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QTL Mapping of Key Agronomic Traits in Potato

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Abstract The potato is a globally important food crop, and its key agronomic traits, such as tuber shape, yield and stress resistance, have a significant impact on agricultural production and market value. Quantitative trait loci (QTL) analysis, as an important means to reveal the genetic mechanism of complex traits, provides theoretical support and technical guidance for the improvement of potato traits. This review systematically compiles the research progress on QTL mapping of key agronomic traits of potatoes in recent years, with a focus on summarizing the distribution and functional analysis of the main QTLS that control tuber shape, yield, and disease and stress resistance, and clarifying the key genetic loci and genes related to these traits. For instance, the Ro site on chromosome 10 is significantly correlated with the shape of the tuber, and multiple QTLS have been confirmed to make significant contributions to tuber yield and disease and stress resistance. Meanwhile, by integrating multi-omics methods such as genome-wide association studies (GWAS), transcriptomics, and epigenetics, the molecular mechanisms of trait regulation were further elaborated in depth. This review also explores the influence of gene-environment interactions on QTL expression, as well as the application prospects of marker-assisted selection (MAS) and gene editing techniques in potato breeding. By integrating genetic and environmental factors, it is expected that the development of superior potato varieties will be accelerated in the future, providing support for food security and sustainable agricultural development.

Keywords Potato; Quantitative trait locus (QTL); Genetic diversity; Marker-assisted selection (MAS); Breeding improvement

1 Introduction

Speaking of potatoes (*Solanum tuberosum* L.), this thing is actually quite interesting. You may not know that although it can now be grown all over the world, it was originally wild in the Andes Mountains of South America. In terms of output, it is indeed inferior to rice and wheat. However, it can adapt to various climates and grow from tropical to cold regions (Jaganathan et al., 2020). Although it ranks only fourth among food crops, in many places it is a life-saving staple food. Of course, there are exceptions. For instance, some particularly humid tropical regions are not very suitable for planting. As for economic value, it goes without saying. From Europe to Asia, countless farmers have relied on this to make a living. To be honest, when it comes to the ability to feed the population, potatoes are no worse than those major grains.

Those engaged in potato breeding all know that the yield is of course very important-after all, more and more people are eating nowadays. But to be honest, a high yield alone is not enough. Who would want the tubers that grow crooked? The size should be uniform, the shape should be good-looking, and the nutritional indicators such as starch content and vitamins should also meet the standards; otherwise, it simply won't sell in the market (Yamakawa et al., 2021). When it comes to disease resistance, it's even more of a headache, especially for late blight. A single outbreak can destroy an entire field. There is also the issue of drought. In recent years, the climate has become increasingly strange, with floods today and droughts tomorrow (Gebhardt, 2023). The most troublesome thing is that these characteristics are not determined by a single gene; they often involve the interaction of a large number of genes. So nowadays, those engaged in breeding are constantly struggling with these complex traits.

When it comes to QTL positioning, it's actually quite interesting. Nowadays, people conducting potato research are all using this technique. To put it simply, it is to compare the genes of well-growing and poorly growing potatoes (Ahmad et al., 2022). This job was not easy to do before. But since the advent of new tools like next-generation sequencing, the positioning accuracy has improved significantly. However, to be honest, even if the relevant gene regions are identified, it will still take a lot of effort to determine exactly which gene is at work. Important characteristics such as yield and disease resistance (Massa et al., 2015) are often the result of the combined action of multiple genes. The commonly used approach nowadays is to develop molecular markers, so that during breeding, it can be known in advance which seedlings may be more outstanding. Of course, in actual operation, various unexpected situations will still be encountered. After all, living beings are just too complex. But in any case, this technology has indeed saved a lot of time for breeding experts.

This research mainly focuses on several key indicators of potatoes-yield, quality, as well as disease and drought resistance. To be honest, these characteristics cannot be determined by just one or two genes. Therefore, we use QTL mapping to understand the genetic patterns behind them. Although the mechanism of action of some sites has not been fully understood yet, some important associated regions have indeed been identified. With these discoveries, we will be able to select materials more precisely when doing breeding in the future. Of course, practical application may still need to be combined with traditional breeding methods. After all, there will always be some unexpected situations in the field performance. Overall, however, these data should be helpful for cultivating more high-yielding and disease-resistant potato varieties, especially in the current situation where climate change is so frequent. Ultimately, the most important thing is to be able to truly apply the laboratory achievements to the fields and enable farmers to grow better potatoes.

2 Materials and Methods

2.1 Study materials: germplasm sources and target trait selection criteria

The materials used in this experiment are quite interesting. They were obtained by crossing the processing 12601ab1 and the fresh potato Stirling parents. To be honest, there are certain considerations when choosing these two parents. One is good at processing characteristics, and the other has good edible quality. The purpose is to see if the offspring can inherit both advantages. Finally, 227 different hybrid offspring were obtained, each of which looked quite different-some had particularly high yields, some had very regular tuber shapes, and some had particularly good disease resistance (Hurtado-Lopez et al., 2015). We focused on observing several practical traits: the yield level, whether the tubers were round or not, the dry matter content, and whether they could be harvested early. These indicators are very practical for both growers and processing plants. After all, who wouldn't want potatoes that are both high-yielding and good-looking? However, to be fair, the manifestations of these traits in hybrid offspring are truly diverse, and some combinations are completely unexpected.

2.2 Phenotypic measurement and evaluation methods for key traits

To ensure the reliability of the data, we have made a lot of efforts. These potatoes have been grown for a full three years and in different places-after all, the performance of the same variety can vary greatly in different environments. Each harvest is carried out according to a uniform standard. For instance, the yield is calculated by digging out and weighing each potato plant honestly. The shape of the tubers is rather interesting. It has to be examined one by one by hand, mainly to see if they are round and if the eyes of the sprouts are deep. Sometimes, there can be a long argument over a "standard appearance" potato (Yamakawa et al., 2021). The dry matter content is really high. Just slice the potatoes, dry them and weigh them. As for early maturity, we would walk around the fields every day to see when half of the plants had flowered. To be honest, this kind of field work is the most exhausting, but the data quality is indeed much more reliable than that of laboratory data alone.

2.3 Construction of genetic linkage maps and selection of marker types

When it comes to constructing the genetic map, we have put all the available marker techniques to use. At the very beginning, I used AFLP markers and spent a long time fiddling with 38 sets of primers. Later, six more SSR tags were added. Although these traditional techniques are time-consuming, the results are quite stable. However, the most powerful part was the SNP markers added later, which involved several thousand genome-wide loci at once (Hu et al., 2020), significantly improving the resolution of the map. The final map pieced together contains 514 valid markers, divided into 12 linkage groups-this number is quite interesting and exactly matches the chromosome number of potatoes. To be honest, the most annoying thing about making a graph is that some markers just won't obediently join the chain group no matter what, and you have to verify them repeatedly.

Fortunately, there is now high-throughput sequencing, which is much more convenient than using traditional methods in the past. However, the workload of data analysis has actually increased.

2.4 QTL mapping methods: multi-environment data analysis and statistical models

When doing QTL positioning, we tried several methods. The interval plotting method is a basic skill, but relying solely on it still feels insufficient. Therefore, single-label analysis was added for cross-validation. The most troublesome factor is the environmental one-the same genotype may show vastly different manifestations in different plots. Therefore, in our analysis, we pay special attention to those QTLS that can be detected in multiple environments. These sites are usually more reliable (Li et al., 2019). The composite interval mapping method (CIM) was used to eliminate background interference. Later, the multi-QTL mapping method (MQM) was also attempted to see if those sites with small effects could be identified. In addition to the conventional additive effect, we also focused on the dominant effect and the upper-level effect-sometimes when two sites without a significant effect come together, they can produce unexpected results. To be honest, each of these statistical methods is more challenging to use than the last, but to avoid missing any important loci, all the necessary analyses must be carried out.

2.5 Software and analytical tools: genome data processing and visualization platforms

When it comes to data analysis, we have really tinkered with software. TetraploidMap, a software specifically designed for tetraploids, is the main force. After all, ordinary diploid analysis tools would have problems when used to process potato data. Interval mapping mainly relies on QTL Cartographer. This veteran software is easy to use, but extra caution is needed when setting parameters. R/qtl is mainly used for drawing graphs for statistics, and the visualization effect is indeed good (Li et al., 2018a). Later, feeling it wasn't enough, I conducted a genome-wide association analysis using TASSEL and PLINK, hoping to find something new. To be honest, each of these software programs has its own advantages and disadvantages. We often have to verify the results with each other-sometimes the same data can be run with different software, and the results can vary quite a lot. The most troublesome thing is that when the software reports an error, just checking for bugs consumes a whole day. Fortunately, there are now many open-source tools available, so I can finally get a thorough understanding of the data.

3 Genetic Characteristics of Key Agronomic Traits in Potatoes

3.1 Genetic regulation and environmental adaptability of yield-related traits

When it comes to potato yields, it's actually quite complicated. Not only should the genes of the variety itself be considered, but also the influence of the planting environment. Some varieties perform well in the laboratory but wilt as soon as they are in the field-that's why we pay special attention to environmental adaptability. Studies like those in Ethiopia have found that although the yield of local varieties is not the highest, genetic variability is particularly rich (Tessema et al., 2022), which is a treasure for breeding. Interestingly, there is a QTL locus related to maturity on the V chromosome (Hermeziu et al., 2023), and this discovery has been of great help because early-maturing varieties can avoid many pests and diseases. This is more obvious in drought years, and certain chromosomal markers are closely related to drought resistance. However, to be honest, even if these markers are found, they still need to be tested repeatedly during actual breeding. After all, there is always some unclear relationship between genotype and phenotype.

3.2 Genetic mechanisms of quality traits

The quality of potatoes is no simple matter-especially the starch and dry matter content, which are the most valued indicators by processing plants. It is often found in the laboratory that the starch content of potatoes grown in the same plot of land can vary greatly. Through QTL localization, we did identify several key loci (Vanishree et al., 2021), some of which had a particularly significant impact. This was an unexpected gain. Interestingly, these quality traits are relatively less affected by the environment; it is mainly genes that play a role. It was recently discovered that the starch content varies with different cytoplasmic types (Alvarez-Morezuelas et al., 2023), which is quite surprising. To figure out the specific mechanism, we also investigated quite a few genes involved in sugar metabolism. Although the process was quite troublesome, at least now we know which markers to focus on for screening. However, to be fair, even if we know these genetic rules, it still takes a lot of effort to truly cultivate a perfect variety.

3.3 Genetic diversity of stress-resistance traits

When it comes to the stress resistance of potatoes, wild varieties are truly a treasure trove. During the years of conducting disease-resistant breeding, it was found that the resistance genes of cultivated varieties were extremely monotonous. On the contrary, those unremarkable wild potatoes (Li et al., 2018b) contained quite a few good things. For devastating diseases like late blight, many of the resistance markers we use now have been dug out from wild species (Afshari et al., 2017). However, wild materials also have their drawbacks. They often bring along some undesirable traits and have to be repeatedly returned for screening. The issue of drought has drawn increasing attention in the past two years. By comparing the performance of leaves when they are short of water, some interesting SNP markers were identified (Zhao, 2024). The most troublesome thing is the prevention and control of nematodes. These substances cause damage underground, and by the time they are discovered, it is often too late. Fortunately, with the advancement of genetic testing technology nowadays, the strength of the plant's resistance can be predicted without waiting for the plant to fall ill. Of course, for these discoveries to be truly applied in the fields, they still need to be verified over a long period of time-after all, the laboratory is the laboratory and the field is the field.

4 QTL Mapping Results

4.1 Identification and contribution analysis of QTLs related to yield traits

This QTL localization is quite interesting. The newly discovered site on chromosome III is particularly eye-catching-its impact on yield variation is much greater than expected. However, a more typical case is the situation on chromosomes I and IV (Figure 1), where each locus contributes a portion of the effect, with the least being just over 5% and the most reaching around 16%. This indicates that the yield of potatoes is not determined by just one or two genes; rather, it's more like a group of genes working in coordination. Interestingly, some of these sites control the number of tubers, while others control the weight of individual tubers. Only when combined do they determine the final yield. The laboratory data looks quite clear, but there are always some unexpected incidents in the fields-perhaps there are still some minor sites that we haven't detected. This also explains why high-yield breeding is so difficult, as so many genetic factors have to be gathered together.

4.2 Distribution and effect evaluation of key QTLs for quality traits

This analysis of QTL related to potato quality revealed that the key loci for starch content were mainly concentrated on chromosomes I, II and VIII. Interestingly, these loci are all stable in different planting environments (Hara-Skrzypiec et al., 2018), which is good news for breeding. The situation regarding dry matter content and specific gravity is rather complicated-although these two traits seem related, their QTL positions do not overlap at all, indicating that there are two different genetic mechanisms controlling them behind the scenes. The most surprising thing is the genetic pattern of the shape of the tubers. The loci on chromosomes III and X have a particularly significant impact on the appearance of the tubers. However, field observations have found that even if the genotypes are the same, the shape of the tubers is still affected by soil conditions, which indicates that phenotypic prediction cannot rely solely on genotypes. Overall, the genetic regulation of quality traits is more refined than imagined, and each indicator needs to be optimized separately.

4.3 Identification of major QTLs for stress-resistance traits and environment interaction analysis

Several findings in this QTL mapping of stress resistance traits are particularly notable. The precocious QTL on chromosome 5 is a "big guy"-it alone can explain 33.55% of the phenotypic variation (Manrique-Carpintero et al., 2018), which is rare among complex traits. However, the resistance to scab disease is relatively scattered. The contribution of loci on chromosomes I and IV is not significant, and it may be necessary for more potent loci to act together. The most troublesome issue is the interaction between genes and the environment: the same early-maturing genotype stands out in cool regions but becomes unremarkable in warm ones. Traits such as plant height and flowering period are even more dependent on the weather. Sometimes, the influence of the environment even exceeds that of genetic factors. These findings indicate that conducting stress-resistant breeding cannot merely focus on laboratory data; it is more reliable to carry out multi-frequency and multi-season field verifications.

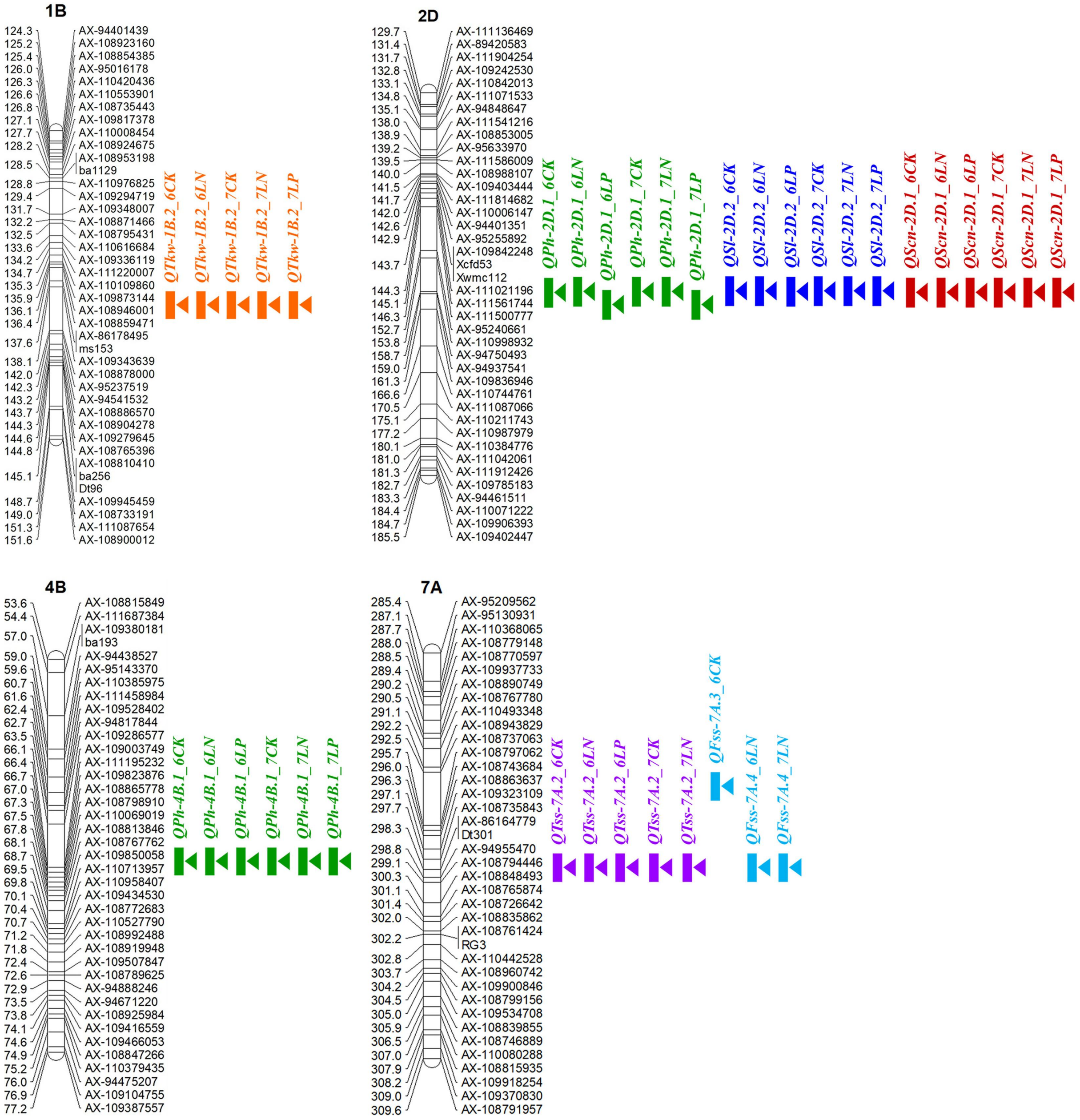

Figure 1 Location of four environmentally stable QTL in at least five environments (Adopted from Ma et al., 2023)

4.4 Hotspot identification of overlapping QTL regions for multiple traits

The most exciting aspect of this research is the discovery of several QTL" hotspots ". There is a magical region on chromosomes IV and VII that can simultaneously affect above-ground growth (such as emergence rate and stem quantity) and underground tuber yield. This pleiotropic gene is truly a treasure for breeders (Mei et al., 2021). On chromosome V, there is even more activity. The QTLS of two unrelated traits, maturity and starch content, are actually very close to each other on the genome-although fine localization reveals that they are actually at different sites. However, to be fair, although these hotspots are convenient, one still needs to be cautious when using them. Sometimes, when a superior site is chosen, it may accidentally bring in a chain of adverse traits. Our laboratory has encountered such a situation: we selected a high-yield site, but as a result, the plants became particularly late-maturing. Nowadays, when making marker-assisted choices, all these chain relationships must be taken into account to avoid neglecting one aspect for another.

5 Validation of Candidate QTLs and Gene Discovery

5.1 Validation of key QTLs across different environments and germplasm

Verifying QTL, in essence, means repeatedly testing in different places and among different varieties before it can be effective. We have suffered-some QTLS that performed well in the laboratory group failed to adapt to the field (Martinez et al., 2016). Sites like those that control flower color and leaf characteristics were found to have their effects discounted when verified in tetraploid materials when the environment changed. Now I've learned my lesson. During the verification, I deliberately chose different materials ranging from diploid to tetraploid. New technologies such as high-throughput sequencing and BSA have indeed been of great help, especially for difficult traits like precocious puberty, which can quickly identify candidate regions. However, the most practical approach still requires more experiments. For instance, the same early-maturing QTL might perform outstandingly under long-day conditions in the north but be rather unremarkable in the south. So now when making mark-assisted selections, it is necessary to first ask clearly: In which environments has this QTL been verified? Otherwise, the bred varieties are very likely to suffer from "water and soil incompatibility".

5.2 Screening and annotation analysis of candidate genes in QTL-associated regions

Identifying the candidate genes in the QTL region is like playing a detective game in the genome. We have tried various methods-the old technique of cDNA-AFLP can still bring surprises from time to time, especially when tracking transcripts that occur simultaneously with precocious traits. However, nowadays simplified genome sequencing combined with high-density mapping is more commonly used, which can narrow the QTL interval to a very small range (Yamakawa et al., 2021). The discovery of the PUB14 ubiquitin ligase gene that time was made possible by this combination of measures. The funniest thing is that sometimes the candidate genes are clearly within the interval and the functions are correct, but they are not responsible for the phenotype-at this time, new methods such as QTL-seq have to be relied on for re-verification (Saini et al., 2021). Nowadays, for precise positioning, it is often necessary to combine resequencing data and compress the interval to within tens of kilobytes before identifying candidate genes. However, to be honest, even if the gene is identified, to prove that it indeed controls the target trait, functional verification is still necessary. This entire process would take at least one or two years to complete.

5.3 Functional validation of key genes through transcriptomics and other analyses

To verify the functions of candidate genes, in essence, it is about catching the "suspected genes" red-handed. The most commonly used method in our laboratory is to compare extreme materials-for example, placing the earliest maturing and the latest maturing potatoes together for transcriptome analysis, and as a result, several key genes were really identified (Sonsungsan et al., 2024). The bch gene that controls the yellow color of potato flesh is particularly interesting. I never thought that carotene metabolism is so important in potatoes. Verifying the TLRP gene was even more challenging. Just building the BAC library took more than half a year. However, it was eventually confirmed that it does affect the quality of cooking, and all the efforts were not in vain. Nowadays, functional verification increasingly emphasizes the combination of multiple omics. For instance, recently, cross-analysis of transcriptome data and proteome data was conducted, and it was found that although the transcriptional level of some genes remains unchanged, there are significant differences in protein activity. Although these discoveries are time-consuming and labor-intensive, they can provide solid targets for molecular breeding and are still better than blind screening.

6 Applications of QTL Mapping in Potato Breeding

6.1 Development of molecular markers based on QTLs and marker-assisted selection (MAS)

QTL positioning technology has indeed brought new ideas to potato breeding. Now, variety improvement is much more precise than before. By analyzing those potato materials with high yield, disease resistance or outstanding quality, we found quite a few useful DNA markers (Kulkarni et al., 2020). Take the issue of nematode resistance as an example. The markers developed using the polyploid QTL-seq method have increased the efficiency of screening disease-resistant varieties several times over. There have also been breakthroughs in starch content and tuber quality-the QTL sites shown in Figure 2 have now all been transformed into practical molecular markers. However, in actual operation, it was found that tetraploid and hexaploid crops have different responses to the markers and should be treated differently. The most practical aspect is that these markers can be used for early screening. Without waiting until the harvest season, it is possible to predict which plants have greater potential at the seedling stage. Of course, mark-assisted selection is not a panacea. The field performance is ultimately determined, but at least it significantly narrates the screening range, saving time and effort.

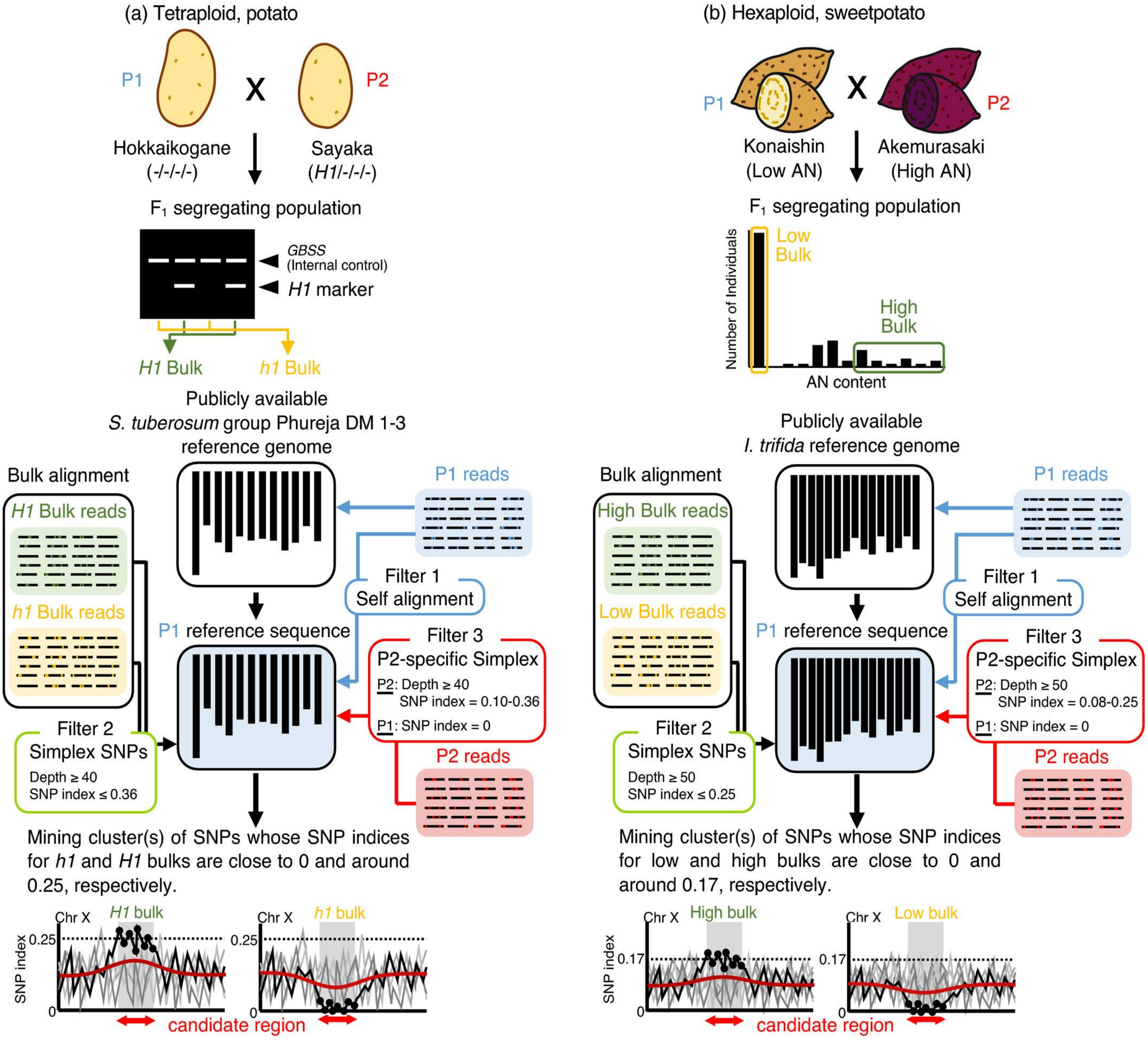

Figure 2 Schematic representation of the polyploid QTL-seq in potato (Adopted from Yamakawa et al., 2021)

6.2 Integration of QTLs with traditional breeding methods

Combining QTL positioning with traditional breeding is like giving veteran farmers a pair of high-tech glasses-it not only retains their accumulated experience but also adds a pair of "sharp eyes". Previously, to select early-maturing varieties, one had to wait until the end of the entire growing season. Now, by detecting those key loci (Korontzis et al., 2020), the seedling stage can be predicted with about 90% accuracy. The screening for late blight resistance is more obvious. Previously, it was necessary to build a dedicated disease garden to inocalize pathogenic bacteria. Now, with the help of consensus map data, the first round of screening can be completed in the laboratory. However, the veterans always remind us that no step of the trait observation that should be done in the field can be omitted, because some QTLS show unstable performance under different genetic backgrounds. The most successful case is the introduction of disease-resistant QTLS identified through meta-analysis into superior varieties, which not only retains the original high-yield characteristics but also enhances the resistance. This "walking on two legs" strategy is indeed much more reliable than choosing solely based on phenotypes.

6.3 Enhancing breeding efficiency using QTLs and gene-editing technologies

The combination of QTL mapping and CRISPR technology has simply equipped potato breeding with a "GPS navigation system "and a" molecular scalpknife "- first, the target gene region is locked by QTL mapping, and then precise editing is carried out by CRISPR (Kim et al., 2017). For instance, the QTL we discovered that controls starch synthesis requires seven or eight generations of breeding in traditional methods. Now, with CRISPR directly editing the key sites, it only takes two or three generations to see results. However, in actual operation, it was found that the editing efficiency of polyploids is much lower than that of diploids, and repeated attempts are often required. Now our team is even more aggressive. By integrating the Bayesian statistical method and conducting hybrid model analysis, we can reduce the QTL interval to a smaller size, thereby enhancing the targeting of CRISPR. Recently, I have been attempting to simultaneously edit multiple QTL loci for both yield and disease resistance. Although it is highly challenging, if successful, the breeding cycle of the variety can be shortened by more than half. Of course, field verification is still indispensable. After all, the final editing effect depends on the performance in the field.

7 Research Challenges and Directions

7.1 Technical bottlenecks in current potato QTL research

Conducting QTL research on potatoes is like playing a high-difficulty jigsaw puzzle-the tetraploid genome makes each genetic locus have four sets of alleles, and the effects produced by their combination are so complex that they are a headache. The most typical example is that the same QTL may exhibit completely different effects in different genetic contexts, and even the direction of action can be reversed (Tiwari et al., 2017). Environmental factors have made things even more complicated. The drought-resistant QTLS detected under drought conditions last year may disappear this year if the rainfall is normal. So we had to set up more than ten test sites across the country and continuously track the data for three years (Yang et al., 2019) in order to distinguish which QTLS were "fixed" and which were "changing". Sometimes, a site that is clearly located in the laboratory becomes "invisible" in the field. This kind of interaction between genes and the environment is the most maddening. However, it is precisely these challenges that make potato genetics research so fascinating-after all, the more complex the problem, the more fulfilling it is to solve it.

7.2 Future prospects of high-throughput omics technologies

It's really a great time to conduct research on potato QTL now. GWAS technology is like assembling a scanner for genes (Deng and Chen, 2024). There is no need to pre-set candidate regions. A scan across the entire genome can identify associated loci. However, the most impressive is the multi-omics collaboration-genomic data sets the stage, transcriptome and proteome data perform the show, and recently even metabolome data has been added (Ma et al., 2023). Our laboratory has recently discovered that there is a QTL site that controls flavor. It is not obvious on the genome, but metabolome data show that it significantly affects the accumulation of glycoside alkaloids. This multi-dimensional verification has made QTL localization increasingly precise, and now it can even distinguish similar loci on homologous chromosomes. Of course, when the volume of data is large, it can be a headache. Just processing these omics data requires several servers. But seeing the positioning accuracy shrink from a few megabytes of bases to just a few hundred kb, the targeting of breeding has indeed improved by more than one level.

7.3 The necessity of global collaboration and germplasm resource sharing

When it comes to potato research, one cannot go it alone. Germplasm banks around the world are like a "treasure chest" (Manrique-Carpintero et al., 2015), especially those local varieties in the remote Andes mountains, which contain many precious genes for disease and drought resistance. Remember that there was a key gene for resisting late blight, which was initially discovered in a local variety in Peru. Now, the collaborative network led by the International Potato Center is doing quite well. Everyone regularly exchanges materials and data and unifies experimental standards-otherwise, the QTLS measured by you might not match mine at all. Recently, a shared database has also been established, where even data on heat-resistant varieties developed by small-scale farmers in Africa can be accessed. The benefits of this open cooperation are obvious: the early-maturing genes from Northern Europe can help improve varieties in South Asia, and disease-resistant materials from the Americas can also be put to use in Asia. Ultimately, to address the challenges brought about by climate change, it requires the joint efforts of scientists around the world.

8 Concluding Remarks

Research on QTL in potatoes has indeed yielded considerable results over the years. Just in the tetraploid population, 39 key loci have been identified-ranging from the appearance of the tubers to their cooking characteristics, and even when they germinate (with high heritability reaching 92% and low at 54%). Interestingly, the QTLS that control flower color always cluster on chromosomes II, III, and V, often adjacent to the sites of leaf maturity. The most powerful one is the "early maturity switch" on chromosome 5 (contributing 33.55%), which is simply a magic tool for shortening the breeding cycle. However, these findings also expose the complexity of potato genetics: the same trait may be regulated by more than a dozen minor QTLS, and some loci are even linked to undesirable traits. Nowadays, making marker-assisted selection is like defusing a bomb; one has to be extremely careful to retain only the favorable alleles. Fortunately, with the improvement of positioning accuracy, these problems are being solved one by one, providing the possibility for cultivating "all-round" varieties.

Potato breeding is becoming increasingly sophisticated nowadays. Those QTL loci that control important agronomic traits are like providing breeders with a "genetic manual". For instance, the traits of early maturity and high starch content were originally thought to restrict each other, but it was found that their QTLS were not in the same position at all-this opened the door to breeding new varieties of "early maturity and high starch". New technologies such as polyploid QTL-seq add the finishing touch. The molecular markers developed have increased the selection efficiency several times over. Now, without waiting for the harvest, it is possible to predict at the seedling stage which plants have the potential for high yield, disease resistance and excellent quality. To be honest, the most practical aspect of these technologies lies in their ability to avoid "chain burdens"-in the past, when selecting disease-resistant varieties, low-yield genes were often accidentally introduced. Now, through precise positioning, only the necessary gene fragments can be retained. Of course, for laboratory achievements to truly benefit farmers, they still need to be verified in the fields. However, it is undeniable that these QTL markers are transforming potato breeding from "empiricism" to "precise design", providing new tools for addressing the challenges of climate change and food security.

The next step in potato QTL research is to explore the "deep water zone". The 471kb target area of the early maturity is like a treasure chest. There must be more delicate regulatory elements that haven't been discovered inside-perhaps some non-coding area is the real "switch". Nowadays, merely looking at the genome is no longer sufficient for research. It is necessary to string together transcriptome data and field phenotypes for analysis, just like piecing together a three-dimensional jigsaw puzzle. CRISPR technology is particularly useful here. It can directly "perform surgery" on candidate genes to verify their functions, which is much faster than the past backcrossover verification. However, the most crucial point is still to expand the scope of verification. The same QTL may perform exceptionally well in local Andean species but cease to exist in modern cultivated species. So we plan to set up experimental sites in different ecological zones of the northern and southern hemispheres, and even include wild relatives in the research. After all, climate change is so drastic that the drought-resistant QTL discovered today might become a lifeline in a few years. Although these tasks are time-consuming and labor-intensive, they enable breeders to obtain truly "resistant" molecular markers.

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Conflict of Interest Disclosure

The author affirms that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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