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A High-Density SSR Genetic Linkage Map and QTL for Sweetpotato Storage-root Yield and Dry Matter Content were Constructed

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Abstract

Ipomoea batatas (L) Lam.'s sweet potato is a common food crop, particularly in developing nations. The crop's primary breeding objective has been to increase dry matter content and storage root yield, which necessitates DNA marker-assisted breeding. Using 601 simple-sequence repeat (SSR) primer pairs, we constructed a high-density genetic linkage map of sweet potato using a mapping population of 500 F1 individuals from a cross between Xushu 18 (female) and Xu 781 (male). The Xushu 18 map had 90 linkage groups with 5547 SSR markers and covered 18,263.5 cM, while the Xu 781 map had 90 linkage groups with 4599 SSR markers and covered 18,043.7 cM. These maps have the highest genome coverage of any sweet potato genome that has been reported so far. Storage-root yield was explained by 33 QTL, while dry matter content was explained by 16 QTL, accounting for 6.5%–47.5% of variation. The foundation for marker-assisted breeding and the fine mapping and cloning of QTL in sweet potatoes is provided by these findings.

Keywords: Sweetpotato; Map of SSR linkages; QTL; Root yield from storage; Dry-matter substance

Introduction

Sweetpotato, Ipomoea batatas (L) Lam., is a food crop particularly significant in emerging nations. It is an allohexaploid that is frequently self-incompatible and highly heterozygous, making it difficult to improve genetically. Quality, disease resistance, and storage-root yield are examples of quantitatively inherited characteristics of sweet potatoes [1]. In order to simultaneously improve these traits, marker-assisted breeding is required because they typically have a negative correlation.

A high-thickness hereditary linkage map is fundamental for quantitative characteristic locus (QTL) planning and marker-helped choice. The whole-genome assembly of Sweet potato is still in its infancy, and the linkage map construction is somewhat sluggish [2]. Several sweet potato linkage maps based on random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), sequence-related amplified polymorphism (SRAP), retrotransposon-based insertion polymorphism (RBIP), simple sequence repeat (SSR), and single-nucleotide polymorphism (SNP) markers have been constructed using F1 populations and a two-way pseudo-testcross mapping strategy. Due to their widespread inclusion in plant genomes, SSR markers have been shown to be useful tools for marker-assisted breeding in crop species like rice wheat and maize. High-thickness SSR hereditary linkage maps are as yet ailing in yams, restricting the utilization of marker-helped reproducing for its improvement.

The goal of QTL mapping is to locate genes or loci that control agricultural traits. In marker-assisted breeding, DNA markers that are tightly linked to QTL can be developed and used [4]. A few QTL planning examinations of agronomic characteristics have been acted in yams. In the guide of Zhengshu 20, distinguished one QTL related with starch content. Utilizing a populace comprising of 240 F1 people from the cross Tanzania × Beauregard, recognized eight QTLs for β-carotene content, 12 for starch content, and 13 for dry-matter substance. Using 202 F1 individuals of Xushu 18 Xu 781, linkage maps primarily based on AFLP markers identified 27 QTL for dry matter content, eight QTL for starch content, and nine QTL for storage-root yield. Using 300 F1 individuals of Jizishu Longshu , seven QTL were identified for root rot resistance. utilizing a high-density linkage map, identified one significant QTL for root-knot nematode resistance in the Tanzania Beauregard F1 offspring.

The targets of the current review were to build a high-thickness SSR-based hereditary linkage guide of yam and to recognize QTL for capacity root yield and dry-matter substance utilizing a planning populace containing 500 F1 people got from the cross Xushu 18 × Xu 781 [4].

Materials and Techniques

Plant materials: A planning populace involving 500 F1 people was created by crossing the business yam cultivar Xushu 18 (as female) with the first class line Xu 781 (as male). A cultivar with a medium dry matter content and high storage root yield, Xushu 18 is widely grown in China. Xu 781 is typically used as a breeding parent due to its low yield of storage roots and high dry matter content. For five years, these two parents and F1 individuals were planted at the Tianji Fenghua Yulong Agricultural Development Co., Ltd. experimental station in Baodi, Tianjin, China. A randomized complete block design with three replications was used in the field trial. In each plot, 20 plants were planted in two rows separated by 25 cm and 80 cm, respectively. After approximately 120 days of growth, the experiments were harvested under standard field conditions.

DNA extraction: Using the cetyltrimethylammonium bromide method, genomic DNA was extracted from the young leaves of two parents and the F1 individuals [5]. The DNA concentration was

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measured with an ultraviolet spectrophotometer, and the gel's quality was evaluated by electrophoresis on a 1% (w/v) agarose gel.

Genotyping and marker scoring: A bunch of 601 SSR preliminary matches including 273 genomic SSRs (gSSRs), 298 BAC-end succession SSRs (bSSRs), and 30 EST-based SSRs (eSSRs), all recently evolved, were utilized to enhance the guardians and F1 people. The following were the conditions for cycling: 95 °C for five minutes, followed by 35 cycles at 95 °C for one minute, 55–59 °C for thirty seconds, and 72 °C for one minute, with a final extension at 72 °C for ten minutes. A 6% vertical denaturing polyacrylamide gel and silver staining were utilized to score SSR markers.

Markers were scored 1 or 0 based on their presence or absence in the F1 individuals, with ambiguous or missing bands recorded as 2. Markers are polymorphic between the parents. Using a GeneRuler 100-bp DNA Ladder marker, the DNA fragments were sized [6]. The following three groups of polymorphic markers were identified based on their presence in both parents: Only Xushu 18 has maternal markers, only Xu 781 has paternal markers, and both parents have double-simplex markers. In light of the isolation proportions tried with the chi-square test, markers were partitioned into four gatherings: simplex markers in the offspring), triplex markers (present in one parent in three copies with a hexasomic (19:1), tetrasomic (11:1), or disomic (7:1), and double-simplex markers (present in both parents in a single copy with a 3:1 ratio, denoted by s, d, t, and ds, respectively), which are present in one parent in two copies with a hexas Contorted markers were set apart with postfixes, meaning tremendous changes at the 0.05 and 0.01 likelihood levels, separately.

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Result and Discussion

Outcomes marker data: Out of the 601 SSR primer pairs, 509 produced a mean of 5.55 polymorphic bands consisting of 2826 polymorphic bands. At long last, 1967 SSR markers were utilized for building the Xushu 18 guide: The Xu 781 map was constructed using 2116 SSR markers, 507 simplex markers, 187 duplex markers, 23 triplex markers, 1250 double-simplex markers, and 22 triplex, 1250 double-simplex, 670 simplex, and 174 duplex markers. the proportions of simplex markers in each case. These SSR markers could be used to create a genetic linkage map of the allohexaploid sweet potato because they were consistent with the values expected for an allohexaploid (75% simplex and 25% non-simplex).

Construction of genetic linkage maps: Utilizing the simplex and double-simplex markers, a framework map of each parent was constructed using JoinMap [10]. The final 90 genetic linkage maps for each parent were then created by inserting duplex and triplex markers into the framework map. On the Xushu 18 map, 90 linkage groups identified a total of 5547 SSR markers, including 238 simplexes, 4686 duplexes, 159 triplexes, and 464 double-simplexes. For Xushu 18, there were 1761 (31.7 percent) distorted markers at the 0.05 probability level. The total length of the map was determined to be 18,263.5 cm, and the marker density was 3.3 cm. The length of the linkage group ranged from 88.5 to 268.6 cm, with a mean length of 202.9 cm. There were 9–110 mapped markers in the linkage groups, with a mean of 62.

There were 4599 SSR markers on the Xu 781 map, divided into 90 linkage groups. There were 225 simplexes, 3645 duplexes, 385 triplexes, and 344 double-simplexes. At the 0.05 probability level, segregation distortion was observed in 1391 (30.2%) markers in Xu 781 [11]. The length of the entire map was 18,043.7 cm, and the marker density was 3.9 cm. The average length of the linkage group was 200.5 cm, and it ranged from 87.8 to 301.3 cm. There were 6–131 mapped markers in linkage groups, with a mean of 51.

Homologous linkage groups: Duplex and triplex markers were used to identify each parental map's. In the Xushu 18 and Xu 781 maps, 15 homologous groups were established, which corresponded to the number of allohexaploid sweet potato chromosomes. The links between the 50 linkage groups on the Xu 781 map and the 52 linkage groups on the Xushu 18 map were assigned using the 214 double-simplex markers.

The 500 F1 individuals' storage-root yield and dry-matter content: varied over the course of the five years. The average storage-root yield for F1 individuals was 2.27, while the average storage-root yield for Xushu 18 and Xu 781 was 3.35 and 1.05 kg, respectively [12]. The average dry-matter content of F1 individuals was 30.99%, while the average dry-matter content of Xushu 18 and Xu 781 was 27.32 percent and 33.63 percent, respectively. Xushu 18 had a significantly lower dry matter content than Xu 781, despite having a significantly higher storage root yield than Xu 781. Capacity root yield and dry-matter

substance followed a typical conveyance in the F1 populace. A few people showed offensive isolation for the qualities, recommending that these two characteristics were constrained by various loci [13]. Storage-root yields in various years were highly correlated, and dry matter contents were also correlated across years. These correlations gradually decreased as the number of years increased.

QTLs analysis

Over the course of the five years, 33 QTLs for storage-root yield were identified. From qYIEF_1 to qYIEF_17, the 17 QTL were located on 16 linkage groups of Xushu 18. All of them had a positive effect, accounting for between 6.5 and 31.1 percent of the variation in storage-root yield [14]. From qYIEM_1 to qYIEM_16, 16 QTL that explained 11.2%–47.5% of the variation in storage-root yield were mapped on 13 linkage groups for Xu 781. qYIEM_2 and qYIEM_15, which were co-located to gSSR0720-2d and gSSR0066-4d respectively and mapped on XU781(02.09) and XU781(14.82), had negative effects on storage-root yield out of the 16 QTL. The fact that Xu 781 has a lower storage-root yield than Xushu 18 is consistent with these findings. qYIEM_3 made sense of the greatest phenotypic variety, representing 47.5% of the variety away root yield.

In just five years, sixteen QTL for dry matter content were found, and eight of them were found on eight linkage groups of Xushu 18, accounting for between 4.2% and 18.9% of the variation. Xu 781's eight linkage groups were mapped to eight additional dry-matter content QTL, accounting for 3.2%–17% of the variation. Fifteen of the 16 QTL applied a constructive outcome on dry-matter substance, with just qDMM_1 showing an adverse consequence [15]. The potential for fine mapping and cloning exists for a number of significant QTLs for storage-root yield and dry matter content that were discovered in Xushu 18 and Xu 781.

Conclusion

In this review, qBN-1, a significant QTL controlling BN on soybean chromosome 6, was fine-planned to 115.67-kb in the RIL populace and affirmed in the backcrossing populace of KF19BC3F2 and KN24BC2F2. During this time, two possible candidate genes were examined. Expression analysis indicated that Glyma06G208900 might be the candidate gene in the qBN-1 region. The discoveries of this study clarify the possibility to execute qBN-1 into other soybean reproducing lines utilizing marker-helped choice. In addition, our findings provide useful information for the upcoming identification of the qBN-1 candidate gene for BN.

Acknowledgement

None

Conflict of Interest

None

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