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Functional Identification and Molecular Mechanism Analysis of BHLH Transcription Factor ABP7-like in Maize Leaf and Grain Development

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Abstract: Corn, the world's third largest grain, has many USES, and demand is growing. How to improve the yield of maize is becoming a research focus, and the final yield of maize is closely related to the grain traits, so it is essential to carry out the functional identification and molecular mechanism analysis of BHLH transcription factor abp7-like in maize leaf and grain development. The purpose of this paper is to solve the problem of how to improve maize yield by analyzing and studying in detail the factors related to leaf and grain development. Based on the original study of BHLH transcription factor ABP7, the function identification and molecular mechanism analysis of a homologous gene abp7-like in maize leaf and grain development were discussed. Through sequence comparison with other known BHLH transcription factors and surface analysis of three constructed transgenic maize crops, the important role of BHLH transcription factor abp7-like in the development of maize leaves and embryos and its influencing principle were systematically discussed. The results showed that BHLH transcription factor abp7-like is a g-box binding transcription activator of BHLH, which plays an important role in the development of maize and embryo. In addition, the leaf and embryo development of the three transgenic corn crops constructed according to this method was significantly better than that of the ordinary corn crops. The experimental results showed that the yield of the transgenic corn crops was 25% higher than that of the ordinary corn crops.

1. Introduction

Since the 1980s, driven by the reform and opening up policy, China's economy has begun to develop at a high speed, and the demand for food has gradually increased. Maize is the third most important cereal crop in the world (after wheat and rice) and can grow in a variety of climates [1].

Corn has a variety of uses, such as human food, animal feed, and the manufacture of products for the pharmaceutical industry. In many countries, corn is used as a staple food. Due to the high energy and nutritional value of grains, leaves and stems, it is very suitable as animal feed. It can be used to produce starch, ethanol and plastic, and as a basic antibiotic [2]. As a C4 (tropical) plant, corn uses carbon dioxide, solar radiation, water, and nitrogen is more efficient in photosynthesis than C3 (temperate) crops. Maize grown on the same site at this water source is about twice as efficient as C3 crops. The essential things in life, such as oxygen, food, fiber, fuel and other products, are very dependent on photosynthesis [3]. The leaves of the plant are almost flat organs, designed to effectively capture light and perform photosynthesis. The photosynthesis process of land plants is accomplished by the leaves of the plants, which can capture light and use energy to reduce the formation of carbon dioxide and nitrate ions and carbohydrates and amigo acids. This function is achieved by special tissues that are placed in a layer with top (front) focus on light capture and gas exchange on the bottom (back) side. In nature, there are a variety of leaves of different shapes and sizes. Depending on the leaves, the leaves can be simple or complex organs that can not be divided or divided into leaflets [4]. The leaves are usually based on their general shape (round, oval or lancet), edges (smooth, lobed, or jagged), and curvature (planar or non-planar). The basic structure of the leaf generally develops along three axes, that is, near, far, middle, lateral, and positive dorsal axes. Therefore, plants appear to be exploiting a common mechanism responsible for establishing these axes in leaf development. The final size and shape of a plant's leaves involves three main developmental events: starting with the leaves, then growing the leaves, and finally expanding and maturing the leaves. The factors found behind the leaf size and shape at the bottom layer are inherently inherited: pin1 and knob1 indicate leaf initiation, KANADI, and YABBY are leaf birth, ANGUSTIFOLIA3, and growth regulator 5 control leaf expansion and maturation, respectively.

As for BHLH transcription factors, BHOPAL-type transcription factors are a large class of transcription factors that are named because they contain highly conserved domains. This domain contains 60 amigo acids, including a basic region at the N-terminus that is rich in basic amigo acids responsible for binding transcription factors to DNA, and two hydrophobic regions separated at the C-terminus by a loop of different length Residues constitute a helical structure that is both necrophilia and lollipop[5]. HAH-containing proteins usually form homo- or hydrometers. Dimer formation is necessary for DNA recognition and specific binding. The highly conserved Leu23 residues and Leu52 residues are required for materialization of human MAX protein and Archbishops PAR1 protein. Although BHLH usually forms dimes, BHLH can still interact with some other non BHLH proteins [6]. BHLH is the second largest class of transcription factors in plants, and most bind specifically. The Archbishops genome encodes over 150 BHLH proteins and regulates biological processes such as development, hormone signal response, and biotic abiotic stress response. For example, ZmR-like transcription factors are involved in the bio synthesis of flavonoid, the formation of tachometers and root hairs. BHLH transcription factors usually have introduction activation or inhibition activity, and this activity is related to the formation of dimer [7]. It is a constitution expressed BHLH gene. ICEL regulates stalemate development through interaction with MUTEFAMA and SPCH. Although some BHLH transcription factors have the characteristic of constitutive expression, there are also some BHLH transcription factors whose expression is S patio temporal or tissue-specific [8]. The BHLH gene in corn is specifically expressed in Aleutian cells and green tissues, respectively. ZOU can interact with ICE1, and this hetero dimer is necessary for recognition of target genes. In maize, the BHLH transcription factor, ZmZOf, which is specifically expressed in endosperm; decreased expression will lead to degradation of the embryo and the embryological region. Although Zm ZOU can interact with the ICE homo-logs Zm ICEb and Zm ICEc in maize, the interaction efficiency between Zm ZOU and Zm ICEa is more severe.

In order to explore how to efficiently and intelligently extract Web information from agricultural product quality and safety systems, this paper conducts a study on a scheme that can automatically extract Web information from agricultural product quality and safety systems based on templates. Among them, Yong ming made a detailed introduction to BHLH transcription factors, analyzed the current problems in increasing corn yield, and explained related research methods and technologies. It also shows that the national government attaches great importance to increasing corn yield, and indicates the importance of BHLH transcription factors and the significance of research [9]. Xin Cui proposed in his article the functional identification and molecular mechanism analysis of BHLH transcription factors in the development of camellia leaves and grains, and expounded the problems existing in the analysis experiments, especially in gene extraction and medium culture. In addition, it showed the significance and importance of BHLH transcription factor to improve the quality of agricultural products, and made a solution to the improvement and problems [10]. Haiping Ding detailly explained the gene information comparison of BHLH transcription factor ABP7 and ABP7-Like in this article, and put forward the importance and impact of BHLH transcription factor ABP7 on improving corn yield, and the necessity of carrying out related research [11]. Agnese Rabissi proposed the technology and related principles of using BHLH transcription factor ABP7-Like to transgenic new plants in corn, and pointed out the advantages and disadvantages of this transgenic crop. Some common problems in the cultivation of genetically modified crops were raised, and the problems and related performances encountered in the application of plant cultivation were briefly introduced [12].

To put it simply, in this paper, we seek ways to increase maize yield, and carry out functional identification and molecular mechanism analysis of BHLH transcription factor ABP7-Like in maize leaf and grain development. Specifically, the main research content of this article is roughly divided into five parts: the first part is the introduction part, which aims to systematically review the main research content of this article from the research background, research purpose, research ideas and methods; the second part is The theoretical basis, a detailed and systematic summary of the current functional identification and molecular mechanism analysis of maize leaf and grain development and the current research status of BHLH transcription factors, and the introduction of the basic ABP7 of BHLH transcription factors ABP7-Like. The third part is related research, through querying data and conducting relevant experiments to explain the effect of BHLH transcription factor ABP7-Like on the development of maize leaves and grains. The fourth part is the analysis of the data. Through the specific survey data and research results, the superiority of the three transgenic corn crops constructed using the BHLH transcription factor ABP7-Like was verified from various aspects such as leaf color traits and grain traits. Part is the summary and suggestions of this article, the summary of the results of the article and the prospects for the better use of BHLH transcription factor ABP7-Like in the yield of corn.

2. Proposed Method

2.1. BHLH Transcription Factor ABP7-Like Medium

In order to better study the BHLH transcription factor ABP7-Like, there must be a lot of experimental materials, so the medium is the method that must be used. LB liquid culture medium (1L): 10 g of pep tone; 5 g of yeast extract; 10 g of Na Cl; 800 ml of ddH20 was dissolved, and the pH was adjusted to 7.2-7.5 with 1M Na OH, and the volume was adjusted to 1 L with ddH20, and autochanger at 121C for 20 min. For solid media, add 1.5% agar powder. Preparation of 1M 3-AT storage solution: Weigh out 4.204g of 3-AT, dissolve it in 50mL ddH20, and filter sterilize. Yeast-deficient medium was prepared according to the formula on the instructions: each packet was dissolved in 500mL ddH20 and sterilized at 121C for 15min. When the medium containing 3-AT is

cooled to 50C, a corresponding volume of 3-AT mother liquor is added to make the final concentration reach the requirements, and then the plate is reserved. Cinnamon / Ampicillin storage solution: 0.1g / ml, 0.22m filter sterilized by filtration, and stored at-20 after dispensing. When used, it is added to sterilized LB liquid or solid medium at a ratio of 1: 1, and the final concentration of antibiotics is 100mg / LLO, and the preparation of 0.5M EDTA at pH 7.5: Weigh 18.61g EDTANa2H20 in 80mL ddH20 After using Na-OH to adjust the pH to 7.5, make up to 100mL and sterilize. The solution ratio adjustment formula is shown in formula 1:

$$M = DM\frac{u_1}{u_2}V.M \tag{1}$$

For the preparation of protestation K solution: 0.1g protestation K was weighed and dissolved in 10mLddH2O, and stored at -20C after aliquot. Preparation of MES: Weigh 21.325g of MES in 400mLddH20, adjust the pH to 5.7 with KOH and set the volume to 500mL. Preparation of 1M Tris-HCl: Weigh 12.11g Tris in 80mL ddH20, adjust the pH to 6.5 or 8.0 with HC1, then set the volume to 100mL and autoclave. Oxer preparation: Mix 2mL of 1MTris-HCl, 0.4mL of 0.5M EDTA, and dilute to 10mL. Preparation of 2MKC: Weigh 14.9g of KC1, add ddH20 to dissolve and make up to 100mL, and autoclave. 1M Ca Cb preparation: Weigh 14.7g CaCl2, add ddH20 to dissolve and make up to 100mL, and autoclave sterilization. Preparation of 0.8M manning (Manning): Weigh 14.574g manning, add ddH2O to dissolve and make up to 100mL, and autoclave. The formula of the dilution ratio of the dissolving solution is shown in formulas 2 and 3:

$$N = C.VF.0.5/C\,V\,S \tag{2}$$

$$VAD = VF - VS \tag{3}$$

In addition, some materials need to be cultivated. Preparation of 1MMgCb: Weigh 20.33g MgCl2x6H20, add ddH20 to dissolve and dilute to 100mL, and autoclave. Preparation of 50% PEG4000: 5g PEG4000 plus ddH20 was dissolved and the volume was adjusted to 10 ml. Preparation of Lobelia: Weigh 6.599g Li Ac, add ddH2O to dissolve, adjust the pH to 7.5 with acetic acid, and make it to 100mL, then autoclave. Preparation of 2M sucrose: Weigh 68.5g sucrose, add ddH20 to dissolve and make up to 100mL, and store at 4C after autoclave. Preparation of 212M glycerin: Weigh 15g glycerin and ddH20 to dissolve and make up to 100mL, filter sterilize by 0.22pm filter membrane. Preparation of 0.1MPMSF: Weigh 1.74g of PMSF in 100mL of absolute ethanol, aliquot and store at -20C. 5MLiCl preparation: Weigh 21.2g Li Cl, add ddH20 and make up to 100 ml, 0.22 pm filter membrane filter sterilization. Preparation of 20% NP40: Pipette 20mL of NP40, add ddH20 to volume to 100mL, and autoclave. Preparation of 10% SDS: Weigh 10g SDS, add 80mLddH20 and place it on a heated magnetic stirrer. After it is completely dissolved, make up to 100mL. Preparation of 10% sodium chocolate: Weigh 10g sodium chocolate, add dd Hob to dissolve and make up to 100mL. The establishment of the culture medium provides a large amount of research materials for subsequent research.

2.2. Cloning and Vector Construction of BHLH Transcription Factor ABP7-Like Gene

The cloning and vector construction of the BHLH transcription factor ABP7-Like gene is also the basis for research, and there are many methods in this regard. Among them, DNA extraction generally uses corn leaves from the 3-leaf stage to the 5-leaf stage as materials, and about 1 cm2 of the leaves are placed in a 2 ml centrifuge tube containing steel balls, and the liquid nitrogen is quickly frozen and then ground using a grinder. Then follow the instructions of the DNA extraction kit. All clone PCR reactions were amplified using Fast Pfc. The amplification reaction system was as follows: DNA template (1.5ul), 2.5mm DNTPS (5.5ul), primers (12uM), 5xFastPfu buffer (10ul),

Faustus DNA polymerize (2ul), ddH2O (50ul), etc. The PCR reaction procedure is as follows: (1) 94 C, 2min; (2) 94C, 20s; (3) 56 C, 20s; (4) 72 C, the extension time depends on the fragment length (2kb / 1rain), Cycle 30 times from 2 to 4; (5) 72C, 5min. After all amplification products are detected by electroplate, the target band is cut and recovered using the DNA recovery kit according to the instructions. The total DNA is estimated according to the brightness of the initial electroplate band, and an appropriate amount of eloquent is added to make the final DNA concentration meet the subsequent test . The formula for predicting DNA mass and moles is shown in formulas 4, 5, and 6:

$$\mathrm{ds}DNA = M/(L*617.96+36.04) \tag{4}$$

$$\mathrm{ss}DNA = M/(\mathrm{nt}*308.97+18.02) \tag{5}$$

$$\mathrm{ss}RNA = M/(NT*321.47+18.02) \tag{6}$$

Vector construction mainly uses restriction nonnuclear digestion and T4DNA ligate ligation and homologous recombination. The former mainly uses the corresponding restriction enzyme to digest the vector fragment and the target fragment. The digestion system for the vector and the target fragment is as follows: DNA (1ug vector fragment), nonnuclear (0.5ul), 10x buffer Liquid (2ul), ddH2O (20ul) and so on. After reacting for 1 h at the optimal reaction temperature of restriction enzymes, the digested products were detected by agaric gel electroplate and recovered. The recovered DNA was quantified, and the quantified DNA was ligated according to a 1: 5 molar ratios of the target fragment to the carrier fragment. All were transformed into E. Colic competent. The transformation process is as follows: add the ligation product to 50jxL competent E. Colic competent cells thawed on ice, mix lightly and place on ice for 20min; heat-shock at 42C for 60s, re-place on ice for 3-5min, add 500hLLB liquid Culture medium.

After that, the temperature needs to be adjusted for vector construction. First, activate E.coli by shaking at 200C for 7 min at 7C. If you use ampicillin for resistance screening, skip this step. After centrifuge at 4000xg for 3min, discard 400uL of the supernal; re suspend the remaining bacterial solution with the remaining medium and spread it on ampicillin or kanga resistant plates; dry the plate in a clean bench and invert and incubate at 37 C. Cultivate in a box for 8-16h; pick a single colony and culture it in 3mL of corresponding resistant liquid LB medium for 8-16h, extract the plasma, and perform enzyme digestion or PCR identification and sequencing; the method of homologous recombination is through design and vector Primers with a minimum of 15 NT homologous sequence that can amplify the target fragment at the same time after amplification of the target fragment, homologous recombination with the linear vector. Recombine products were also transformed into E. Colic competent cells and coated on corresponding resistant plates, and monoclonal were picked and verified by sequencing. The mixing ratio of DNA fragments and plaids and the insertion quality are shown in Equation 7:

$$G = \lg * \mathrm{g} * \frac{C_1}{C_2} \tag{7}$$

3. Experiments

3.1. Related Processing of Experimental Data

The object of this experiment was corn from an experimental planting base. The influence of BHLH transcription factor ABP7-Like on the functional identification and molecular mechanism analysis of maize leaf and grain development was examined. During the experiment, there is a large

amount of experimental data to be processed, and there must be errors in these data. It is also very important to handle the errors appropriately. Therefore, before using these experimental data for forward and reverse analysis, the error should be processed and analyzed on the original data[13]. Generally, the errors of the experimental data can be divided into three types: system error, random error and gross error[14]. Among them, random errors are often caused by random factors, and their signs and absolute values are irregular. However, as the number of experiments increases, random errors are generally considered to be normally distributed. The gross error mainly refers to the fact that in the statistical data, due to the observer's carelessness, or sudden changes in environmental conditions, unstable instrumentation and other factors, the observation error does not conform to a certain statistical distribution rule, which is usually a measurement error. System error is the error caused by the measurement instrument, the change of the measurement reference and the influence of external conditions. At present, the systematic error of observations is generally composed of corresponding statistics based on the statistical characteristics of observations, and then test hypotheses are made based on the characteristics of their probability distributions, and judgments are made by comparing actual calculated values with quantifier values[15].

At present, when resolving this kind of problem at home and abroad, the least square method is usually used to process the experimental data twice. The basic idea of the least square method is to first assume that the observations only contain accidental errors, but this is basically not true in reality. Possibly, for this reason, a new theory has been developed to study systematic errors and gross errors. At present, the more effective method for processing systematic errors is the additional parameter method; there are two methods for processing gross errors. One is the data detection method that still belongs to the category of least squares, and the other is the method of robustness estimation that is different from the least square's method. Or robust estimation. In addition, in the actual situation, various social work-related links are constantly changing, and the information collection system is also in a moving state, which means that the entire collection process is dynamically changing, so there will be relative errors in experimental management. It is inevitable. Modern error theory generally believes that the measured true value cannot be determined, and the existence of the quantum effect excludes the existence of the unique true value, so the error cannot be accurately obtained.

3.2. Experimental Model Establishment

After obtaining the information of the BHLH transcription factor ABP7-Like, important work analyzes the effect of this factor on the leaves and grains of corn from the genetic level, and then achieves high yield of corn. It is often the case that some information is not updated in time and some information is not transparent. Therefore, it is a very complicated problem to collect the correct experimental results in a timely manner and evaluate the experimental standards. The relationship between BHLH transcription factor ABP7-Like and maize yield is a mathematical model. The influence mechanism and role of BHLH transcription factor ABP7-Like is the key to determine the new transgenic corn crops. Therefore, to explore the impact of ABP7-Like on corn yield at the molecular level, a reasonable mathematical model is mainly established. The purpose of establishing a mathematical model is to establish the function relationship between the activity or content of the BHLH transcription factor ABP7-Like and the yield of corn, that is, to use the information obtained from various channels to determine the influence of various factors on leaf traits, embryo traits, etc., and to establish the response effect Sexual function model. After obtaining the relevant experimental corn traits, a better genetically modified corn crop can be constructed based on its own dynamic adjustments.

Commonly used methods for establishing statistical models include stepwise regression, multiple

regression, weighted regression, and so on. There are many factors that influence the final experimental results. In addition, the established GM model was used to predict the information in the future, and there are many ways to increase corn yield. It is also important that this genetically modified corn crop that uses the influence mechanism of the BHLH transcription factor ABP7-Like is reliable and has a market prospect . Domestic and foreign statistics on the quantitative data of agricultural product quality and safety system market size have only begun in recent years, so there are very few data that can be used to predict the future application of agricultural products. The article uses gray prediction models to use BHLH transcription factors. ABP7-Like's impact mechanism is predicted for the development of the GM corn crop application market, and the effectiveness and accuracy of the impact mechanism is verified from the side. On the premise of qualitative research on the impact mechanism of the BHLH transcription factor ABP7-Like, further Enrich the quantitative research theory.

In addition, the functional identification of BHLH transcription factor ABP7-Like in the development of maize leaves and grains and the establishment of information collection indicators related to molecular mechanism experiments were established. After the establishment of a statistical model, the collection indicators can be determined. From the knowledge of mathematical statistics, it can be known that when the statistical model established based on the least square method satisfies the conditions of Gaussian assumption and the normal distribution of residuals, the obtained statistical model is the best unbiased estimation. This model can be used for overall estimation and prediction. Under normal circumstances, there is no abnormality in the residual sequence obtained after the observations are fitted; if there are abnormal values, it may indicate a precursor of instability. The upper and lower limits for judging whether the collected information value is abnormal are called collection indexes. There are two common methods for establishing collection indicators based on statistical models: confidence interval method and small probability method.

3.3. Experimental Conditions and Equipment

The functional identification and molecular mechanism analysis of the BHLH transcription factor ABP7-Like in the development of corn leaves and grains discussed in this article. The experimental data analysis and related automated experimental devices mainly use the Internet of Things perception and identification technology, the Internet of Things communication and application layer technology. These technologies and the equipment needed are the main experimental conditions and equipment for this experiment. The so-called Internet of Things perception and identification technology refers to the Internet of Thing's collection of information through perception and identification, and is the main data source of the Internet of Things. Commonly used technologies are: two-dimensional code technology, radio frequency identification RFID technology, infrared sensing technology, GPS satellite positioning technology, audio and visual identification technology, biometric identification technology, etc. Sensing technology mainly embeds sensors around or on an object, collects data of the object or the surrounding environment, and senses various physical or chemical changes. Commonly used technologies include sensor technology, radio frequency identification technology, and so on. The sensor is the main source of information for the application of the Internet of Things. It senses the status information of the measured object, and converts the perceived information into electrical signals or other forms of information, and then outputs it. , Display and control requirements, and finally achieve automatic detection and automatic control functions. The node information table structure of the sensors used in this paper is shown in Table 1:

Table 1. Sensor node information table structure

The field names	Field type	Field meaning
SENSOR-TYPE	Small int (5)	The sensor type of the node
NWK ADDR	Small int (5)	The network address of the node
EXT ADDR	Small int (5)	The MAC address of the node20-27mm
TIME	Time stamp	Data information update time

The Io T communication and application layer technology used in the BHLH transcription factor ABP7-Like-related automated experimental device refers to that communication technology can be divided into two categories according to the transmission medium: wired communication technology and wireless communication technology. With the widespread use of mobile communication equipment in recent years, wireless communication has become the fastest-growing and most widely used communication method. It uses electromagnetic wave signals to transmit information from one place to another in the atmospheric space, thereby achieving data. The main technologies of wireless transmission include radio communication, infrared communication, microwave communication and optical communication. A wireless communication network is a communication network composed of wireless communication devices connected to each other based on communication standards and protocols. In the network, the communication terminal communicates by accessing the network and relying on the network. According to the way of accessing the network, it can be divided into two types: self-organizing network and centralized network with a central control point.

4. Discussion

4.1. ABP7-Like Sequence Cloning and Molecular Characterization

Gene function often has an important relationship with its expression pattern, and gene expression is often specifically regulated by promoters. Therefore, in order to explore the expression pattern and find clues about its function, the promoter was cloned. With reference to the upstream sequence of the P7 start co don in the genome of maize B73 inbred line, primers ABP7-Like-OE and ABP7-like-RNAi were designed to clone the promoter of the P7 gene in the maize inbred line 319 genome and used for biological information Analysis and vector construction. Among them, ABP7-Like-OE is located about 200 downstream of the start co don to increase the specificity of the promoter clone. ABP7-like-RNAi is located about 1.6 Kb upstream of the starting ATG, and the expected size of the product is about 1.8 Kb. DNA fragments of corresponding size were recovered after PCR amplification and detected by electroplate, ligated with the EASY-Blunt cloning vector to form PEASY-Pabp7, transformed into E. Colic competent cells, and spread on LB medium containing cinnamon. Monoclonal clones were selected and identified, and the identified colonies were sent for sequencing. A 1885bp fragment was confirmed by analysis, of which 1,646bp was located upstream of the starting ATG. This segment was used as the promoter of QI19 and named Pabp7-1.6k. The genetic structure of ABP7-Like is shown in Table 2.

Table 2. Genetic structure and basic information for ABP7-Like

Code starting point	Cloning sequence	Number of exons	Number of endows
ATG	1761	10	9

The data in Table 2 compare the ABP7-Like sequence with the cloned gnomic sequence. It is found that ABP7-Like has 10 exons and 9 introns. The basic information is not much different from ABP7. It can be seen that it is indeed a homologous gene of ABP7. .

Later, the developmental expression profile analysis of ABP7-Like in QI 319 was studied. The

QPCR results showed that the expression of JSP7 in QI 319 was basically consistent with the B73 digital expression profile data obtained from the previous database, which was different at different stages in the corn development It was expressed in tissues, but in QI 319, J5P7 was expressed at the early stage of seed germination and seedling stage. Based on the analysis of the expression patterns of ABP7-Like in QI 319 and B73, it is speculated that ABP7-Like may have important relations with seed germination, seedling growth, and grain development. The experimental results are shown in Figure 1 below.

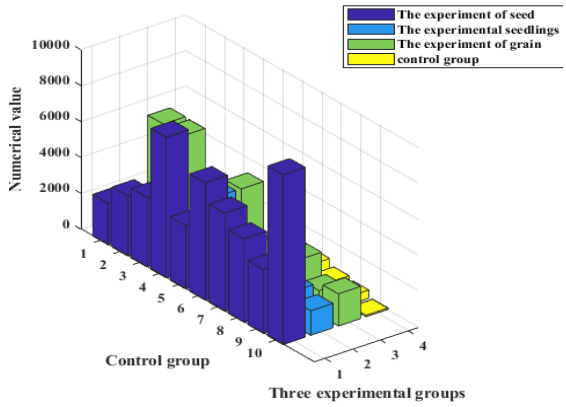

Figure 1. Expression of abp7-like during the development of QI 319

From the data in Figure 1, it can be seen that the expression of ABP7-Like is determined by the expression in corn seed coats. Furthermore, through experimental tests, it can be seen that ABP7-Like is closely related to seed germination, seedling growth, and grain development, which determines The seed germination rate, seedling growth, and grain development speed, etc., and the experimental group that specifically enhanced the ABP7-Like interference of corn, its seed germination rate was 15% higher than that of ordinary corn seeds.

In order to study the seed germination process that ABP7-Like actually participates in and why it promotes seedling growth, it is important to carry out the selection of ABP7-Like interaction proteins. Maize as a Eucharistic transcription initiation often requires multiple proteins to assist each other, Since ABP7-Like has activating activity and can grow on a defective medium containing 125mM3-AT, and all interactions Protein screening was performed on a defective medium containing 100 mm 3-AT. and a total of 175 positive colonies were screened. The experimental statistical results are shown in Figure 2.

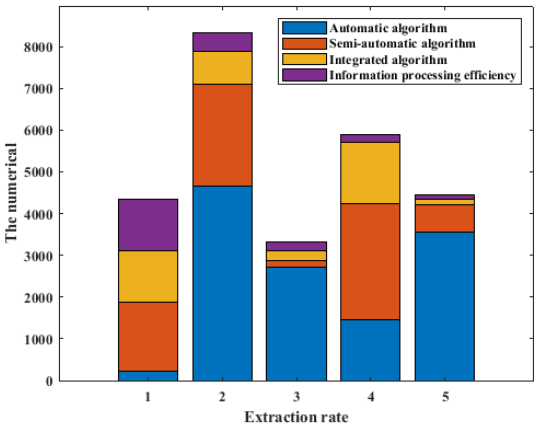

Figure 2. ABP7-Like protein performance analysis

From the data in Figure 2, it can be seen that there are many types of ABP7-Like-related interaction proteins, and the interaction proteins are related to embryonic development, oxidant phosphorylation of Mondrian, and interactions between nuclear and Mondrian. It participates in the process of osmotic adjustment in the later stage of seed maturation, which also explains why ABP7-Like is closely related to seed germination, seedling growth, and grain development. According to statistical analysis, there are about 758 types of ABP7-Like interaction proteins.

4.2. ABP7-Like Transgenic Materials and Plant Phenotype Analysis

The analysis of ABP7-Like transgenic materials and plant phenotype s is the focus of research. Previous laboratory results have shown that ABP7-Like can promote the development of transgenic Archbishops Italianate, can increase the size of fruit clips and grains, and through expression profiles The analysis found that ABP7-Like was expressed throughout the development process and was particularly highly expressed in the seed coat at the stage of grain development, a series of ABP7-Like plant expression vectors were constructed, and related transgenic materials were created in cooperation with DA BEI Agricultural Company. After multiple plantings and years of planting, the related phenotype was examined to clarify ABP7- Like's function in corn laid the foundation. The experimental results of the planted ABP7-Like-VP64 related data are shown in Table 3:

Table 3. List of overlapped genes between ABP7-Like-VP64 up-regulated and down-regulated

Gene	Annotation	OE	RNAI
Zm00001d009178	Expansin-B4	1.27709	-1.492756
Zm00001d017495	Protein	2.0955	-1.71562
Zm00001d023994	Expansin-B4	1.24684	-1.0187588
Zm00001d028348	Expansin-B4	1.30911	-1.8254988
Zm00001d035390	Protein	2.28062	-1.3109144

As can be seen from Table 3, the results of MA sequencing of ABP7-Like-VP64 leaves revealed that the number of leaves was 1,531, and the genes were deferentially expressed. Among them, 1,007 genes were up-regulated and 524 regulatory cells were expressed. In addition, 2297 genes were deferentially expressed in the RNA-Seq of ABP7-Like-SRDX leaves. The difference between the transgenic group and the control group was 877 genes up-regulated and 1420 genes down-regulated.

In addition, the expression of some PA7, OE and RNAI transgenic plants was identified during the planting process. The 3cm RNA from the tip of the eighth leaf of the 11th period was extracted and QPCR was found. In the PA7 transgenic event, ABP7-Like did not appear to be over expressed, and it is recognized that it can reduce the weight of grains. This proves that ABP7-Like is a transcontinental activator and plays a positive role in regulating grains. The experimental results are shown in Figure 3.

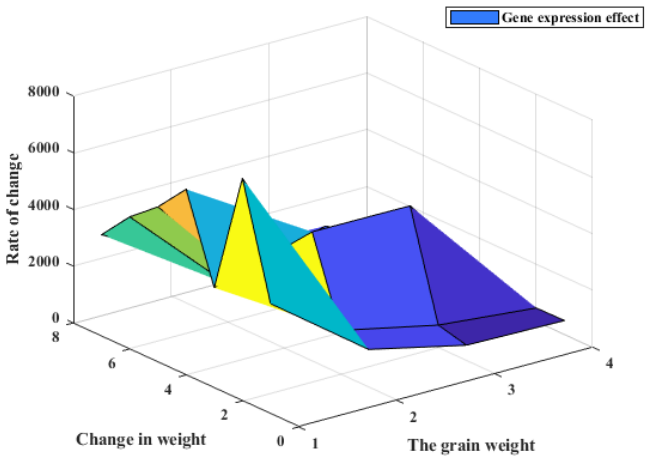

Figure 3. Regulation of corn kernels for ABP7-Like

From the data in Figure 3, it can be seen that ABP7-Like has a very important regulatory effect on corn kernels, which proves that ABP7-Like is a transplantation activator and that it plays a positive role in regulating grain regulation. In addition, compared with the experimental group, it can be seen that the weight of the genetically modified corn kernels is heavier than ordinary corn, about 15%. In addition, the yield of transgenic corn was much higher than the average corn yield of the experimental control group, and the yield increased by 25%.

Secondly, after analysis, it was found that the expression of several other transgenic lines J5P7 had reached the expectation except that the down-regulation of RNA i-c was not obvious. In PYE-DOG, J and P7 are 3.4 times the control, and in DE-ICE, J5P7 expression is about 42 times that of the control; in RNA i-PG, it is half of the control, but slightly higher than the control in RNA c. The expression of ABP7-Like in PG was 6 times that of IC in wild type, which also explained that the expression of PG in all over expressing lines was only a few times higher than that of the control, while the number was increased in IC Ten times because of the high background expression of ABP7-Like in PG. The effect of ABP7-Like on leaf traits is shown in Figure 4 after statistical analysis:

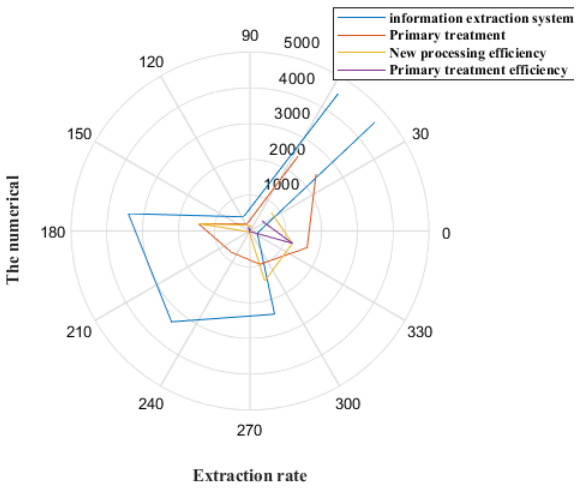

Figure 4. Phenotype analysis of transgenic materials of ABP7-Like

It can be seen from FIG. 4 that the three types of transgenic corn plants cultured according to

ABP7-Like have darker leaves and are less prone to senescence compared with non-transgenic corn plants, and the leaf characteristics of this plant are better. The total yield of the three transgenic corn plants cultivated by ABP7-Like was higher than that of ordinary corn, and the yield increased by 24.5%.

5. Conclusion

(1) This article analyzes the common problems existing in corn planting at present, discusses these problems without solving them, and proposes corresponding solutions. The development and impact of various technologies for increasing maize yield were briefly introduced, and the effect of BHLH transcription factor ABP7 on maize yield was studied. The gene comparison information of ABP7 and ABP7-Like was analyzed. The QPCR results showed that the expression of JSP7 in Qi 319 was basically consistent with the B73 digital expression profile data obtained in the previous database. It was expressed in different tissues at various stages during the development of corn, but in Qi 319 J5P7 was in the early stage of seed germination and Higher expression at seedling stage.

(2) The key part of the functional identification and molecular mechanism analysis of BHLH transcription factor ABP7-Like in maize leaf and grain development studied in this thesis is the analysis of ABP7-Like sequence cloning and molecular characteristics, and the corresponding influence mechanism and theory are proposed. Guidance confirmed the effect of ABP7-Like on maize leaf and grain development. Compared with non-transgenic corn plants, the three transgenic corn plants grown according to ABP7-Like have darker leaves and are less prone to senescence. This plant has better leaf characteristics, and the final experimental results show that the three transgenic corns grown according to ABP7-Like The total plant yield was higher than that of ordinary corn, and the yield increased by 24.5%.

(3) The core part of the functional identification and molecular mechanism analysis of bHLH transcription factor ABP7-Like in the development of maize leaves and grains was discussed and explained. ABP7-Like transgenic material and plant phenotypic analysis. It has been experimentally verified that the bHLH transcription factor ABP7-Like is a bHLH-like G-box binding transcription activator, which plays an important role in maize and embryo development. In addition, the leaf and embryo development of the three genetically modified corn crops constructed accordingly was significantly better than that of ordinary corn crops and the total yield increased by 25%.

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Data Availability

Data sharing is not applicable to this article as no new data were created or analysed in this study.

Conflict of Interest

The author states that this article has no conflict of interest.

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