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Quantitative Trait Locus (QTL) Mapping for Common Wheat Plant Heights Based on Unmanned Aerial Vehicle Images

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Abstract: The application of unmanned aerial vehicle (UAV) remote sensing technology for high-throughput acquisition of phenotypic values of field plant height is of great significance in plant height monitoring of wheat varieties (lines). Based on the UAV, mounted with high-resolution digital cameras, a low-altitude remote sensing platform was built to obtain images of the Berkut/Worrakatta recombinant inbred lines (RIL) wheat population (297 lines). The optimal digital surface model (DSM) for plant height extraction was constructed by combining the actual wheat plant heights measured in the field. Using a wheat 50K SNP chip, quantitative trait locus (QTL) analysis was performed for field plant height of the RIL population using UAV plant height data to detect the locus related to plant height. We verified the effectiveness of QTL analysis using the UAV plant height data. The results of the DSM plant height extraction method showed that the plant height extraction models during the entire growth period had a highly significant correlation ($p < 0.001$); the measured plant height correlated with the predicted plant height, with prediction model accuracy $R^2 = 0.7527$ and verification model accuracy $R^2 = 0.8214$. QTL analysis was conducted on the manually and UAV-measured plant height traits. For the manually measured plant height phenotypes, one locus related to plant height was detected on wheat chromosome 6A and explained 13.12% of phenotypic variation. For the UAV-measured phenotypes, one locus related to plant height was also detected on wheat chromosome 6A and explained 9.62% of phenotypic variation. The *QPH.xjau-6A* locus on chromosome 6A, which featured in the results of the two measurement methods, is a stable locus, indicating that the mapping results obtained using the actual plant height values were in good agreement with those obtained using the UAV extracted values. Three candidate genes related to plant height were screened: they encode protein kinase, NAC domain protein, and cytochrome P450, respectively. Therefore, this study provided reference information for monitoring plant phenotype and growth of wheat and also for the extraction of plant height for wheat breeding in the future.

Keywords: digital image; plant height; quantitative trait loci; *Triticum aestivum* L.; unmanned aerial vehicle

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1. Introduction

Wheat (*Triticum aestivum* L.) is an important food crop that is widely cultivated globally and is of great significance to national economies and social development [1,2]. However, demand for food has increased notably due to the rapid increase in the world population, and it is expected that by 2050, global food demand will increase by 70% [3]. Although the rapid development of biotechnology has promoted an increase in wheat yield, supporting global food security, the demand for wheat continues to increase. Researchers are also considering how to conduct accurate and high-throughput measurement of important phenotypic traits of wheat plants to ensure more efficient and rapid genetic improvement in important wheat traits [3,4]. Research on crop phenotypes, which are the basis of breeding, contributes to the accurate selection of new varieties that meet the requirements of breeding programs. With cross-application of crop phenotypic identification based on remote sensing technology used in crop breeding programs, the advantages of unmanned aerial vehicle (UAV) remote sensing in realizing high-throughput identification of important phenotypes in crop field have gradually been realized, making it an increasingly popular research method in wheat breeding [5–8].

Plant height (PH) is an essential crop phenotypic parameter and an important trait for evaluating plant growth and yield. Reduced plant height and improved lodging resistance have always been important breeding goals [9,10]. From the 1960s to the 1980s, the promotion of dwarf and semi-dwarf wheat varieties played a key factor in increasing global wheat production [11–13]. At present, the measurement of wheat plant height using the manual method is time-consuming and labor-intensive, and it suffers a certain degree of subjectivity. High-throughput monitoring of wheat plant height using UAV remote sensing technology can help to achieve timely, accurate, and efficient growth monitoring and yield prediction, which are of great importance in the genetic improvement of wheat traits [14,15]. The commonly used sensors for remote sensing monitoring in agriculture include high-resolution digital cameras, multi-spectral cameras, and thermal infrared sensors, each with different applications, working performance, and indicators [16,17]. Digital cameras can take high-resolution orthophotos of crops, which can be used to plan breeding programs and monitor crop growth, the crop planting area, and the lodging area; agricultural multi-spectral cameras can produce crop reflectance of red, green, and near-infrared bands for information analysis of crop growth, yield, diseases, and insect pests, and thermal imagers can accurately determine the crop canopy temperature for monitoring crop transpiration and drought [8,18,19]. Owing to its rapid development, UAV remote sensing technology has been widely applied in the detection of important crop traits, and detection of crop height is increasingly becoming an important research problem [16,20–22]. Yang et al. [18] found that the phenotypic values extracted from UAV images can be used to measure the phenotypic traits of crops. Niu et al. [23] used UAV digital images in combination with ground control points (GCP) to generate a digital surface model (DSM) to extract the plant height of maize, and they confirmed the efficiency and accuracy of crop prediction analysis based on UAV remote sensing technology. With regard to crop height monitoring, Zarco-Tejada et al. [24] and Luo et al. [25] obtained high-resolution images through visible light (RGB) digital cameras and LIDAR, attached to fixed-wing aircraft, and used them to estimate the height of olive trees and the plant height of low wetland vegetation, respectively. Verhoeven [26] and Weiss and Baret [27] acquired high-resolution images through visible light cameras mounted on UAVs, constructed a DSM for crops using dynamic structural algorithms and a 3D reconstruction method, and calculated plant height of crops and vines. The aforementioned studies all reflected the advantages of UAVs, such as carrying convenience, high flexibility, and short operating cycles [27,28]. The use of linkage maps for gene mapping has also been widely applied in research on the height traits of wheat [21,22,29]. An increasing number of reports have identified quantitative trait loci (QTL) for the plant height of wheat using different genetic populations [30–32]. Liu et al. [33] discovered seven QTLs affecting plant height, which are located on chromosomes 1B, 4B, 6A, 6D, and 7A, and each QTL explained 5.2–50.1% of the phenotypic variation. Bőrner et al. [34] detected some major QTLs controlling plant height on wheat chromosomes 1AS, 2DS, 4AL, and 6AS. Few existing studies have used high-throughput phenotypic identification to obtain QTLs in crops [20].

In this study, linkage analysis was conducted using UAV remote sensing-measured plant height of wheat and field-measured height phenotypes of wheat. The comparison of phenotypic identification and QTL analysis demonstrated the accuracy of UAV remote sensing data in the determination of phenotypes, and it also revealed the practicality of using UAV remote sensing data in the genetic improvement of crops. This study aimed to provide a fast, efficient, and large-scale phenotypic identification method for complex traits of wheat varieties (lines) and effectively solve the problems of large-scale and accurate phenotypic identification in the genetic improvement of wheat.

2. Materials and Methods

2.1. Test Materials and Design

The wheat materials used in this study were recombinant inbred lines (RIL) of the F6 generation with 297 lines developed from parents Berkut and Worrakatta using the single seed descent method. The plant height of the parent Berkut was significantly higher than that of the parent Worrakatta. The parents and their populations came from the International Maize and Wheat Improvement Center (CIMMYT) and were donated by the Wheat Research Institute of the Chinese Academy of Agricultural Science and the Wheat Genetics and Breeding Research Group of the College of Agriculture, Xinjiang Agricultural University.

In 2019, phenotypic identification tests on plant height of wheat using UAV remote sensing were conducted at the Snapping Research Base of Xinjiang Agricultural University. The site is located at 87°21′08″ to 87°21′11″ E, 43°56′19″ to 43°56′22″ N. Wheat RIL populations of 297 lines were sown on 5 April 2019 and harvested normally on 8 July 2019. The field was designed with random blocks, containing 2 replicates and 3 row zones (each of size 2 m × 0.9 m). In addition, each zone was spaced 0.2 m apart. Field management was carried out in accordance with the local conventional cultivation management mode, and the wheat field showed good growth. Fertilizer application, drip irrigation, insect control, and weed control were also followed in local field management practices.

2.2. Image and Ground Data Acquisition

A DJI Genie 4A four-rotor electric drone, mounted with a high-resolution digital camera, was used as a UAV remote sensing data acquisition platform. The UAV platform had a position and orientation system (POS) for data acquisition in real time. The model of the high-resolution digital camera was FC 6310, and its main parameters included 20 million real pixels, 5472 × 3648 resolution, f/5.6 aperture value, and 9 mm focal length. Specific parameters of the UAV image acquisition system are listed in Table 1. On the days of image acquisition (5 April 2019 and 6 July 2019), solar radiation was stable, and the weather was sunny and cloudless. During the data acquisition at the mature period (6 July 2019), the plant height was measured at 96 evenly distributed sampling points. Four plants were selected at equal intervals along the diagonal of each material block and measured using a tape; the average height of the four plants was taken as the mean plant height (PH) of the measuring plot. The height of the top of the spikes surrounding the wheat was taken as the height of the plant during the measurement.

Table 1. Main parameters of the UAV remote sensing image acquisition system.

Main Parameter	Value
Maximum takeoff weight	1368 g
Duration of flight	25–30 min
Flying height	20 m
Horizontal and vertical overlapping rate	80%
Ground resolution	1 cm

2.3. Plant Height Data Extraction

Using acquired high-resolution digital images, in combination with GCP data and Pix4Dmapper stitching software, stitching of UAV high-resolution digital images was performed to generate a digital orthophoto map (DOM) and digital surface model (DSM) of bare land and wheat during the mature period in the field, denoted as DSM_0 and DSM_1, respectively. DSM_0 was the bare land image immediately after sowing, which could be used as a datum of the field undulation. The difference between DSM_1 and DSM_0 could be used to determine the plant height (PH) of wheat varieties (lines) at each sampling point, as shown in Equation (1). The specific image stitching process is shown in Figure 1.

$$PH = DSM_1 - DSM_0, \tag{1}$$

where DSM_1 is the DSM at the mature period, and DSM_0 is the estimated DSM of the bare land after sowing.

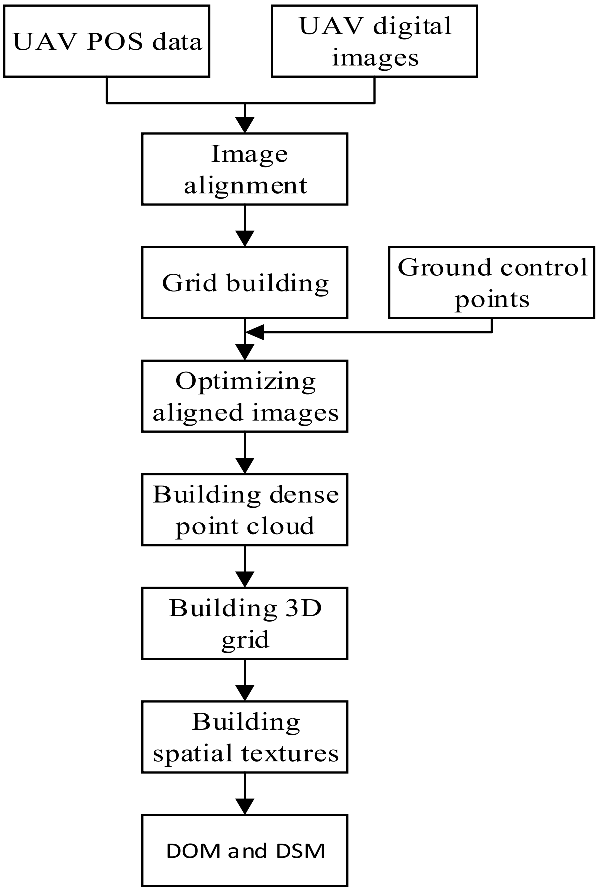

Figure 1. Unmanned aerial vehicle image stitching process.

2.4. Plant Height Data Modeling

Using the method of simple linear regression analysis, 70% of the sample data were randomly selected for modeling, and a wheat plant height estimation model was constructed. The remaining 30% of the sample data were used for verification, and a wheat plant height verification model was also constructed to test the model estimation ability. Estimated plant height of wheat and field observation values were used for model regression analysis. The determination coefficient (R^2) was selected as the evaluation index of the estimation and verification model. The higher the R^2 value of the model, the better the fitness of the model. The calculation method of R^2 is shown in Equation (2):

$$R^2 = \frac{\sum_{i=1}^{n} (X_i - \overline{X})^2 (Y_i - \overline{Y})^2}{n \sum_{i=1}^{n} (X_i - \overline{X})^2 \sum_{i=1}^{n} (Y_i - \overline{Y})^2} \tag{2}$$

where X_i and $\overline{X}$ are the measured value of sample i and the mean of the measured values, respectively; Y_i and $\overline{Y}$ are the estimated value of sample i and the mean of the estimated values, respectively; and n is the total number of samples.

2.5. QTL Mapping

Linkage analysis, based on a high-density genetic map constructed by our research group, was conducted using a 50K SNP chip. The entire map used 11,375 markers to construct a genetic map containing 1604 bin markers and 28 linkage groups, covering 21 chromosomes of common wheat. The length of the genetic map was 2220.26 cM, and the average distance between each marker was 1.38 cM. By combining the phenotypic values with the chip data, inclusive composite interval mapping (ICIM-ADD) was completed to estimate major QTL using ICIM Mapping V4.1 software, where the logarithm of the odds (LOD) threshold was set at 2.5; default values were used for other settings. The results were jointly evaluated based on the values of phenotypic variation explained (PVE) and LOD to obtain the QTL of plant height. A QTL was named by Q + abbreviation of the trait + abbreviation of the work unit (xjau) + the chromosome where the QTL was located. For example, the QTL detected on the short arm of wheat chromosome 6A was named *QPH.xjau-6A*.

2.6. Candidate Genes

The detected SNP markers that significantly correlated with yield-related traits were used to detect the candidate genes. Physical positions of population markers were mapped on the wheat genome, and a BLAST comparison was performed using the significant SNP marker sequence detected in multiple environments based on the Chinese Spring Wheat Reference Genome Database (http://www.wheatgome.org/ (accessed on 13 February 2023)) and NCBI website (http://www.ncbi.nlm.nih.gov/ (accessed on 19 February 2023)) for functional annotation of candidate genes.

3. Results

3.1. Phenotypic Evaluation

The mean plant height of the parent Berkut, determined using traditional field measurement, was 68.0 cm, and that of parent Worrakatta was 56.0 cm. The plant heights of the two parents were significantly different ($p < 0.05$), and the range of variation in the plant height of the RIL population was 49.4–78.3 cm, showing a bidirectional transgressive segregation (Table 2). The mean plant height of parent Berkut, determined using UAV remote sensing measurement, was 69.4 cm, and that of parent Worrakatta was 60.0 cm. The plant heights of the two parents were also significantly different ($p < 0.05$), and the range of variation in the plant height of the RIL population was 54.5–76.5 cm, showing a bidirectional transgressive segregation (Table 2). The values of the field-measured plant height and UAV remote-sensing-measured plant heights of the population both showed a normal distribution with continuous variables (Figure 2). The plant heights of the two parents and the mean plant height of the population measured using UAV remote sensing were all higher than the plant heights measured manually in the field. However, the field-measured plant height of the population exhibited a larger variation range than did the UAV remote-sensing-measured heights. Correlation analysis showed that the correlation coefficient between the field-measured plant height and UAV remote-sensing-measured plant height was as high as 0.92, indicating that UAV remote sensing can be used to effectively reflect the phenotype of plant height among individuals. Variance analysis showed that the genotypic differences between the field-measured plant height and UAV remote-sensing-measured plant height of the Berkut/Worrakatta RIL population both reached a significant level ($p < 0.001$) (Table 3), and the broad-sense heritability of both was 0.76, indicating that the plant height of wheat was greatly affected by genetic factors.

Table 2. Basic descriptions of the plant height of wheat Berkut/Worrakatta parents and the population.

	Parent		RIL Population						
	Berkut	**Worrakatta**	**Mean**	**Minimum**	**Maximum**	**Standard Deviation**	**Standard Error**	**Kurtosis**	**Skewness**
Measured	68.0 cm	56.0 cm	61.2 cm	49.4 cm	78.3 cm	5.92	0.34	−0.27	0.45
UAV	69.4 cm	60.0 cm	64.3 cm	54.5 cm	76.5 cm	4.42	0.26	−0.27	0.45

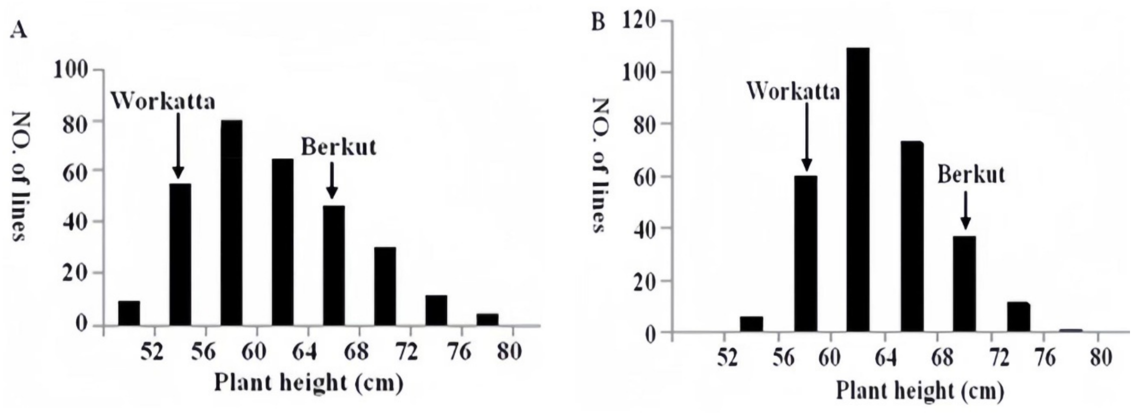

Figure 2. Distribution frequency of the measured plant height (**A**) and the predicted plant height based on DSM extraction (**B**).

Table 3. Variance analysis and broad-sense heritability of plant height traits.

Index	**Mean Square**			**Heritability**	**Correlation Coefficient (r)**
	Genotype (G)	**Replicate**	**Error**	**(h^2)**	
Measured	70.19 ***	3.47	15.74	0.76	0.92
UAV	39.03 ***	1.91	8.75	0.76	

*** indicates significance at $p < 0.001$.

3.2. Plant Height Model Analysis

Linear regression analysis was carried out on 297 lines of the wheat RIL population, and a plant height estimation model was constructed. A total of 70% of the data were randomly selected for model construction (Figure 3A), and the remaining 30% of the data were selected for model verification (Figure 3B). Scatter plots of the results were produced, and R^2 values of the models were calculated, as shown in Figure 3. The R^2 values of the model data and verification data were 0.7527 and 0.8214, respectively. This result also indicated that the models all had high prediction accuracy. Figure 3A also illustrates that the wheat plant height data extracted by DSM were generally smaller than the manually measured values. However, the overall deviation was not large. This may have been caused by factors such as full ear grains with increased grain weight, reduced vegetation coverage, and withered and yellow leaves after the end of the wheat growth period, leading to a high bending degree of the wheat stem and reduction in the image extraction effects, thereby lowering the plant height of wheat extracted by DSM.

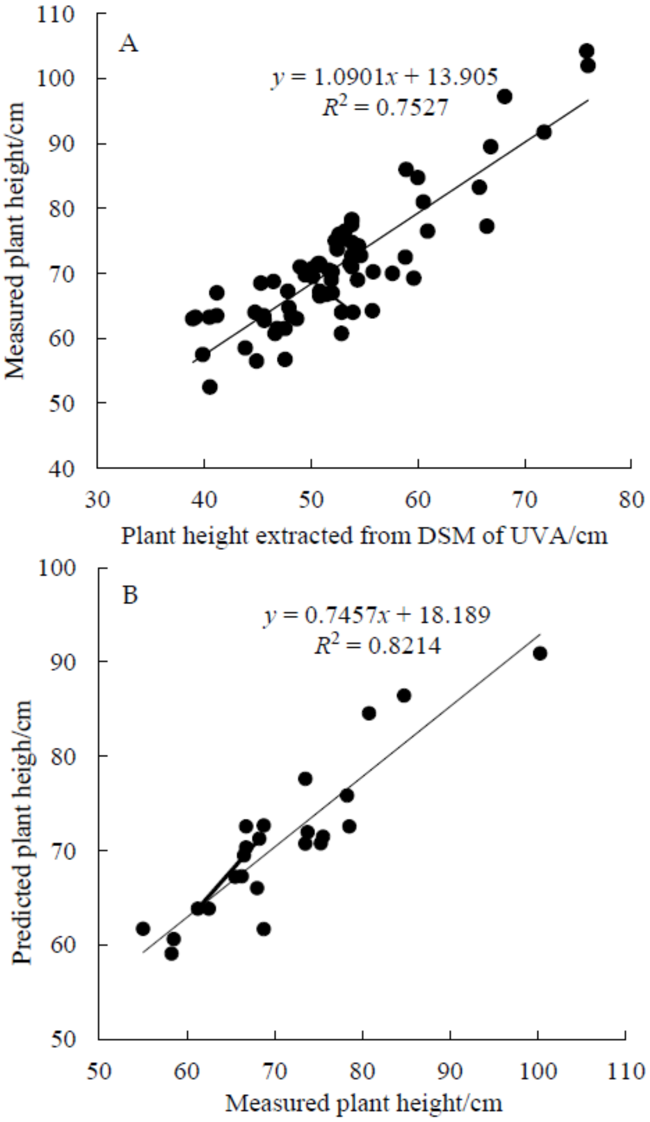

Figure 3. Comparison of the measured plant height and the plant height extracted from DSM of UAV (**A**) and the measured plant height and the predicted plant height by model (**B**).

3.3. QTL Mapping for Plant Height

The 297 lines of the Berkut/Worrakatta RIL population were subjected to whole-genome analysis for the manually measured plant height and UAV measured plant height. The results showed that in the manually measured plant height phenotypes, one plant height-related QTL *QPH.xjau-6A* was detected, and it is distributed on wheat chromosome 6A between *AX-109447932* and *AX-95023286* with a PVE of 13.12%. In the UAV remote sensing measured phenotypes, the same locus related to plant height was also detected on wheat chromosome 6A, with PEV of 9.62% (Table 4 and Figure 4). The same QTL detected in the two methods was located in a total area of 155.0 Mb between *AX-109447932* and *AX-95023286*. The PEV of manually measured plant height and UAV-measured plant height was basically the same, indicating that chromosome 6A is an important effector locus of plant height. This verified the accuracy of plant height measurement using UAV remote sensing and showed the similar trend of genome prediction for plant height from UAV remote sensing measurement and traditional field measurement. Moreover, the number and position of major QTLs obtained were basically consistent with the QTL mapping results under conventional plant height measurement. The experimental results also showed that the high-throughput detection of wheat plant height can be accurately realized by UAV, which provides a theoretical basis for the development of the technology of remote sensing to monitor wheat phenotype.

Table 4. QTL mapping of plant height in the wheat Berkut/Worrakatta RIL population.

Treatment	QTL [a]	Chr [b]	Position	Left Marker	Right Marker	LOD [c]	PVE (%) [d]	AE [e]
Measured	*QPH.xjau-6A*	6A	44	*AX-109447932*	*AX-95023286*	8.91	13.12	−2.16
UAV	*QPH.xjau-6A*	6A	44	*AX-109447932*	*AX-95023286*	6.39	9.62	−1.50

[a] QTLs that extend across single one-log support confidence intervals were assigned the same symbol. [b] Chr Chromosome. [c] LOD Logarithm of odds (LOD) score. [d] PVE is phenotypic variance explained by individual QTL in percentages. [e] AE Additive effect of LOX activity.

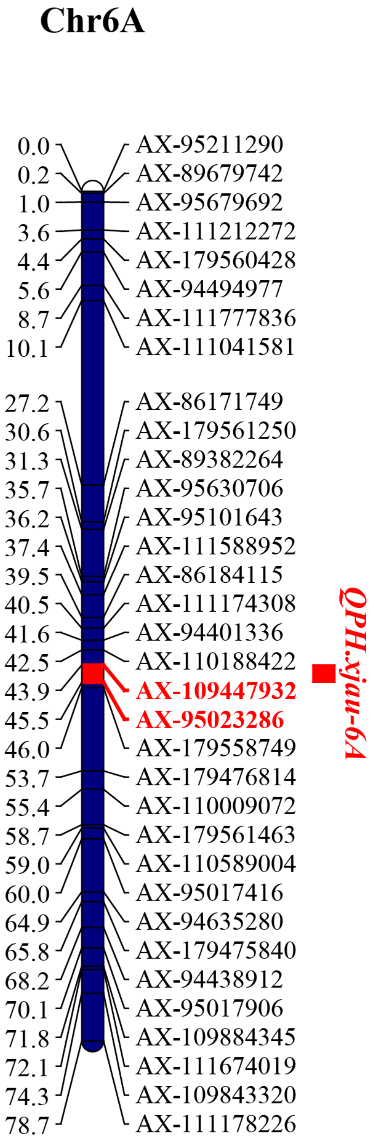

Figure 4. Location of wheat plant height on chromosome 6A.

3.4. Candidate Genes

Based on the fact that *QPH.xjau-6A* was repeatedly detected in both the manually and UAV remote-sensing-measured plant height and was closely linked with SNP markers *AX-109447932* and *AX-95023286*, the sequence information in this area was analyzed using the IWGSC Ref Seq Annotations database of wheat to screen the candidate genes. According to the gene functional annotation information, three candidate genes (*TraesCS6A01G196400*, *TraesCS6A01G208900*, and *TraesCS6A01G210500*) related to the plant height of wheat were obtained, as listed in Table 5. The three candidate genes included: (1) *TraesCS6A01G196400*, the gene encoding protein kinase, which regulates normal growth and development of plant organs and participates in hormone signal transmission in plants, playing a role in promoting growth and development of wheat; (2) *TraesCS6A01G208900*, the gene encoding the NAC domain protein, which regulates plant growth and development and negatively regulates plant height by affecting the accumulation of gibberellic acid (GA); and (3) *TraesCS6A01G210500*, the gene encoding cytochrome P450, which promotes the increase in plant height and increases grain yield by promoting cell proliferation (Table 5).

Table 5. Candidate genes for SNPs significantly associated with plant height.

Marker [a]	Chr [b]	Position (Mb)	Gene	Candidate Gene
AX-109447932AX-95023286	6A	287.31	*TraesCS6A01G196400*	Protein kinase family protein
		377.86	*TraesCS6A01G208900*	NAC domain-containing protein
		381.53	*TraesCS6A01G210500*	Cytochrome P450

[a] Marker shard markers were detected in MLM models at the threshold $-\log10$ (p) = 3.0. [b] Chr Chromosome.

4. Discussion

Plant height is a vital agronomic trait of wheat, affecting biomass and yield. The conventional method of measuring plant phenotypic traits (e.g., plant height, etc.) requires manual field investigation, which is inefficient and time-consuming. In recent years, the combination of spectral features (e.g., RGB, multispectral, and hyperspectral, etc.) and traits has more accurately extracted the phenotypic information of crops [35]. Satellite-based phenotyping depends on the planting area of the crop and weather conditions. UAV-based field phenotyping of crops makes it possible to collect crop heights with higher precision, frequency, and efficiency. In many studies, images collected by UAV-based high-resolution cameras were generated into digital orthophoto maps (DOMs), digital surface models (DSMs), crop surface models (CSMs), and digital terrain models (DTMs), which are used to analyze the data of crop height [36–38]. Xie et al. [39] and Feng et al. [40] reviewed recent applications of UAV remote sensing with various sensors for plant high-throughput phenotyping traits (plant height, etc.). The final purpose of phenotyping is to select the best genome lines [39]. However, Wang et al. [20] pointed out that few existing studies have used high-throughput phenotypic identification to obtain QTLs in crops. This study combined this method with field measured plant heights of wheat, and an optimal digital surface model (DSM) was constructed for plant height extraction based on UAV images. Moreover, QTL analysis was performed for field plant height of the RIL population and UAV plant height data to detect the locus related to plant height and we also verified the effectiveness of QTL analysis using the UAV plant height data.

Plant height, which is an important phenotypic feature of plants, can be used to evaluate growth status and estimate the yield of plants, and it is also one of the important evaluation criteria of breeding value and germplasm resources [2,9,10,33]. Plant height is a basic observable and measurable agronomic trait in wheat. There have been many reports on gene mapping of plant height by previous researchers. Most of the 21 chromosomes of wheat are related to genetic variation in plant height [27,33]. Despite limiting factors, such as the low density of molecular markers, large variation of traits affected by the environment, and linkage drag, there are few loci available for molecular marker-assisted selection obtained through linkage analysis or association analysis [41,42]. Using a high-density integrated physical map as the basis, the common loci controlling yield-related traits can be detected using two methods: single marker–trait association (SNP-GWAS) and segment–trait association (Haplotype-GWAS). A comparison of the detected loci with previously reported loci on a genetic map and physical map, and the analysis of the genetic correlation between different traits, can provide a reliable basis for analyzing the effects of different loci and assist in the selection of molecular markers [31,33,43]. Despite the genetic linkage map saturation of wheat and the genetic background differences between the parents (the parental plant height was not of extreme types), only one QTL related to the plant height variation of wheat was detected in this study. Some QTLs, especially micro-effect QTLs, were not detected. In this study, a plant height-related QTL *QPH.xjau-6A* was detected between the markers *AX-109447932* and *AX-95023286* on chromosome 6A. Although this QTL is on the same chromosome as the one detected by Liu et al. and Wang et al., it is not on or near the same marker [30,33]. It is speculated that this QTL may be a new locus. Therefore, further study on this type of loci would be of great significance in analyzing the genetic mechanisms that regulate the plant height of wheat and in cultivating new high-yield wheat varieties.

Plant height is an important agronomic trait of wheat. Although 13 Rht major genes have been discovered and mapped, the plant height of most varieties is controlled by multiple genes and is characterized by typical quantitative and genetic features, and it is easily affected by environmental factors [30]. Identification and selection of plant height phenotypes using traditional methods are constrained by the need for field work, which makes it difficult to achieve large-scale identification, and the reliability of the method is low [44]. Phenotypic traits of plant height are easy to observe, while their genetic research is progressing slowly, and cloning of the genes regulating the related traits is even more difficult. So far, the QTLs of plant height that can be repeatedly detected are limited to a few major loci, such as *Rht-B1b* and *Rht-D1b*. A large number of QTLs have been obtained on other loci, but their stability is poor. Their reliability still needs further verification, and they are far from being able to be applied in production [41]. UAV remote sensing technology has potential application value in the phenotypic analysis of plants and achieves rapid acquisition of spatial information in large-scale crop breeding plots. With guaranteed accuracy and effectiveness of phenotypic identification, this method has advantages such as fast maneuvering speed, low costs of usage, and simple maintenance and operation. It has already played an important role in the large-scale identification of crop phenotypes [9,10]. In this study, through a correlation analysis between the traditionally-measured plant height and the UAV remote-sensing-measured plant height, we found that both methods for plant height prediction can accurately reflect the differences between varieties. The accuracy and practicality of analyzing plant height traits through UAV remote sensing images were justified. In addition, in this study, based on the plant height phenotypic data obtained by UAV remote sensing image analysis, in combination with the wheat 50K SNP chip, the major QTLs of plant height could be accurately obtained. The number and position of major QTLs obtained were basically consistent with the QTL mapping results under conventional plant height measurement. The major locus related to plant height, *QPH.xjau-6A*, was detected on chromosome 6A using both methods.

Three possible genes (*TraesCS6A01G196400*, *TraesCS6A01G208900*, and *TraesCS6A01G 210500*) associated with plant height candidates in chromosome 6A were identified by linkage analysis in this study. *TraesCS6A01G196400* and *TraesCS6A01G208900* are regulated protein kinases; the proteins of this family have important roles in physiological processes such as phytohormone signaling, light signaling, and floral organ development [45]. *TraesCS6A01G210500* encodes cytochrome P450 protein. Cytochrome proteins not only participate in biosynthetic pathways in plants, but also act as key enzymes in the degradation of foreign toxic substances and cellular defense systems, which have a certain impact on crop height [46]. This result also revealed the practicality of using UAV remote sensing data in the genetic improvement of crops.

5. Conclusions

In this study, a remote sensing platform was established using a UAV carrying a high-resolution digital camera to acquire images of a Berkut/Worrakatta RIL wheat population (297 lines). The best digital surface model (DSM) for extracting plant height was constructed by combining field measurements of actual wheat plant heights. Quantitative trait loci (QTL) analyses were then performed on the field plant height and drone plant height data of the RIL population using a wheat 50K SNP chip to detect loci associated with plant height. The value of R^2 between the field measured plant height and the predicted plant height by the DSM model reached 0.7527. This indicated that the accuracy of UAV-based measurement of wheat plant height was higher. Both the field measured data and the predicted data using the UAV mined the *QPH.xjau-6A* locus on chromosome 6A. This verified the utility and feasibility of UAV-based remote sensing in gene mining. Moreover, the QTL we identified might be a new QTL locus associated with wheat plant height. This study also provided a fast, efficient, and large-scale phenotypic identification method for complex traits of wheat varieties, and it solved the problems of large-scale and precise phenotypic identification in the genetic breeding of wheat.

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Data Availability Statement: The data supporting the findings of this study are available from the first authors upon reasonable request.

Conflicts of Interest: The authors declare no conflict of interest.

Abbreviations

DOM	Digital orthophoto map
DSM	Digital surface model
GCP	Ground control points
hB2	Broad-sense heritability
ICIM-ADD	Inclusive composite interval mapping
LOD	Logarithm of odds
PH	Plant height
POS	Position and orientation system
PVE	Phenotypic variance explained
QTL	Quantitative trait loci
RIL	Recombinant inbred line
SNP	Single nucleotide polymorphism
UAV	Unmanned aerial vehicle

References

1. Ma, F.F.; Xu, Y.F.; Wang, R.F.; Tong, Y.P.; Zhang, A.M.; Liu, D.C.; An, D.G. Identification of major QTLs for yield-related traits with improved genetic map in wheat. *Front. Plant Sci.* **2023**, *14*, 1138696. [CrossRef]
2. Edae, E.A.; Byrne, P.F.; Haley, S.D.; Lopes, M.S.; Reynolds, M.P. Genome-wide association mapping of yield and yield components of spring wheat under contrasting moisture regimes. *Theor. Appl. Genet.* **2014**, *127*, 791–807. [CrossRef]
3. Yang, Y.H.; Zhang, J.Q.; Wu, K.G.; Zhang, X.X.; Sun, J.; Peng, S.B.; Li, J.; Wang, M.T. 3D Point Cloud on Semantic Information for Wheat Reconstruction. *Agriculture* **2021**, *11*, 450. [CrossRef]
4. Colomina, I.; Molina, P. Unmanned aerial systems for photogrammetry and remote sensing: A review. *ISPRS J. Photogramm. Remote Sens.* **2014**, *92*, 79–97. [CrossRef]
5. Jang, G.; Kim, D.W.; WonPyo, P.; HakJin, K.; Chung, Y.S. Heterogeneity Assessment of Kenaf Breeding Field through Spatial Dependence Analysis on Crop Growth Status Map Derived by Unmanned Aerial Vehicle. *Plants* **2023**, *12*, 1638. [CrossRef]
6. Yang, G.J.; Liu, J.G.; Zhao, C.J.; Li, Z.H.; Huang, Y.B.; Yu, H.Y.; Xu, B. Unmanned aerial vehicle remote sensing for field-based crop phenotyping: Current status and perspectives. *Front. Plant Sci.* **2017**, *8*, 1111. [CrossRef] [PubMed]
7. Niu, Y.X.; Zhang, L.Y.; Han, W.T.; Shao, G.M. Fractional vegetation cover extraction method of winter wheat based on UAV remote sensing and vegetation index. *Trans. Chin. Soc. Agric. Mach.* **2018**, *49*, 212–221.
8. Jin, X.L.; Zarco-Tejada, P.J.; Schmidhalter, U.; Reynolds, M.P.; Hawkesford, M.J.; Varshney, R.K.; Yang, T.; Nie, C.W.; Li, Z.H.; Ming, B.; et al. High-throughput estimation of crop traits: A review of ground and aerial phenotyping platforms. *IEEE Geosci. Remote Sens. Mag.* **2020**, *9*, 200–231. [CrossRef]

9. Chen, Z.X.; Ren, J.Q.; Tang, H.J.; Tang, H.J.; Shi, Y.; Leng, P.; Liu, J.; Wang, L.M.; Wu, W.B.; Yao, Y.M. Progress and perspectives on agricultural remote sensing research and applications in China. *J. Remote Sens.* **2016**, *20*, 748–767.
10. Watanabe, K.; Guo, W.; Arai, K.; Takanashi, H.; Kajiya-Kanegae, H.; Kobayashi, M.; Yano, K.; Tokunaga, T.; Fujiwara, T.; Tsutsumi, N.; et al. High-throughput phenotyping of sorghum plant height using an unmanned aerial vehicle and its application to genomic prediction modeling. *Front. Plant Sci.* **2017**, *8*, 421. [CrossRef]
11. Law, C.N.; Snape, J.W.; Worland, A.J. The genetical relationship between height and yield in wheat. *Heredity* **1978**, *40*, 133–151. [CrossRef]
12. Zhu, X.K.; Guo, W.S.; Li, C.Y.; Feng, C.N.; Peng, Y.X. Relationship of plant height component indexes with grain yield and quality in wheat. *J. Triticeae Crops* **2009**, *29*, 1034–1038.
13. Lu, Y.; Xing, L.P.; Xing, S.J.; Hu, P.; Cui, C.F.; Zhang, M.Y.; Xiao, J.; Wang, H.Y.; Zhang, R.Q.; Wang, X.E.; et al. Characterization of a putative new semi-dominant reduced height gene, Rht_NM9, in wheat (*Triticum aestivum* L.). *J. Genet. Genom.* **2015**, *42*, 685–698. [CrossRef]
14. Araus, J.L.; Cairns, J.E. Field high-throughput phenotyping: The new crop breeding frontier. *Trends Plant Sci.* **2014**, *19*, 52–61. [CrossRef] [PubMed]
15. Shen, Y.L.; Benoît, M.; Cao, Z.; Paul, K.; Guo, L.F.; Yao, H.X.; Cheng, Q. Improving wheat yield prediction accuracy using LSTM-RF framework based on uav thermal infrared and multispectral imagery. *Agriculture* **2022**, *12*, 892. [CrossRef]
16. Wang, P.; Luo, X.W.; Zhou, Z.Y.; Zang, Y.; Hu, L. Key technology for remote sensing information acquisition based on micro UAV. *Trans. Chin. Soc. Agric. Eng.* **2014**, *30*, 1–12.
17. Du, M.M.; Noguchi, N. Monitoring of Wheat Growth Status and Mapping of Wheat Yield's within-Field Spatial Variations Using Color Images Acquired from UAV-camera System. *J. Remote Sens.* **2017**, *9*, 289. [CrossRef]
18. Yang, G.J.; Li, C.C.; Yu, H.Y.; Xu, B.; Feng, H.K.; Gao, L.; Zhu, D.M. UAV based multi-load remote sensing technologies for wheat breeding information acquirement. *Trans. Chin. Soc. Agric. Eng.* **2015**, *31*, 184–190.
19. Salah, E.H.; Nasser, A.S.; Salah, E.; Yahya, R.; Majed, A.; Hassan, D.Y.; Wael, H. Combining biophysical parameters, spectral indices and multivariate hyperspectral models for estimating yield and water productivity of spring wheat across different agronomic practices. *PLoS ONE* **2019**, *14*, e0225294.
20. Wang, W.; Gao, X.; Cheng, Y.; Ren, Y.; Zhang, Z.; Wang, R.; Cao, J.; Geng, H. QTL Mapping of Leaf Area Index and Chlorophyll Content Based on UAV Remote Sensing in Wheat. *Agriculture* **2022**, *12*, 595. [CrossRef]
21. Forsmoo, J.; Anderson, K.; Macleod, C.A.; Wilkinson, M.E.; Brazier, R. Drone-based structure-from-motion photogrammetry captures grassland sward height variability. *Appl. Ecol.* **2018**, *55*, 2587–2599. [CrossRef]
22. Hassan, M.A.; Yang, M.J.; Fu, L.P.; Rasheed, A.; Zheng, B.Y.; Xia, X.C.; Xiao, Y.G.; He, Z.H. Accuracy assessment of plant height using an unmanned aerial vehicle for quantitative genomic analysis in bread wheat. *Plant Methods* **2019**, *15*, 37. [CrossRef] [PubMed]
23. Niu, Q.L.; Feng, H.K.; Yang, G.J.; Li, C.C.; Yang, H.; Xu, B.; Zhao, Y.X. Monitoring plant height and leaf area index of maize breeding material based on UAV digital images. *Trans. Chin. Soc. Agric. Eng.* **2018**, *34*, 73–82.
24. Zarco-Tejada, P.J.; Diaz-Varela, R.; Angileri, V.; Loudjani, P. Tree height quantification using very high resolution imagery acquired from an unmanned aerial vehicle (UAV) and automatic 3D photo-reconstruction methods. *Eur. J. Agron.* **2014**, *55*, 89–99. [CrossRef]
25. Luo, S.Z.; Wang, C.; Pan, F.F.; Xi, X.H.; Li, G.C.; Nie, S.; Xia, S.B. Estimation of wetland vegetation height and leaf area index using airborne laser scanning data. *Ecol. Indic.* **2015**, *48*, 550–559. [CrossRef]
26. Verhoeven, G. Taking computer vision aloft—Archaeological three-dimensional reconstructions from aerial photographs with photoscan. *Archaeol. Prospect.* **2011**, *18*, 67–73. [CrossRef]
27. Weiss, M.; Baret, F. Using 3D point clouds derived from UAV RGB imagery to describe vineyard 3D macro- structure. *Remote Sens.* **2017**, *9*, 111. [CrossRef]
28. Hassan, M.A.; Yang, M.J.; Rasheed, A.; Jin, X.L.; Xia, X.C.; Xiao, Y.G.; He, Z.H. Time-series multispectral indices from unmanned aerial vehicle imagery reveal senescence rate in bread wheat. *Remote Sens.* **2018**, *10*, 809. [CrossRef]
29. Wang, X.Q.; Zhang, R.Y.; Song, W.; Han, L.; Liu, X.L.; Sun, X.; Luo, M.J.; Chen, K.; Zhang, Y.X.; Yang, H.; et al. Dynamic plant height QTL revealed in maize through remote sensing phenotyping using a high-throughput unmanned aerial vehicle (UAV). *Sci. Rep.* **2019**, *9*, 3458. [CrossRef] [PubMed]
30. Wang, Z.H.; Wu, X.S.; Ren, Q.; Chang, X.P.; Li, R.Z.; Jing, R.L. QTL mapping for developmental behavior of plant height in wheat (*Triticum aestivum* L.). *Euphytica* **2010**, *174*, 447–458. [CrossRef]
31. Xu, Y.H.; Yang, Y.Z.; Wu, S.; Liu, D.C.; Ren, Y.Z. QTL Mapping for Root Traits and Their Effects on Nutrient Uptake and Yield Performance in Common Wheat (*Triticum aestivum* L.). *Agriculture* **2023**, *13*, 210. [CrossRef]
32. Roncallo, P.F.; Akkiraju, P.C.; Cervigni, G.L.; Echenique, V.C. QTL mapping and analysis of epistatic interactions for grain yield and yield-related traits in *Triticum turgidum* L. var. *durum*. *Euphytica* **2017**, *213*, 277. [CrossRef]
33. Liu, D.C.; Gao, M.Q.; Guan, R.X.; Li, R.Z.; Cao, S.H.; Guo, X.L.; Zhang, A.M. Mapping quantitative trait loci for plant height in wheat (*Triticum aestivum* L.) using a F2:3 population. *Acta Genet. Sin.* **2002**, *29*, 706–711. [PubMed]
34. Börner, A.; Schumann, E.; Fürste, A.; Cöster, H.; Leithold, B.; Röder, S.; Weber, E. Mapping of quantitative trait loci determining agronomic important characters in hexaploid wheat (*Triticum aestivum* L.). *Theor. Appl. Genet.* **2002**, *105*, 921–936. [CrossRef]

35. Hasan, U.; Sawut, M.; Chen, S. Estimating the leaf area index of winter wheat based on unmanned aerial vehicle RGB-image parameters. *Sustainability* **2019**, *11*, 6829. [CrossRef]
36. Panday, U.S.; Shrestha, N.; Maharjan, S.; Pratihast, A.K.; Shahnawaz; Shrestha, K.L.; Aryal, J. Correlating the plant height of wheat with above-ground biomass and crop yield using drone imagery and crop surface model, a case study from Nepal. *Drones* **2020**, *4*, 28. [CrossRef]
37. Tao, H.; Feng, H.; Xu, L.; Miao, M.; Yang, G.; Yang, X.; Fan, L. Estimation of the yield and plant height of winter wheat using UAV-based hyperspectral images. *Sensors* **2020**, *20*, 1231. [CrossRef]
38. Wang, D.; Li, R.; Zhu, B.; Liu, T.; Sun, C.; Guo, W. Estimation of wheat plant height and biomass by combining uav imagery and elevation data. *Agriculture* **2023**, *13*, 9. [CrossRef]
39. Xie, C.; Yang, C. A review on plant high-throughput phenotyping traits using UAV-based sensors. *Comput. Electron. Agric.* **2020**, *178*, 105731. [CrossRef]
40. Feng, L.; Chen, S.; Zhang, C.; Zhang, Y.C.; He, Y. A comprehensive review on recent applications of unmanned aerial vehicle remote sensing with various sensors for high-throughput plant phenotyping. *Comput. Electron. Agric.* **2021**, *182*, 106033. [CrossRef]
41. Li, T.; Deng, G.B.; Su, Y.; Yang, Z.; Tang, Y.Y.; Wang, J.H.; Qiu, X.B.; Pu, X.; Li, J.; Liu, Z.H.; et al. Identification and validation of two major QTLs for spike compactness and length in bread wheat (*Triticum aestivum* L.) showing pleiotropic effects on yield-related traits. *Theor. Appl. Genet.* **2021**, *134*, 3625–3641. [CrossRef]
42. Chen, S.L.; Gao, R.H.; Wang, H.Y.; Wen, M.X.; Xiao, J.; Bian, N.F.; Zhang, R.Q.; Hu, W.J.; Cheng, S.H.; Bie, T.D.; et al. Characterization of a novel reduced height gene (Rht23) regulating panicle morphology and plant architecture in bread wheat. *Euphytica* **2015**, *203*, 583–594. [CrossRef]
43. Shi, Y.; Ji, S.P.; Shao, X.W.; Tang, H.J.; Wu, W.B.; Yang, P.; Zhang, Y.J.; Ryosuke, S. Framework of SAGI agriculture remote sensing and its perspectives in supporting national food security. *J. Integr. Agric.* **2014**, *13*, 1443–1450. [CrossRef]
44. Hu, P.C.; Chapman, S.C.; Wang, X.M.; Potgieter, A.; Duan, T.; Jordan, D.; Guo, Y.; Zheng, B.Y. Estimation of plant height using a high throughput phenotyping platform based on unmanned aerial vehicle and self-calibration: Example for sorghum breeding. *Eur. J. Agron.* **2018**, *95*, 24–32. [CrossRef]
45. Sukumaran, S.; Dreisigacker, S.; Lopes, M.; Chavez, P.; Reynolds, M.P. Genome-wide association study for grain yield and related traits in an elite spring wheat population grown in temperate irrigated environments. *Theor. Appl. Genet.* **2015**, *128*, 353–363. [CrossRef]
46. Sun, C.W.; Zhang, F.Y.; Yan, X.F.; Zhang, X.F.; Dong, Z.D.; Cui, D.Q.; Chen, F. Genome-wide association study for 13 agronomic traits reveals distribution of superior alleles in bread wheat from the Yellow and Huai Valley of China. *Plant Biotechnol. J.* **2017**, *15*, 953–969. [CrossRef]