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Sweetpotato Research Front

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Contents

Do names and natures often agree?

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When parents name their child, they must consider it very carefully. It is their first, and quite important, gift to their baby. Parents wish their child such things as good fortune, happiness, health, wealth, and so on.

As breeders, we give names to new sweetpotato cultivars with feelings like those of parents. For example, 'Fukumurasaki' (fuku+murasaki) —introduced in this paper— means 'Happy-Purple'. We hope that its sweetness makes people who eat it feel happy. In the case of 'Koganesengan', it is the most-produced cultivar in Japan and is mainly used for spirits (imo-shochu). 'Kogane' means 'gold' in English, and its name refers to both its creamy-white skin color and its value. 'Sengan' means a very high yield; however, the word literally means the weight of 'one thousand kan'. 'Kan' is an old unit of weight in Japan; 1 kan was set at 3.75 kg.

When we release a new cultivar, we know its characteristics in detail because we have been cultivating it over 10 years. Thus, we try to give the cultivar a name that can express its characteristics simply and precisely. For example, 'Tamaakane' (tama+akane) means ball+madder-red. Its name is derived from its round shape and orange-colored skin and flesh. 'Quick Sweet' can be cooked more quickly than ordinary cultivars because the gelatinization temperature of its starch is about 20°C lower than that of other sweetpotato cultivars. Even if cooked in a microwave, it will become sufficiently sweet.

However, there are many cultivars named based on our impressions of them and not based on their specific characteristics. We often add the words 'otome' and 'komachi' to the names of cultivars for table use; the words mean 'young lady' and 'beautiful lady', respectively. We expect the names 'Beniotome' or 'Benikomachi' to imply their beautiful appearances and good tastes. In addition, 'Beni' means red skin color.

'Beniharuka' is also named from our impression; 'haruka' means 'by far' or 'much'. We tried to signify that this cultivar is 'much better than previous cultivars in various characteristics'.

'Kokei No. 14', which is a leading cultivar for table use in Japan, has many other names. It was named differently in each production area because farmers try to appeal to consumers by including their area's name. It is called 'Miyazakibeni' in Miyazaki prefecture, 'Benisatsuma' in Kagoshima prefecture (formerly 'Satsuma Domain'), and 'Narutokintoki' in Tokushima prefecture. 'Naruto' is a production area of Tokushima, and 'kintoki' means an excellent sweet potato with red skin and yellow flesh. Consumers expect good quality from their names; therefore, these areas are known as good production areas for sweetpotatoes.

'Beniharuka' also has many other names because it is widespread in Japan like 'Kokei No. 14'. For example, it is named 'Benitenshi', 'Beniyuka', 'Imosienne', among others. Furthermore, some local names of 'Beniharuka' guarantee a certain quality of the product. For instance, 'Kanta-kun' is used at the production area in Oita prefecture. 'Kanta' means 'sweet and fat', and 'kun' is a kind of honorific for boys. 'Kanta-kun' must be sold only after 40 days of storage to sufficiently increase its sugar content.

Producing good quality 'Beniharuka' in various places in Japan is a great pleasure for consumers and breeders alike. However, we cannot help but feel dissatisfied when our cultivars are only called by other names. We hope our precious cultivar names are shown along with local names as much as possible.

Fukumurasaki: A New Sweetpotato Cultivar with Purple Flesh for Table Use

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Introduction

Fukumurasaki, developed by the Kyushu Okinawa Agricultural Research Center, is a new sweetpotato cultivar with purple flesh. The texture of its baked root is slightly wet with a good taste (Fig. 1).

Fig. 1 Baked root of Fukumurasaki

Origin

Fukumurasaki is the progeny of the maternal parent Kyukei 255 and the paternal parent Purple Sweet Lord, and this cross was carried out in 2005. Purple Sweet Lord is the most widespread purple-fleshed sweetpotato for table use in Japan, and Kyukei 255 has a particularly sweet taste. A total of 35 seeds were obtained from the crossing. Fukumurasaki was selected based on evaluation of its field performance, taste, and appearance. These good characteristics may have been inherited from its parents, both of which have been selected for table use.

Characteristics

Fukumurasaki has intermediate sprouting ability and is a semi-upright plant type. The stem diameter is relatively large with a short internode length. The anthocyanin coloration of the internode and node is weak. Young, dark green leaves mature into green five-lobed leaves. The storage root shape is ovate. Its skin is purple-red, and its flesh is purple. The texture of the steamed root is intermediate.

Fig. 2 Storage root of Fukumurasaki

Performance

Compared to Kokei No. 14 and Purple Sweet Lord, Fukumurasaki shows lower root yield and smaller root size. The root contains more dry matter and attains much higher brix when steamed (Table 1). Its resistance to root-knot nematodes is intermediate, whereas it is slightly resistant to root-lesion nematodes.

Table 1. Yield and other traits of Fukumurasaki in yield trial (2009–2011 and 2013–2017, standard cultivation)

Traits	Fukumurasaki	Kokei No. 14	Purple Sweet Lord
Root yield (t/ha)	20.1	24.9	29.8
Root size (g)	127	192	194
Number of roots per hill	4.2	3.5	4.2
Dry-matter content (%)	37.2	31.6	34.3
Brix (%)[1)]	24.8	16.6	13.4
Root-knot nematode resistance	Intermediate	Slightly Susceptible	Slightly Resistant
Root-lesion nematode resistance	Slightly Resistant	Intermediate	Slightly Resistant
Storability	Intermediate	Intermediate	Slightly High

1) Four times the value measured of exudates from steamed root mashed with three volumes of water.

Research Paper

Development of PCR-Based DNA Markers Associated with Resistance to Southern Root-Knot Nematode in Sweetpotato

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The southern root-knot nematode (SRKN) *Meloidogyne incognita* is an intractable pest and causes severe damage to sweetpotato, affecting yield and quality. Sano et al. (2005) detected nine SRKN races (SP1 to SP9), and Tabuchi et al. (2017) revealed that SP6 included at least two races, SP6-1 and SP6-2. Of these 10 races, SP1, SP2, SP4, and SP6-1 are the major ones in Japan. Because the use of resistant sweetpotato cultivars is a low-cost and effective method of controlling SRKN damage, DNA markers associated with this trait are in demand. However, genetic analysis, which is essential for developing DNA markers, is difficult in sweetpotato because of its complex genome structure, i.e., hexaploid, outcrossing, highly heterozygous, and large genome (~3 Gb). Recently, next-generation sequencing (NGS) systems have become proficient at dealing with enormous amounts of DNA-polymorphism data and carrying out genetic analyses. We constructed a high-density linkage map based on retrotransposon insertion polymorphism (RIP), simple sequence repeat (SSR), and single nucleotide polymorphism (SNP) markers generated by NGS and 113 F_1 plant progeny of J-Red and Choshu (Sasai et al. 2019). J-Red and Choshu are resistant and susceptible to the major SRKN races, respectively, and the resistance of 107 F_1 plants was tested. We carried out quantitative trait locus (QTL) analysis and a genome-wide association study (GWAS) and detected highly effective QTLs for resistance to SRKN races SP1, SP4, and SP6-1. We developed a PCR-based DNA marker that can identify SNP genotypes in this QTL region. This DNA marker could discriminate between resistance and susceptibility to SRKN races SP1, SP4, and SP6-1 of F_1 plants at a rate of 70% (Fig. 1 shows part of these results). We are also developing PCR-based DNA markers to discriminate between resistance and susceptibility to SRKN races SP2, SP3, and SP6-2. These markers could be helpful for marker-assisted selection of SRKN resistance.

References

1) Sano et al., Jpn. J. Nematol. 35, 1-12 (2005).
2) Tabuchi et al., Nematol. Res. 47, 29-33 (2017).
3) Sasai et al., DNA Res. 26(5), 399-409 (2019)

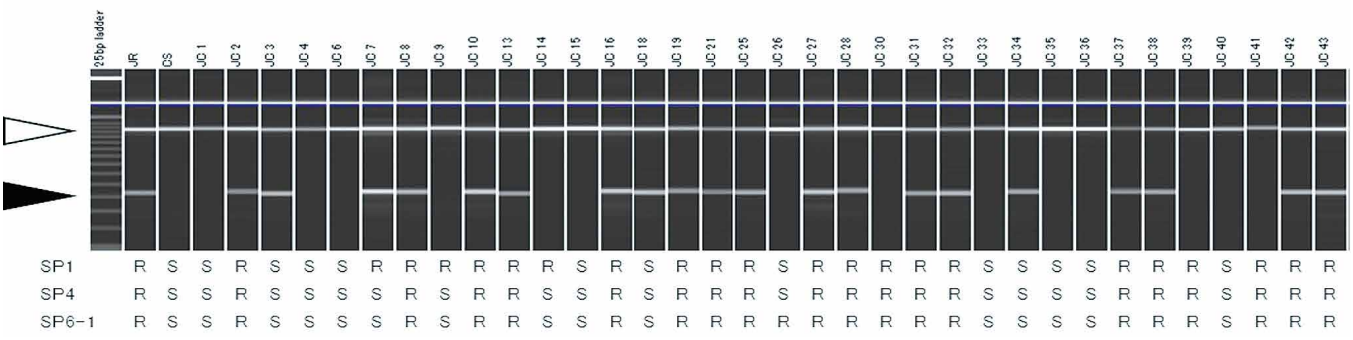

Fig. 1 Identification of SNP genotypes in the QTL region for resistance to SRKN races SP1, SP4, and SP6-1 by a DNA marker and resistance/susceptibility to these SRKN races in F_1 (JC#) progeny of J-Red (JR) and Choshu (CS). ▲, PCR fragments of the DNA marker associated with SRKN resistance (206 bp). △, fragments confirming successful PCR amplification (418 bp). R, resistance. S, susceptibility

Genetic Analysis of Agronomic Traits in Sweetpotato using Genome-Wide SNP

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Introduction

Recent studies on the draft genome sequence of diploid *Ipomoea trifida* (Hirakawa et al. 2015) followed by a high-density single-nucleotide polymorphism (SNP) genetic map in hexaploid sweetpotato (*I. batatas* L.) covering the whole genome (2n=6x=90) (Shirasawa et al. 2017) has ushered in a new era in the genetic study of the world's 7th most important food crop. We performed QTL analysis and GWAS of storage root β-carotene content (BC), dry matter (DM), and starch content (SC) with genome-wide 5,991 and 6,450 SNPs obtained from the F_1 progeny of the 'J-Red' and 'Choshu' cultivars, respectively (Haque et al. 2020).

Materials and Methods

'J-Red' and 'Choshu' and their 52 F_1 progeny (JCF_1) were grown in plastic pot in a greenhouse. DM and SC were measured as percentages. Relative BC was analyzed as absorbance at 455 nm (A_{455}). QTL analysis and GWAS were done according to Haque et al. (2020).

Results and Discussion

The DM and SC contents of the JCF_1 progeny were distributed normally, whereas BC was highly biased (Fig. 1). BC was negatively correlated with DM (r = -0.45) and SC (r = -0.51), whereas DM was positively correlated with SC (r = 0.94). In both parental maps, a total of five, two, and five QTL regions on linkage groups (LGs) 7 and 8 were associated with BC, DM, and SC, respectively (Table 1). In GWAS of BC, one strong signal ($P = 1.04\times10^{-9}$) was observed on LG 8, which co-located with one of the above QTL regions. In comparison to field experiment, BC showed a strong correlation (r = 0.96), whereas moderate correlations were found for DM (r = 0.68) and SC (r = 0.66), suggesting the necessity of genetic analysis for DM and SC under field conditions. These SNP markers, particularly for β-carotene, would be useful base resources for marker-assisted selection programs.

References

1) Haque et al. (2020) Breed. Sci. 70: 283–291
2) Hirakawa et al. (2015) DNA Res. 22: 171–179
3) Shirasawa et al. (2017) Sci. Rep. 7: 44207

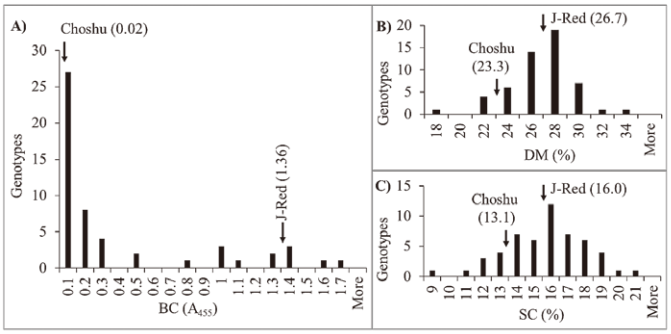

Fig. 1. Histograms of BC (A), DM (B), and SC (C).

Table 1. QTLs controlling BC, DM, and SC in JCF1 progeny

Traits and maps	Locus			ANOVA	Interval-Mapping		*P*-value of GWAS
	LG	Marker name	Position		LOD	PVE	
BC_J-Red	Ib07_4	Itr_sc001596_10966	67.75	** ($P < 0.05$)	4.69	68.0	1.06×10^{-3}
	Ib08_4	Itr_sc000066_68839	164.21	*** ($P < 0.001$)	7.74	49.6	1.04×10^{-9}
	Ib08_6	Itr_sc000227_94993	65.68	*** ($P < 0.001$)	3.24	29.3	3.09×10^{-4}
BC_Choshu	Ib08_3	Itr_sc000227_94989	565.29	*** ($P < 0.001$)	3.83	28.7	3.09×10^{-4}
		Itr_sc000066_1754	620.05	** ($P < 0.05$)	3.21	24.8	6.04×10^{-5}
DM_J-Red	Ib07_4	Itr_sc000546_59175	77.20	*** ($P < 0.001$)	3.04	25.2	3.45×10^{-4}
	Ib08_4	Itr_sc000057_157946	57.15	*** ($P < 0.001$)	3.31	50.9	0.0045
SC_J-Red	Ib07_4	Itr_sc000546_59175	77.20	*** ($P < 0.001$)	2.93	25.5	4.74×10^{-4}
	Ib08_4	Itr_sc000057_157946	57.15	*** ($P < 0.001$)	3.31	50.9	7.67×10^{-4}
SC_Choshu	Ib07_2	Itr_sc000393_73439	90.03	*** ($P < 0.001$)	3.07	23.8	0.0074
		Itr_sc004815_16417	118.76	*** ($P < 0.001$)	3.20	24.7	0.0061
	Ib07_4	Itr_sc000216_53020	0.00	*** ($P < 0.001$)	3.30	25.3	0.0015

Evaluation of Early Vigor under Direct Planting Cultivation in Sweetpotato

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In general, sweetpotato is propagated using stem cuttings. Direct planting—in which small storage roots are planted instead of transplanting stem cuttings—has been studied as a labor-saving system in sweetpotato and is similar to the propagation system of potato. In contrast to potato, this type of planting has not been widely adopted for sweetpotato. A major problem is 'mother root enlargement'. This problem has been reduced through breeding efforts, and some cultivars with low 'mother root enlargement' were released. In addition to 'mother root enlargement', early vigor is important for cultivars used in direct planting because it affects their ability to compete with weeds. Compared with 'mother root enlargement', early vigor has received little attention in breeding programs. In this study, we aimed to identify genotypes with good early vigor in direct planting by examining traits such as emergence and shoot yield.

A total of 12 genotypes were tested in 2018 and 2019. Four of the 12 were major cultivars ('Koganesengan', 'Norin No. 1', 'Norin No. 2', and 'Shiroyutaka'); the other eight were cultivars or lines adaptable to direct planting ('Murasakimasari', 'Suzukogane', 'Tamaakane', 'Chugoku No. 25', 'Kyukei 327', 'Kyukei 335', 'Kyukei 342', and 'Kyushu No. 198'). The number of emergent shoots was counted at least every three days until full emergence. Shoot dry-matter yield and plant height were recorded 43 days after planting in 2018 and 62 days after planting in 2019.

Significant differences in days to emergence and shoot dry-matter yields were observed among genotypes in both years (only shoot dry matter is shown in Fig. 1). 'Kyushu No. 198', 'Norin No. 1', and 'Kyukei 335' were outstanding in terms of early vigor (Fig. 1). Of these genotypes, 'Kyushu No. 198' and 'Kyukei 335' should be promising as breeding material for improving growth competition with weeds in direct planting.

A strong relationship between plant height and shoot dry-matter yield was observed (Fig. 2). In breeding programs, the shoots cannot be cut until harvest time. Therefore, this predictive curve for shoot dry-matter yield is helpful for excluding clones with inferior early vigor in actual breeding programs.

This research was supported by grants from the Project of the Bio-oriented Technology Research Advancement Institution, NARO (the special scheme project on advanced research and development for next-generation technology).

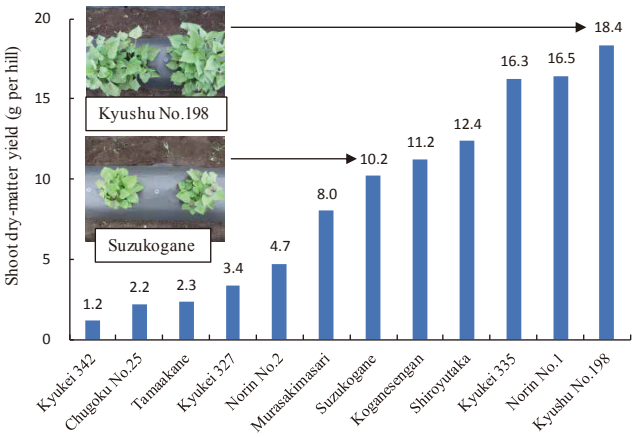

Fig. 1 Shoot dry-matter yield at early growth stages in direct planting. Average values from two years' experiments are shown.

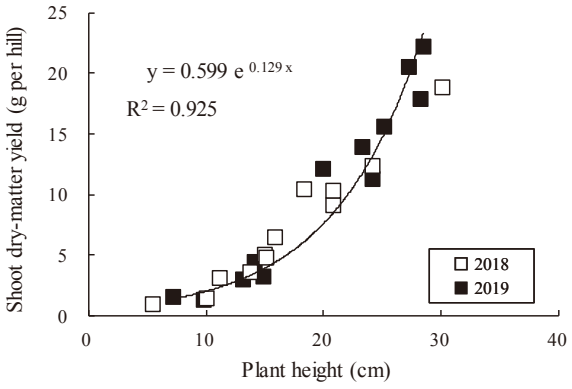

Fig. 2 Relationship between plant height and shoot dry-matter yield. R^2 indicates the coefficient of determination.

References

Sakaigaichi et al. (2020) Plant Prod. Sci. https://doi.org/10.1080/1343943X.2020.1797511

Historical and Recent Progress in Genetic Linkage Analysis of Hexaploid Sweetpotato

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Sweetpotato (*Ipomoea batatas* (L.) Lam) is one of the most important crop species in the world with an annual production over 1 million tons (FAO, 2018)[1]. However, its genetic analysis and linkage map construction using molecular markers have been challenging because of the species' complex genomic architecture: high heterozygosity, self-incompatibility, and hexaploidy, with a large number of small chromosomes (2n=6x=90). This manuscript summarizes research progress related to the genetic analysis of sweetpotato from traditional methods to recent advances.

The first genetic linkage map of sweetpotato was constructed by Ukoskit and Thompson (1997) using randomly amplified polymorphic DNA markers in a pseudo-testcross-mapping strategy[2]. Following this report, several research groups performed linkage map construction using amplified fragment length polymorphism (AFLP), simple sequence repeat (SSR), and sequence-related amplified polymorphism (SRAP) markers. Basically, researchers applied the same analytical methods for linkage map construction: simplex markers were first used to construct a framework map, and then the duplex, triplex, and double-simplex markers were inserted to detect homologous groups. Zhao et al. (2013) constructed the first map that included 90 complete sweetpotato linkage groups (LGs) using AFLP and SSR markers, and quantitative trait locus (QTL) mapping was performed to identify QTLs for agronomically important traits, such as dry matter, starch content, and yield[3].

Recent advances in next-generation sequencing (NGS) technologies have enabled high-throughput genotyping for genome wide association studies (GWASs) and high-density linkage map construction in sweetpotato. Shirasawa et al. (2017) first constructed high-density linkage maps using a double digest restriction-site associated DNA sequencing (ddRAD seq) method in which 28,087 single-nucleotide polymorphism (SNP) markers were mapped onto 96 LGs[4]. Shortly thereafter, Sasai et al. (2019) reported the construction of a high-density linkage map using SNP, SSR, and retrotransposon-based markers, and the identification of genomic regions controlling nematode resistance by QTL mapping and GWAS. This group successfully developed a PCR-based DNA marker for nematode-resistance selection with a focus on the identified QTL[5]. The same linkage maps and genome-wide SNP data also helped identify genomic regions controlling several agronomic traits, including storage root β-carotene content, dry matter, and starch content[6].

Recently, several research groups have developed new analytical tools for autopolyploid species. Yamamoto et al. (2020) developed R package software for the genetic mapping of polyploids using low-coverage NGS data; allele dosage probabilities are calculated from read counts in association analysis to detect loci associated with agronomic traits[7]. In addition, researchers at North Carolina State University reported the new tools MAPpoly and QTLpoly for linkage analysis and QTL mapping of polyploids, respectively[8),9]. Altogether, these recently developed algorithms and methodologies open the door for genetic studies in high-level polyploid species such as sweetpotato.

References

1. http://www.fao.org/.
2. Ukoskit and Thompson, J. Am. Soc. Hortic. Sci. 122, 822–828 (1997).
3. N. Zhao et al., Mol. Breed. 32, 807–820 (2013).
4. K. Shirasawa et al., Sci. Rep. 7, 44207 (2017).
5. R. Sasai et al., DNA Res. 26, 399–409 (2019).
6. E. Haque et al., Breed. Sci. 70, 283–291 (2020).
7. E. Yamamoto et al., G3 10, 2661–2670 (2020).
8. M. Mollinari and A. A. F. Garcia, G3 9, 3297–3314 (2019).
9. G. da Silva Pereira et al., Genetics 215, 579–595 (2020).

Editor's Note

The 9th International Sweet Potato Symposium (formerly the Japan–China–Korea Sweet Potato Workshop) scheduled for October 2020 in China has been postponed because of COVID-19. The new date is still TBD. (Dec 9, 2020, M.T.)

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