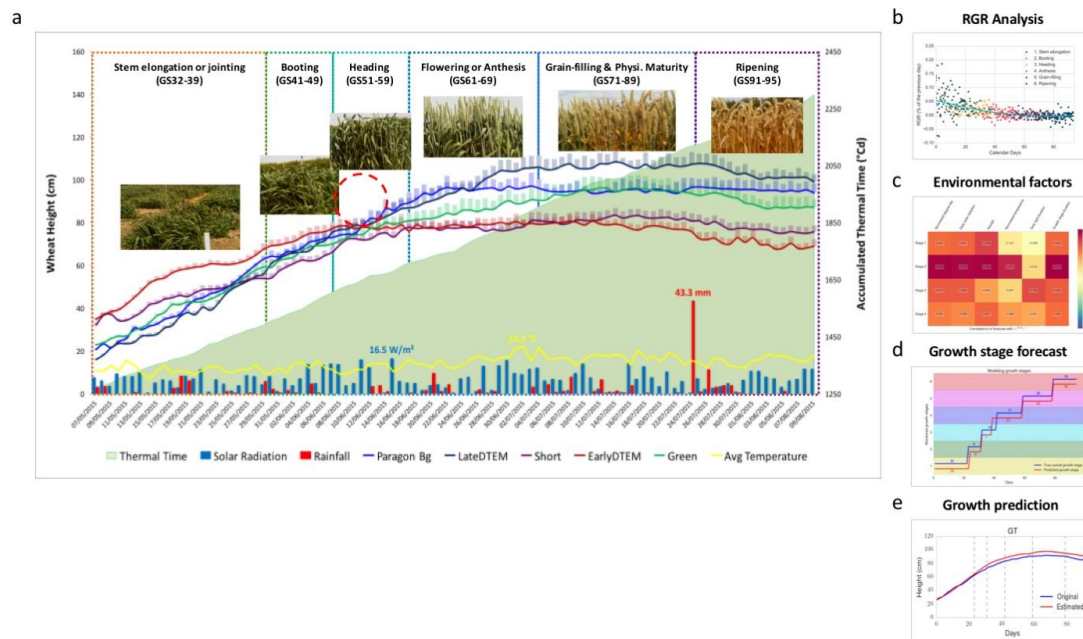
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### 232 **Monitoring NILs of wheat using CropQuant**

233 The radically different nature of environments where wheat is grown provides a  
234 unique opportunity to study the genetic diversity of wheat in connection with yield  
235 and stress tolerance through phenotypic differences<sup>24</sup>. Hence, we have chosen Near-  
236 isogenic lines (NILs) of wheat from our genetic stocks<sup>25</sup> to test the platform. Between  
237 May and August 2015, we monitored five NILs: Late-DTEM, days to ear emergence  
238 with *Ppd-1* loss of function (lof); Early-DTEM, *Ppd-D1a* photoperiod insensitivity;  
239 Short, *Rht-D1b* semi dwarfing; Stay-Green, a stay green induced mutant; and,  
240 *Paragon* wild type (WT). All NILs are in the genetic background of *Paragon* (a UK  
241 spring wheat variety) and were constantly monitored over a 95-day period  
242 (**Supplementary Methods** and **Final Publication**). **Figure 3a** illustrates dynamic  
243 developmental profiles of the five lines generated by CropQuant, together with  
244 environmental factors recorded during the period. Based on the developmental data,  
245 we computed daily relative growth rates (RGR) at different growth stages (**Fig. 3b**)  
246 and applied machine-learning based modelling to explore the dynamics between  
247 genotype, phenotype and environmental factors (**Figs. 3c-e**).

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249 **Figure 3**  
 250 **Figure 3. Monitoring wheat performance using the CropQuant platform and exploring the**  
 251 **dynamics between genotype, phenotype and environment.**  
 252 (a) Five NILs of wheat (Late-DTEM, Early-DTEM; Short, Stay-Green, and *Paragon* WT) and  
 253 their performance in relation to environmental factors such as wind and rainfall, together with  
 254 accumulated thermal time. Six growth stages of *Paragon* WT are used as reference. (b) RGR  
 255 (growth % of the previous day) is used to present the daily growth rate of five NILs at different  
 256 stages. (c,d) Both RGR and canopy height are responses of the correlation models that explore  
 257 wheat growth and environmental factors, including thermal time, solar radiation, rainfall and the  
 258 duration of growth stages, which are statistically significant using *Pearson* correlation ( $p < 0.01$ ). (e)  
 259 A global wheat growth model comparing CropQuant growth measures. (f) A growth stages  
 260 predictive model in comparison to manual phenotyping recording.

263 To measure the rate and sensitivity of wheat growth dynamically in relation to the  
 264 environment, we used *Paragon* WT as the reference and highlight six key growth  
 265 stages (GS32-95, **Fig. 3a**), from stem elongation or jointing (GS 32-39) to ripening  
 266 (GS 91-95), the five growth curves generally followed a sigmoid curve. At the  
 267 beginning of the crop monitoring, *Ppd-D1a* NIL was already at the end of the jointing  
 268 stage (GS37-39) and hence was the first line reaching a maximum height. *Ppd-1* lof  
 269 was the last to stop increasing in height. The heights of five NILs were very similar in  
 270 the middle of June (highlighted by a red dash circle), which has verified what we had  
 271 manually observed in the field as all the NILs were at different growth stages.

273 By cross-referencing five development profiles (based on growth stages, instead of  
 274 calendar days), we notice that, although *Ppd-D1a* NIL and *Rht-D1b* were recorded at  
 275 similar maximum heights (83.4cm and 80.6cm), the latter had a gentle-mannered  
 276 growth pattern. It suggests that this line could be suitable for crop management as  
 277 farmers and growers would have more time to decide whether to apply fertiliser and  
 278 irrigation to assist the growth or to use chemical control to prevent rapid height  
 279 increase<sup>13</sup>. *Ppd-1* lof's growth stages had been shifted back and thus had more time to  
 280 develop. As a result, this line became the tallest in the trial. Although all five lines  
 281 experienced some degree of height reduction due to a significant storm on 24<sup>th</sup> July  
 282 2015, *Paragon* WT presented a much lower lodging risk, as it maintained its height

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283 during ripening (GS91-95). To verify the above observation, we have scored  
284 manually the heading dates and canopy height on the same plots and obtained a strong  
285 correlation (with correlation coefficient of 0.985, see **Final Publication**).

286

287 Moving beyond descriptive phenotypic research, we incorporated genotype (G),  
288 phenotype (P) and environmental (E) datasets into machine-learning based modelling  
289 to explore the dynamics between GxE. First, to understand which environmental  
290 factors were strongly correlated with the growth of the five NILs at every key growth  
291 stage, we computed daily RGR of the lines and associated the growth rate according  
292 with their growth stages. The scatter chart (**Fig. 3b**) shows the growth vigour of the  
293 five genotypes, active from jointing to flowering (GS32-69) and inactive after GS71  
294 (grain-filling). After that, we calculated *Pearson* correlation coefficient and the p-  
295 value based on growth traits such as normalised RGR (nesting three-day rates to  
296 reduce noise) and canopy height at four key stages (i.e. jointing, booting, heading and  
297 flowering). Through this, we have identified six environmental factors that were  
298 significantly correlated with growth traits ( $p < 0.01$ ) out of 14 (**Final Publication**).  
299 They are: normalised degree day, solar radiation, rainfall, normalised temperature,  
300 light duration, and growth stage duration. Two heat maps (**Figs. 3c** and **3d**) were  
301 produced to present the relationship between the identified environmental factors and  
302 two growth traits (RGR and canopy height) in relation to four key growth stages  
303 (GS32-69). As growth traits did *not* change excessively after anthesis (GS71-95),  
304 hence we did not include the later stages in the correlation analysis (**Supplementary**  
305 **Methods** and **Final Publication**).

306

307 Finally, using the six identified environmental factors and growth traits measured  
308 during the growing season, we explored a set of linear regression models to establish  
309 a global predictive model to forecast the growth and development of wheat in the  
310 genetic background of *Paragon*, when interacting with the environment. **Figure 3e**  
311 shows how the model forecasts the overall *Paragon* growth data (GT, mean squared  
312 error: 20.1512, correlation: 0.9991, **Supplementary Methods**). The model uses the  
313 six environmental factors at six stages (GS32-95) as the input to obtain estimates of  
314 the relative growth rates  $y_t$  for every given genotype (**Final Publication**). The  
315 formula  $y_t = X_t^T * \beta_s + c$  was used for prediction, where  $X_t^T$  is the environmental  
316 data at a time point  $t$ ,  $\beta$  is the model parameters for growth stage  $s$ , and  $c$  is a constant  
317 offset. We used ordinary least squares to determine the coefficients of the model. We  
318 also applied the model to predict the growth of the five NILs and compared the  
319 estimated growth with the recorded data generated by CropQuant (**Supplementary**  
320 **Methods** and **Final Publication**).

321

322 On the basis of the first predictive model, we produced a second model to forecast  
323 the timing and duration of key growth stages (GS32-95) to link the crop growth  
324 prediction with real-world agricultural practices. So, farmers, growers and breeders  
325 can make sound decisions based on the difference between the predicted growth curve  
326 and the actual growth pattern measured by CropQuant (**Final Publication**). This  
327 approach could also assist agricultural practitioners in terms of line selection, fertiliser  
328 application, irrigation and harvesting to secure yield production. **Figure 3f** illustrates  
329 the performance of the second model. It has employed a set of support vector  
330 machines (SVM) with radial basis function kernels to classify the timing and duration  
331 of key growth stages (**Supplementary Methods** and **Final Publication**). We tested



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332 the model by comparing the predicted growth stages with the true data measured by  
333 crop physiologists (**Final Publication**).  
334

### 335 **Discussion**

336 The CropQuant platform in combination with networked remote sensing, IoT in  
337 agriculture control systems, advanced bioimage informatics, and machine-learning  
338 based modelling is capable of relieving a major bottleneck in breeding, crop science  
339 and agriculture. The platform enables a future of easy-to-use field phenotyping in  
340 which real-time crop growth and development is now quantifiable. We made a viable  
341 model for IoT in agriculture, which can stretch the imagination of the Agri-Tech  
342 industry to seek cost-effective ways to increase the efficiency and accuracy for  
343 various agricultural practices. With more field trial data feeding into our GxE models  
344 from different regions around the world, we will improve our software solutions and  
345 models, so that we can assist agriculture professionals in making sensible decisions in  
346 their practices. To empower ease of use and wide adoption, we are continuously  
347 improving CropQuant hardware and software to promote our vision in Agri-Tech  
348 innovation, including *mobility* (easy to install and use), *capability* (real-time in-field  
349 analysis), *affordability* (competitive costs) and *durability* (long-lasting in the field  
350 conditions).  
351

### 352 **Methods**

353 Methods and any associated references are available in the online version of the paper.  
354

355 Note: Supplementary information is available in the final published version of the  
356 paper.  
357

### 358 **Author contributions**

359 J.Z., D.R., S.L., T.S., M.C., M.B. and S.G. designed research; J.Z., D.R., O.G., C.L.  
360 and S.O. performed research; J.Z., D.R., T.C. and D.W. contributed hardware design  
361 and the development of analytics software; J.Z., D.R., T.C., D.W., O.G., C.L. M.B.  
362 and S.G. analysed data; and J.Z., D.R., T.C., D.W. and S.G. wrote the paper. All  
363 authors have read and approved the final manuscript  
364

### 365 **Competing financial interests**

366 The authors declare no competing financial interests.  
367

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### 424 **Supplementary Methods**

425

426 **Five wheat NILs** used in the field trial represent a range of genetic variation all with  
427 the genetic background of the UK elite spring wheat ‘*Paragon*’. The development of  
428 the Late-DTEM: Par (Norstar + Gamma 319c) 3c-11, *Ppd-1* loss of function (lof)  
429 lines is described previously<sup>26</sup>. The development of the Early-DTEM NILs: Par  
430 (GS100 2A+CS2B+Son64 2D)-T10 B10 -3b16 and *Ppd-D1a* photoperiod insensitive  
431 has also been published<sup>27</sup>. The novel line Stay-Green is line 2316b selected on the  
432 basis of stay green phenotype from a population of 7000 *Paragon* EMS mutants  
433 carried through single seed descent up to M6 developed under the Wheat Genetic  
434 Improvement Network of the UK Department of Food and Rural Affairs (Defra). The  
435 semi-dwarf NILs (short) were produced by marker assisted backcrossing (to BC6)  
436 using *Rht-B1* and *Rht-D1* KASP markers (LGC). which is available online from  
437 <http://www.cerealsdb.uk.net/cerealgenomics/CerealsDB>. The sources of *Rht-D1b* and  
438 *Rht-B1b* were the UK winter wheat varieties ‘*Alchemy*’ and ‘*Robigus*’ respectively.  
439 The five wheat lines were sown in single 1 m<sup>2</sup> plots in autumn 2014 at Church Farm,  
440 Norfolk UK, and grown according to standard agronomic practice. The manual score  
441 of the date for ear emergence (DTEM) was done when 50% of the plot showed 50%  
442 emergence of the ear from the flag leaf. The manual measurement of plant height was  
443 done from the ear tip to ground level.

444

445 **The CropQuant hardware** contains many components. The centre one of the design  
446 is a *Raspberry Pi 2* or *Pi 3* single-board computer (we are also testing Intel® Edison  
447 in the new version of CropQuant). Based on a mobile ARM processor, the *Raspberry*  
448 *Pi* computer features on-board external connections in the form of USB and Ethernet  
449 to allow expansion using additional peripherals as well as an array of digital GPIO  
450 pins to interface with. The crop growth image acquisition was performed using a 5MP  
451 RGB or NoIR (No Infrared, for night vision) camera module connected via a CSI port  
452 on the *Pi* mother board. Digital temperature and humidity sensors are connected via  
453 manufacturer supplied circuits to the GPIO pins of the *Pi* for interactive control. The  
454 sensors themselves are mounted separate from the circuits, externally on the  
455 CropQuant’s housing, wired through the base of the device and sheltered by a smaller,  
456 open housing unit. The external mounting allows for accurate sensing of ambient air  
457 conditions while sheltering the electronics from direct water damage. The CropQuant  
458 terminal is housed within a weatherproof (IP66 rated) plastic container, sealed around  
459 all openings allowing operation in the field conditions. Physical connection to the  
460 system for data transfer via USB or Ethernet and power (12/5V DC) is facilitated by  
461 water-resistant couplers designed to be sealed against the rain and air moisture.

462

463 **The CropQuant software package** runs on Linux-based operating system *Debian*. It  
464 contains two servers, NetATalk and VNC sever, to facilitate in-field data transfer and  
465 remote systems control, which allows users to connect to every CropQuant terminal  
466 through a wireless (using a tablet or a smartphone) or a wired connection (using a  
467 laptop). To enable real-time systems interactions, a GUI-based imaging program has  
468 been developed and added into the software package to control the RGB or NoIR  
469 camera module for time-lapse crop monitoring. The program can automatically detect  
470 the IP address of a given CropQuant terminal to associate the terminal with its  
471 specific experiment ID of the field trial. After that, the program requests users to  
472 specify information such as genotype, biological replicates and imaging duration via a

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473 GUI dialog box, where users can initiate the image acquisition. The program can  
474 automatically adjust white balance, exposure mode and shutter speed in relation to  
475 variable in-field lighting conditions using the *picamera* package, a pure Python  
476 interface to the *Raspberry Pi* camera hardware. Both image resolution and imaging  
477 frequency (three times per hour in our field trials) can be changed if users want to  
478 modify their experimental settings. The program also conducts the initial quality  
479 control and data backup after every image is captured. The GUI-based imaging script  
480 is freely available for download at (see final publication).

481

482 Besides the image acquisition, the software package also contains functions such as  
483 synchronising with the central server twice within an hour to upload sensor data and  
484 CropQuant hardware information (see CropMonitor). Representative daily images are  
485 routinely selected and transferred to the central server during the night, which  
486 provides a daily snapshot of the monitored crops. Relying on the *crontab* scheduling  
487 system, we can monitor the performance of the software package and resume it  
488 automatically in cases of software interruption or power disruption. The SD card  
489 image running on the current version of CropQuant workstations can be downloaded  
490 via (see final publication).

491

492 **CropMonitor** is the next-generation IoT control system developed to oversee the  
493 field trial. It is performed using a central web server, logging updates received from  
494 individual clients, CropQuant terminals. A Python application on each workstation is  
495 run at regular intervals, scheduled by the native Unix *Cron* system. The application  
496 queries the terminal to determine workstation status information such as uptime,  
497 network addresses and storage usage. Sensor data and more variable system data such  
498 as CPU temperature and processor/memory usage is sampled at a higher frequency  
499 and a mean average of the readings is recorded during the query. Once the application  
500 has collected all necessary data it is encoded into a JSON data object and transmitted  
501 over HTTP to the central server which stores the data in an SQL database running on  
502 HPC. CropQuant status is displayed and automatically updated using a web-based  
503 interface, determining whether each node is online by the time of their last update.  
504 The web interface provides information, including the location of every CropQuant in  
505 the field (a field map needs to be uploaded to the central server), graphs of collected  
506 terminal/sensor data, and facilitates SSH and VNC linking to all active nodes. The  
507 CropMonitor system provides a centralised real-time monitoring system to administer  
508 the network of in-field workstations and collate collected data for visualisation, batch  
509 processing and annotation.

510

511 **The image selection algorithm** is designed to perform speedy assessment of large  
512 image datasets captured in field trials by comparing images to a number of fixed  
513 criteria. The Python-based algorithm can be executed either on a normal computer or  
514 HPC. All images which meet the analysis standards will be collated. In turn, each  
515 image is quantified by brightness, shadow percentage and sharpness, allowing all  
516 images which perform above a set of thresholds to be retained for further traits  
517 analysis. To determine the brightness of an image, the median value of pixel intensity  
518 is taken by transforming the image into HSV colour space. If the median intensity  
519 value is lower than a set threshold, the image is culled and not used from this point  
520 forward. The image clarity is determined by applying a Sobel edge detection<sup>28</sup> to the  
521 image. The detectable edges are calculated and then correlated with sharpness and  
522 exposure range of the image. The result of the clarity detection is also compared to a

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523 set threshold, which will disqualify images if they are out of focus or unclear with ill-  
524 defined edges. The final image test is of the percentage shadow within the visible area.  
525 Dark pixels found in an image with an illumination value of below 20% are either too  
526 dark for feature extraction or containing too much shadow in the monitored plots.  
527 Once all comparisons have been passed, selected images are included in a result  
528 folder with a CSV file recording image metadata for further high-throughput image  
529 analysis. The iPython notebook of the image selection algorithm is freely available at  
530 (see final publication).

531

532 **The plot detection algorithm** detects initial reference positions of monitored plots.  
533 The algorithm identifies the coordinates of white reference canes (the plot region) and  
534 dark height markers on a ranging pole using colour-based feature selection on the  
535 basis of HSV (hue, saturation and value) and *Lab* non-linear colour space. It also  
536 classifies pixels into different groups such as sky, soil between plots, crop canopy,  
537 shadow, and plot regions using unsupervised machine-learning techniques such as K-  
538 Means<sup>29</sup> and spectral clustering<sup>30</sup>. After detecting initial reference objects in the  
539 image, the algorithm establishes a pseudo 3D reference system that records the 2D  
540 coordinates of the plot area, the canopy region, and height markers through a range of  
541 feature selection approaches. The pixel-metric conversion is also computed based on  
542 height markers on the ranging pole. The iPython notebook of the crop plot detection  
543 algorithm is freely available at (see final publication).

544

545 **The CropMeasurer algorithm** employs an adaptive intensity and dynamic gamma  
546 equalisation<sup>31</sup> to adjust colour and contrast to minimise colour distortion caused by  
547 diverse in-field lighting. Then, the algorithm tracks geometric differences between the  
548 plot on a given image and the initial position. If different, a geometric transformation  
549 method<sup>32</sup> will be applied to recalibrate the image, which removes areas outside the  
550 plot area and could generate different sizes of black bars to the top of the given image.  
551 Within a plot, CropMeasurer tracks the crop height by detecting the visible part of the  
552 ranging pole and defines the canopy region through a combined adaptive thresholding  
553 and local Otsu threshold methods<sup>33</sup>. Finally, the algorithm applies Harris and Shi-  
554 Tomasi corner detection methods<sup>34</sup> to locate corner-featured points within the canopy  
555 region. Red pseudo points are generated to represent the tips of erect leaves, reflective  
556 surfaces of curving leaves, heads and the corner points on ears. The main orientation  
557 of a given plot is quantified based on an optimised Canny edge detection method<sup>35</sup>,  
558 which computes the alignment of crop stems. The iPython notebook of the image  
559 selection algorithm is freely available for download at (see final publication).

560

561 **Data interpolation and analysis** have been used to handle minor data loss during the  
562 field experiments. Four days' data gap (at the end of May 2015) has been recorded on  
563 a number of offsite CropQuant workstations, which was caused by SD card crash due  
564 to short-term power failure. We therefore used cubic spline interpolation method<sup>36</sup> to  
565 fill the gap in the phenotypic datasets.

566

567 **The GxPxE interaction model** explores the interactions between the recorded crop  
568 growth of five wheat genotypes and a number of environmental factors. Correlations  
569 are performed for each environmental factor grouped over three days with the  
570 recorded growth data. The reason to group environmental factors into nested three-  
571 day periods is to remove outliers and smooth the input data. The correlations are  
572 determined for each growth stage for five genotypes. The analysis is performed on the

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573 grouped data as particular stages (e.g. booting and heading) contain few recorded  
574 growth data due to the short duration of both stages were present during the growth.  
575 To obtain the dynamic between relative growth rates (RGR) and environmental factors,  
576 we used the formula  $(e^{RGR})^{-1}$  to transfer negative correlation values, as the RGR  
577 series is a decreasing sequence in relation to the increasing nature of growth stages.

578

579 Based on significant environmental factors, a set of linear regression models<sup>32</sup> have  
580 been explored and a single linear regression model is selected to estimate RGR of five  
581 genotypes in relation to given in-field environment conditions. Environmental factors  
582 with insignificant correlations (where  $p > 0.01$ , with respect to the height over the  
583 entire time-series) are removed from the analysis as they provide little predictive  
584 power. Ordinary least squares are used to derive the model coefficients and all the  
585 stages are included as features. The RGR data is normalised to present percentage  
586 changes in height between two consecutive days. To predict the canopy height for a  
587 given genotype, environment data at each growth stage is input to the global model.  
588 To derive the height of the plant over time, successive applications  $h_t = h_{t-1}(1 +$   
589  $y_t)$  are applied, where  $h_t$  is taken from the above equation,  $h_{t-1}$  is the height of the  
590 plant at the previous time-point, and  $h_0$  is equal to the initial height.

591

592 The performance of the model is verified by estimating the growth of all five NILs,  
593 including the overall paragon growth data (GT). The estimation is displayed with  
594 respect to the true canopy height datasets. The mean squared error recorded for G2  
595 (*genotype two*, Late-DTEM), G3 (*genotype three*, Early-DTEM) and G4 (*genotype*  
596 *four*, Stay-Green) shows that the estimated height is close to the true growth curves.  
597 However, the error is much larger for G1 (*genotype one*, Paragon WT) and G5  
598 (*genotype five* Short). This is due to the majority of crop growth happens during the  
599 early stages (GS32-GS59), estimation deviation during these initial stages could affect  
600 the overall height results. As the global predictive model might not be sensitive  
601 towards specific genotypes, we are still seeking a better approach to incorporate all  
602 genotypes with a similar genetic background into the prediction. The iPython  
603 notebook of the **GxPxE** interaction model can be downloaded at (see final  
604 publication).

605

606 **The growth stage predictive model** is based on the GxPxE model described before.  
607 The model is produced to explore how to predict growth stages of different wheat  
608 genotypes on the basis of real growth traits and environment data. It employs support  
609 vector machines (SVM)<sup>34</sup> with radial basis function kernels to classify growth stages,  
610 as SVMs are popular machine learning techniques for classification. The performance  
611 of the model is tested by overall paragon wheat growth data (GT) and *Paragon* WT  
612 (G1), as GT performs well in the GxPxE interaction model whereas G1 performs  
613 poorly. The prediction in comparison with the manually recorded growth stages  
614 suggests a successful prediction of the timing and duration of stem elongation and  
615 jointing (GS32-39) through heading (GS51-59) and flowering (GS61-69) through  
616 Ripening (GS91-95). However, the transition from heading to flowering has  
617 introduced an error, the transition has been predicted three days earlier. The main  
618 reason for this error is due to the short duration of booting (GS41-49) and heading  
619 (GS51-59). All genotypes used for training cannot sufficiently differentiate the two  
620 stages. For this matter, we are planning to add more training datasets from other  
621 varieties such as Watkins and Chinese Spring wheat in other field trials. As the model  
622 can be used to classify growth stages with real in-field data, we have made the model

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623 freely available for other crop research groups to verify as well as jointly improve.  
624 The iPython notebook of the growth stage model can be downloaded at (see final  
625 publication).  
626  
627 **All supplementary movies** mentioned in the manuscript can be freely downloaded at  
628 (see final publication)



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629 **Online methods references**

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