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Relationship between Glossiness and Cooking Liquid Components of Temperate *japonica* Rice

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ABSTRACT

Eating quality is one of the target for rice breeding; it is an important trait to evaluate the quality of rice in recent years. Toyo taste meter emits various electromagnetic waves to cooked rice, and analyzes its reflection and transmission pattern for calculating “Toyo value”. Because of this characteristic, Toyo taste meter is known as a machine to measure the so-called "glossiness" of rice. In this study, we focused on whether it have a significance and a positive correlation between the sensory test and Toyo value. Metabolite profiling using high performance liquid chromatography/mass spectrometry/mass spectrometry (HPLC/MS/MS) was performed to determine the components with significant intensity differences between high eating quality group and low eating quality group, classified by Toyo value. We found twenty-five and twenty of promising components at the positive and the negative mode,

respectively in 2018. Fifteen and ten substances with higher amounts were determined in high eating quality group and low eating quality group, respectively in the positive ion mode and in the negative ion mode, each ten higher amounts of substance were determined in high eating quality group and low eating quality group, respectively by t-test. The substances identified will be useful for evaluating eating quality in rice breeding programs.

Key words: Eating quality, Glossiness, Toyo taste meter, Metabolite profiling

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LIST OF ABBREVIATIONS

CL	Cooking liquid
HPLC	High performance liquid chromatography
MS	Mass spectrometry
TV	Toyo value
HEQ	High eating quality group
LEQ	Low eating quality group

INTRODUCTION

Breeding targets of rice (*Oryza sativa* var. *japonica*) have continuously changed to meet the demands of the times. Especially in Korea, yield was the most important trait; the researcher also paid attention to lodging resistance and disease resistance that could affect to yield. After successful breeding of Tongil and Tongil-type rice which are high yielding varieties and achieving self-sufficiency of production, the breeders pursued complex resistance, high nutrition and processing aptitude based on yield[1].

Eating quality is one of the notable breeding goals, which is literally the answer to 'how delicious is the taste of rice?'. In order to improve taste by breeding, firstly, it is important to define the taste, quantitatively. There are two ways to define the taste of cooked rice. The first is a sensory test judged by humans, and is widely used in the evaluation of characteristics of newly developed rice varieties by researchers. Reliability is gained by applying more than a dozen trained panels although the preference of individual panel may differ to determine the taste. However, the sensory test requires large amount of samples and it has a limitation to handle a large number of samples per day. Another method to define the taste of cooked rice is to use an analyzer. Various measuring devices such as Satake cooked rice taste analyzer and Toyo taste meter have been developed for measuring the taste of white rice (especially *japonica* rice). Compared to the sensory test, it is simpler to perform and consumes relatively small amount of samples. However, the question remains whether

the taste value measured by the instrument is closely related to the actual taste of cooked rice.

Sensory test and measurement using Toyo taste meter were often performed together, in the previous studies. The significant positive correlation was observed between sensory test and Toyo meter test. It means that we can use Toyo value directly to determine the palatability[2,3,4]. Therefore, an identified substance which has a close association or causal relationship with a measured value obtained by a device might be considered as a candidate component which affect to taste of cooked rice. In this study, we sought to find the component(s) that contributed to the glossiness and eating quality from cooked rice using the measuring instruments such as HPLC and Toyo meter.

Glossiness is one of the visible trait in regards of the quality of cooked rice. The degree of glossiness means shines of the surface of cooked rice. Consumers in Japan who often eat *japonica* rice prefer glossy appearance of cooked rice as a property of high eating quality rice. Similarly, Korean customers want to buy superior rice that has glossy surface when it is cooked. In a previous research, researchers showed that glossiness was negatively correlated with amylose content[5] using chromosomal segment substitution lines; this correlation was consistent with the results of previous studies[6]. However, they measured glossiness of polished rice using sensory test and amylose content, not cooked rice[5]; thus we were not able to infer the relationship between glossiness of cooked rice and amylose

content, by extension, another property of cooked rice quantitatively. 인용[7] tried to investigate the correlation between eluted starch of cooked rice and traits including glossiness however, it has not been relatively well studied on the components which are contributed to glossiness.

Analyzers to determine the taste value measure the taste according to each principle and display the result with their own way. In the case of the Toyo taste meter which is widely used to measure the eating quality of cooked rice, a variety of electromagnetic waves are shot on a test-cooked rice to comprehensively analyze the reflection and transmission patterns, and display them as a single Toyo value. In other words, the value of Toyo value represents the “glossiness” of cooked rice. When the electromagnetic waves hit the rice surface, the reflection or transmission pattern is changed according to the film (called a coated layer, surface layer, etc.) on the rice surface, and the Toyo value is determined based on these data. However, studies on analyzing the ingredients in the coated layer of cooked rice in terms of eating quality have not been progressed until now.

In this study, we measured the Toyo value of *japonica* rice cultivars and divided to two eating quality groups. Then, the components in the coated layer of cooked rice were detected by HPLC/MS/MS and analyzed using statistical data analysis to find the components that contribute to glossiness that has been considered as the degree of eating quality.

MATERIALS AND METHODS

1. Plant Materials

A total of 8 cultivars (Koshihikari, Samkwang, Ilpum, Hwaseong, Nampyeong, Hwacheong, Samnam, Giho) were used in this study (Table 1). These cultivars were selected based on the Toyo value of rice cultivars from the previous studies. The plants were grown on the experimental farm of Seoul National University in Suwon, Korea in 2018. Field management was performed according to normal agricultural practice. After heading, the cumulative temperature was calculated with 1,100~1,200℃ and the seeds samples were harvested and dried in drying storage. Grain hull was removed and milled to white rice with a 92.2% of milling rate.

Table 1. List of eight rice cultivars used in this study

No.	Cultivar name	Putative eating quality	Year
1	Koshihikari	High	2018
2	Samkwang	High	2018
3	Ilpum	High	2018
4	Hwaseong	Medium	2018
5	Nampyeong	Medium	2018
6	Hwacheong	Low	2018
7	Samnam	Low	2018
8	Giho	Low	2018

2. Measurement of Toyo Value

One hundred and sixty-five grams of head rice for each variety were selected. Toyo value was measured using Toyo taste meter (MA-90, Toyo Rice Corporation, Wakayama, Japan) in cooperation with Chungcheong-namdo Agricultural Research and Extension Services. The measurement was performed in five replicates.

3. Sample Preparation for HPLC

Cooking method was performed according to modified standard cooking method using National Institute of Crop Science, Rural Development Administration, Korea for the sensory test[8]. Briefly, 150 g of white rice were weighed and washed five times with 450 ml of distilled water. Rice was cooked with an electric rice cooker (WM-0420, CUCHEN, Cheonan, Korea) with distilled water (225g) corresponding to 1.5 times the weight of white rice. When the steam was discharged, the cooking was stopped and the cooking liquid (CL) was collected. The collected CL cooled in a 4℃ refrigerator, and then transferred to a -80℃ deep freezer for storage. All samples were freeze-dried by freeze dryer (PVTFD-10K, IlShinBioBase Corporation, Dong-ducheon, Korea).

Lyophilized CL samples were prepared using modified methods of previous research[9]. Briefly, freeze-dried CL was crashed and grounded by sterilized mortar and pestle. Three hundred mg of lyophilized CL powder was weighed and extracted with 6.0ml 100% MeOH and 70% MeOH(aq)

containing 0.1mg/L lidocaine for lipid-solubility metabolites and water-solubility metabolites, respectively overnight at 4℃. After extracting, all samples were centrifuged at 10,000 g for 10 min and 750 $\mu\ell$ of each extract was mixed and filtrated before HPLC/MS/MS analysis.

4. HPLC/MS/MS operation

The HPLC conditions were as follows: instrument, Ultimate3000 (Thermo Fisher Scientific, Waltham, Massachusetts, USA); column, Kinetex C18 (2.1 mm X 100 mm, 1.7 um)(Penomenex, Torrance, California, USA); column temperature, 45℃; solvent system, 0.1% Formic acid in water:0.1% Formic acid in acetonitrile; gradient change, 95:5 V/V at 0 min, 95:5 V/V at 0.5 min, 50:50 V/V at 10.0 min, 5:95 V/V at 13 min, 5:95 V/V at 16.0 min, 95:5 V/V at 17.0 min, 95:5 V/V at 20.0 min; flow rate, 0.4 ml/min.

The MS conditions were as follows: instrument, Triple TOF 5600+(AB Sciex, California, USA); MS data type, MS1 and MS2; ionization mode, positive and negative; MS scan type, full scan and information dependent acquisition (IDA) Scanning; ionization source, Electrospray ionization(ESI); MS scan range, 50~2,000 m/z; MS/MS scan range, 50~2,000 m/z; pressure of ion source 1(nebulizing gas), 50 psi; pressure of ion source 2(heating gas), 50 psi; pressure of curtain gas, 25 psi; desolvation temperature, 500℃; ionspray voltage floating, 5.5kV(positive) & 4.5kV(negative); declustering potential(DP), 60(positive) & -60(negative); collision energy(CE), 10(positive) & -10(negative); Collision gas, N_2.

5. Metabolite Profiling

The following method describes the contents of the publish tab in the metdb format file which contains processed data.

5.1 Raw Data Processing

Raw data files were converted to mz5 format using ProteoWizard[10] version(s) pwiz_Reader_ABI: 3.0.9987.

Feature finding (a.k.a peak picking) was performed using Elements[11] (version 2.1.1, Proteome Software Incorporation, Portland, Oregon, USA). Feature finding was conducted over a mass range of 50.0 to 2000.0 and the entire retention time range. A noise threshold value of 0.5% of max signal and a minimum time between scans of 0.5 sec was used. MS2 spectra were detected for some features. Features were organized into isotopic clusters, and all appropriate MS2 spectra were associated to appropriate features.

MS1 Peak Groups were formed within individual samples using a same-charge inclusion threshold of 1.0 sec and a cross-charge inclusion threshold of 1.0 sec.

Retention time alignment was not performed. Consensus MS1 Peak Groups were formed using a maximum RT Difference of 30.0 sec. Cross-sample gap filling feature reextraction was performed. Analyte clusters were formed containing all analytes associated with a single consensus MS1 Peak Group. Analyte groups were formed containing all analytes with the same set of ions (peaks in the MS1 Peak Group).

5.2 Spectral Library Searching

Candidate analyte identifications were generated by matching experimental data to spectral library data using exact mass with a mass tolerance of 20.0 ppm. If both the experimental and library data contained MS2 spectra, MS2 peaks were matched between experimental and library spectra using a fragment mass tolerance of 0.5 Da. The following five libraries were searched to generate candidate analyte identifications:

- 20170615_MoNA-export-LC-MS_-_MS-MS_-_Positive_Mode.msp .libdb(29945 entries)
- nist_libraryV2017_elements.libdb(536823 entries)[12]
- 20170615_MoNA-export-LC-MS_-_MS-MS_-_Negative_Mode.msp .libdb(13599 entries)
- 20170615_MoNA-export-LC-MS_-_MS-MS.msp.libdb(43544 entries)
- hmdb_library_elements.libdb(45905 entries)

The following ion types were considered when matching features to library analytes: [M+HCO2]-, [M+Na]+, [M-H-NH3]-, [M+H-NH3]+, [M-H]-, [M-H-H2O]-, [M+H]+, [M+H-H2O]+, [M+NH4]+ and In-source fragments (at least 20% of reference MS2 spectrum max intensity).

Features that did not match to any analytes contained in the spectral libraries were discarded.

5.3 Scoring

To gauge confidence in candidate analyte identifications, an Analyte ID score was calculated from individual feature - library entry matches, incorporating mass accuracy, isotopic distribution, and fragmentation pattern. Analyte identifications that were identified with more ion types received a higher score than identifications made with fewer ion types.

Analyte identifications with an ID Score below zero were discarded.

5.4 Criteria for Analyte Identification

Each technical replicate groups' intensities were normalized to align the median intensities and the inner quartile widths with a bilinear mapping in log space. Identifications were accepted if they could be established with an Analyte ID Score of 0.7, based on peaks with log10 intensity levels of 0.0 or higher which are identified in 1 or more samples.

5.5 Candidate Selection

The components and clusters with the highest ID scores that represent the best match with the compounds in the database were selected from each cluster. Substances found in two or more of three replicates in the blank were excluded. Technological replicates of each biological replicate were averaged when two or more of the three technological replicates exist. Calculated biological replicates were used in statistical data analysis.

6. Statistical Data Analysis

K-mer cluster analysis, normality test, independent two sample t-test and nonparametric test were performed using IBM SPSS Statistics for Windows, Version 25.0 (IBM Corporation, Armonk, New York, USA). K-mer cluster analysis was used for dividing rice varities into two eating quality groups. Normality test was performed because the number of biological replicates was not enough. Independent two sample t-test was used to determine whether there was a significant difference in the amount of individual component between the two eating quality groups. Nonparametric test was performed for confirming the distribution of compounds that did not pass the normality test.

RESULTS

1. Toyo Values and K-mer Cluster Analysis for EQ

The results of TV measurements of the eight rice varieties are shown in the Table 2 and Figure 3. Nampyeong showed the highest TV value of 69.82 ± 1.07, and Samnam showed the lowest TV value of 55.22 ± 0.41. K-mer cluster analysis was performed with k=2 in order to classify them into two eating quality groups. As a result, five varieties of Koshihikari, Samkwang, Ilpum, Hwaseong and Nampyeong were classified into one group, and three varieties of Hwacheong, Samnam, and Giho were classified into another group. Since the former average TV was higher, we put the former as HEQ and the latter as LEQ.

Table 2. The Toyo values of eight rice cultivars

No.	Cultivar name	Mean ± SD	Group
1	Koshihikari	65.02 ± 0.76	HEQ
2	Samkwang	64.22 ± 1.44	HEQ
3	Ilpum	69.78 ± 0.85	HEQ
4	Hwaseong	67.44 ± 1.17	HEQ
5	Nampyeong	69.82 ± 1.07	HEQ
6	Hwacheong	60.94 ± 1.60	LEQ
7	Samnam	55.22 ± 0.41	LEQ
8	Giho	59.94 ± 0.86	LEQ

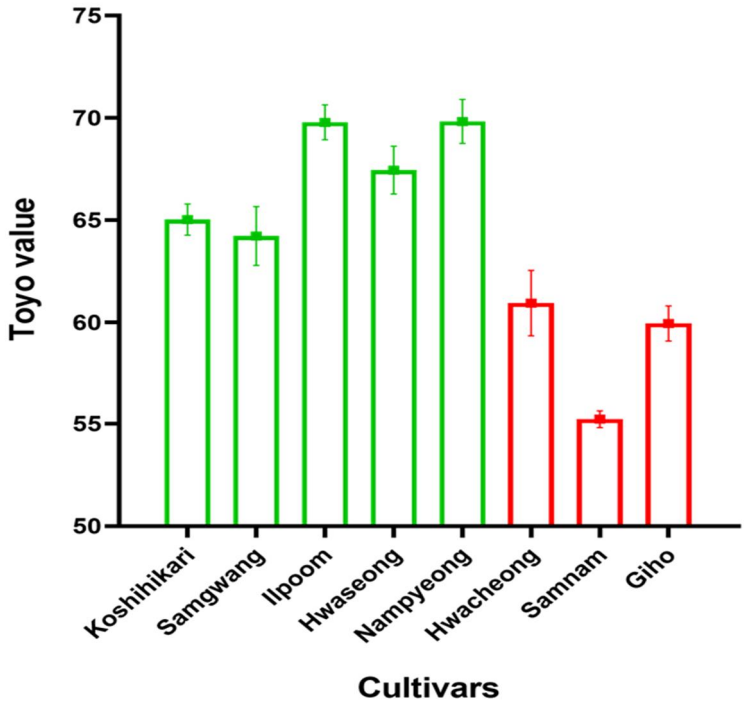

Figure 1. The mean and standard deviation of Toyo value for eight rice cultivars, with K-mean clustering result(k=2). Cultivars included in HEQ are shown in green. Cultivars included in LEQ) are shown in red.

2. Metabolite Profiling in the Positive Ion Mode

As a result of metabolite profiling in the positive ion mode, 25 compounds with significant differences in normalized intensity mean between HEQ and LEQ were found (Table 3). Among them, there were 15 components showed more intensity in HEQ and 10 components showed more intensity in LEQ. 13 lipids, one protein, and one carbohydrate were detected in the broken down the type of substances with higher intensity in HEQ. The types of substances showed higher intensity in LEQ were two lipids, two nucleotides, two carbohydrates, and four organic acids.

Table 3. Candidate metabolites showed significant difference in independent t-test between eating quality group in the positive ion mode

Serial number	Analyte name	Type	t value	p value
P1	3-Polyprenyl-4-hydroxy-5-methoxybenzoate_RT1	Lipid	4.041	0.001
P2	Cluster of 5(6)-Butyl-1,4-dioxan-2-one		3.697	0.001
P3	Cluster of Didodecyl 3,3'-thiodipropionate oxide		3.638	0.001
P4	Didodecyl 3,3'-thiodipropionate oxide		3.638	0.001
P5	Cluster of Phosphatidylethanolamine lyso 18:2		3.634	0.002
P6	Phosphatidylethanolamine lyso 18:2		3.634	0.002
P7	endo-1,4-beta-Xylanase	Protein	3.218	0.009
P8	1-Phenyl-1,3-nonadecanedione	Lipid	3.119	0.005
P9	5(6)-Butyl-1,4-dioxan-2-one		2.931	0.008
P10	Cluster of Chitobiose	Carbo-hydrate	2.925	0.008
P11	DG(14:0/0:0/20:2n6)	Lipid	2.862	0.009
P12	Cluster of 1-Phenyl-1,3-heptadecanedione		2.831	0.01
P13	Androsterone		2.494	0.021
P14	1-Phenyl-1,3-heptadecanedione		2.441	0.023
P15	Porson		2.217	0.037
P16	Cluster of Adenosine	Nucleo-tide	-2.677	0.022
P17	Adenosine		-2.723	0.012
P18	Cluster of Hydromorphone-3-glucoside	Carbo-hydrate	-3.395	0.008
P19	Hydromorphone-3-glucoside		-3.395	0.008
P20	Cluster of DG(18:2(9Z,12Z)/18:2(9Z,12Z)/0:0)	Lipid	-3.717	0.004
P21	Cluster of Folinic acid	Organic acid	-4.527	<0.001
P22	Folinic acid		-4.527	<0.001
P23	Cluster of Citrate		-5.409	<0.001
P24	gamma-Glutamylcysteinylserine		-5.409	<0.001
P25	DG(15:0/0:0/18:2n6)	Lipid	-5.993	<0.001

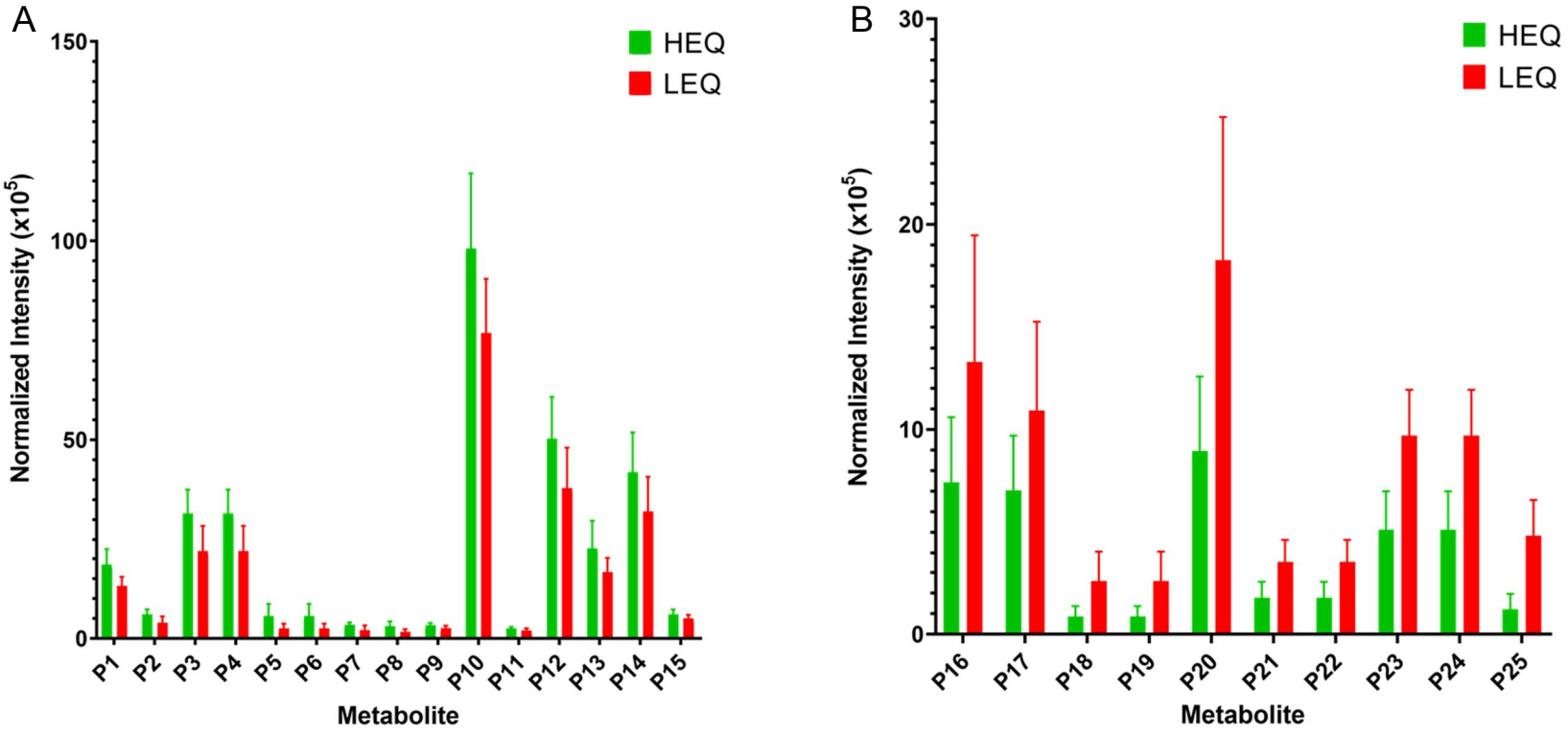

Figure 2. A. The mean and standard deviation of normalized intensity ($x10^5$) of components that intensity is higher in HEQ than LEQ in the positive ion mode. B. The mean and standard deviation of normalized intensity ($x10^5$) of components that intensity is higher in LEQ than HEQ in the positive ion mode. Cultivars included in HEQ are shown in green. Cultivars included in LEQ are shown in red.

3. Metabolite Profiling in the Negative Ion Mode

As a result of metabolite profiling in the negative ion mode, 20 compounds with significant differences in normalized intensity mean between HEQ and LEQ were found (Table 4). Among them, there were 10 clusters or materials showed more intensity in HEQ and 10 clusters or materials showed more intensity in LEQ. Decomposed the type of clusters or substances showed higher intensity in HEQ included eight lipids and two carbohydrates, and divided the type of clusters or substances showed higher intensity in LEQ included four lipids, four acids and two amino acids.

Table 4. Candidate metabolites that showed significant difference in independent t-test between eating quality group in the negative ion mode

Serial number	Analyte name	Type	t value	p value
N1	Senecionine	Lipid	3.615	0.002
N2	Cluster of Phosphatidylethanolamine lyso 18:2		3.166	0.004
N3	Phosphatidylethanolamine lyso 18:2		3.166	0.004
N4	Cluster of Senecionine		3.083	0.005
N5	Avenic acid A_RT2		2.831	0.013
N6	1-Palmitoyl-2-hydroxy-sn-glycero-3-phospho-(1'-rac-glycerol)		2.742	0.012
N7	Valdiate		2.684	0.014
N8	LysoPC(14:0)_RT1		2.664	0.014
N9	Cluster of D-Fructose	Carbohydrate	2.133	0.044
N10	D-Fructose		2.133	0.044
N11	Cluster of Citrate	Organic acid	-2.395	0.036
N12	Citrate		-2.421	0.035
N13	[(2S,3S,4R,5R)-4-hydroxy-2,5-bis(hydroxymethyl)-2-[(2R,3R,4S,5S,6R)-3,4,5-trihydroxy-6-(hydroxymethyl)oxan-2-yl]oxyoxolan-3-yl] (E)-3-(4-hydroxy-3-methoxyphenyl)prop-2-enoate_RT1	Lipid	-2.449	0.023
N14	[(2R,3S,4S,5R,6R)-6-[(2S,3S,4S,5R)-3,4-dihydroxy-2,5-bis(hydroxymethyl)oxolan-2-yl]oxy-3,4,5-trihydroxyoxan-2-yl]methyl (E)-3-(4-hydroxy-3,5-dimethoxyphenyl)prop-2-enoate_RT1		-2.463	0.022
N15	Tyr	Amino acid	-2.502	0.02
N16	Cluster of [(2S,3S,4R,5R)-4-hydroxy-2,5-bis(hydroxymethyl)-2-[(2R,3R,4S,5S,6R)-3,4,5-trihydroxy-6-(hydroxymethyl)oxan-2-yl]oxyoxolan-3-yl] (E)-3-(4-hydroxy-3-methoxyphenyl)prop-2-enoate_RT1	Lipid	-2.506	0.02
N17	Hexacarboxylporphyrin I	Organic acid	-2.562	0.018
N18	Cluster of Tyr	Amino acid	-2.752	0.012
N19	Tosyl-L-lysyl-chloromethane	Lipid	-2.875	0.019
N20	Cluster of NCGC00384990-01!(1S,3R,4R,5R)-3-[(E)-3-(3,4-dihydroxyphenyl)prop-2-enoyl]oxy-1,5-dihydroxy-4-[(E)-3-(4-hydroxy-3,5-dimethoxyphenyl)prop-2-enoyl]oxycyclohexane-1-carboxylic acid	Organic acid	-2.983	0.015

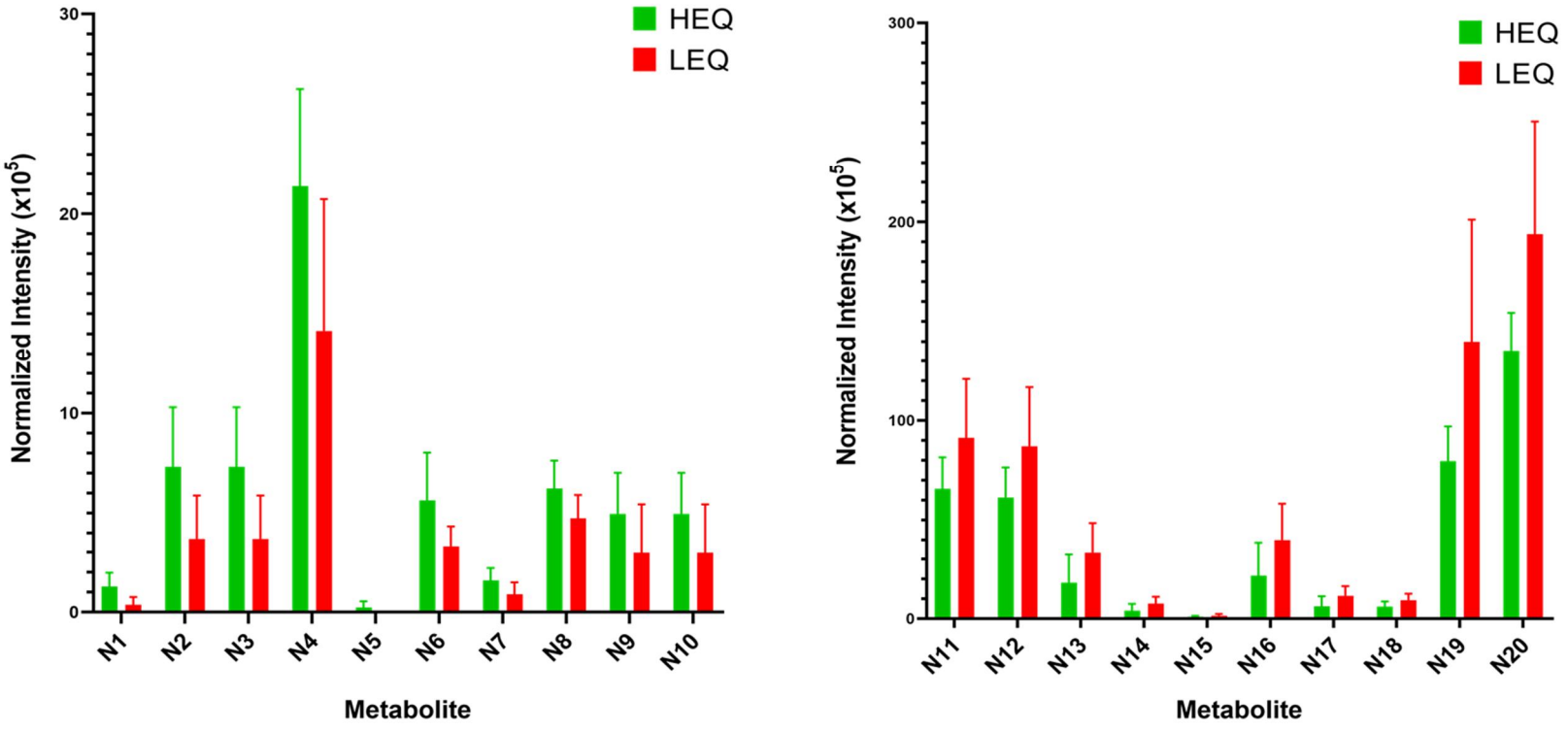

Figure 3. A. The mean and standard deviation of normalized intensity ($x10^5$) of components that intensity is higher in HEQ than LEQ in the negative ion mode. B. The mean and standard deviation of normalized intensity ($x10^5$) of components that intensity is higher in LEQ than HEQ in the negative ion mode. Cultivars included in HEQ are shown in green. Cultivars included in LEQ are shown in red.

DISCUSSION

In order to explore components contributing to the eating quality, we utilized the Toyo value which has a strong and significant positive correlation with eating quality measured by the sensory test. In this study, we analyzed the components of the coated layer which are expected to affect the Toyo value based on the measurement principle, and checked whether there was a significant intensity difference of each substance between the two eating quality groups.

First of all, Toyo values of eight rice cultivars were similar to those predicted Toyo values based on previous studies. However, unlike previous studies, Toyo value of eight varieties were very low, especially Koshihikari. We assume that it might be because the environmental change was effected to experimental field condition of Suwon in 2018. The average temperature of Suwon measured by the Korea Meteorological Administration showed that the heat wave persisted during ripening stage (Table 5[13]). For that reason, environmental condition for seed development may be not suitable than in normal years. In addition, in the process of dry, the grains were dried faster than expected, therefore rice kernels' the moisture content was reduced. Indeed, the Chungcheongnam-do Agricultural Research and Extension Services confirmed the moisture content of white rice before measuring the Toyo value, and recorded a moisture content lower than 14-15%, which is generally expected. According to Toyo instruction, the reliability is the highest when the moisture

content of white rice is 14-15%. If it is lower or higher than that, it was not recommended. It is thought that the Toyo value was measured with low moisture contents of white rice.

The properties of some compounds of the significant differences between HEQ and LEQ in both positive and negative modes were partially explained the results. In the positive mode, 5(6) -Butyl-1,4-dioxan-2-one, Folinic acid and Citrate were included. 5(6) -Butyl-1,4-dioxan-2-one was more common in HEQ and is known to have a fruity flavor[14]. Folinic acid contains L-glutamic acid in its structure, and folinic acid may be negative in taste given the fact that L-glumatic acid contributes to umami. Citrate has a sour taste in itself. In the negative mode, D-fructose, Citrate, and Tyrosine were applicable. D-fructose is widely known to be closely associated with sweet taste, and tyrosine is known to have a bitter taste[15].

Meanwhile, among the components that showed significant difference between two eating quality groups detected in both modes, lipids were generally higher in the high eating quality group, while organic acids and amino acid (Tyr) were higher in the low eating quality group. It might mean that metabolites that are likely to contribute positively to the Toyo value is lipid, which is likely due to a difference in taste.

Although this study was meaningful in suggesting a new way of searching for substances that contribute to the taste, there is a limit to identify the components which explain the relationship between glossiness and taste. This is because only eight varieties' data of one year were used, and experiments with more varieties are required with annual replicate. In

addition, normalized intensity was used as a measure of the significant difference between HEQ and LEQ, which showed the relative difference in the amount of a particular substance, but the absolute amount was unknown and differs from substance to substance. Additional analysis in conjunction with the follow-up experiments will it be possible to select components that differ between the two eating quality groups and to quantitatively analyze them.

Table 5. Maximum temperature and mean temperature in Suwon in July, August and September, 2018

	July		August		September	
	Max(℃)	Mean(℃)	Max(℃)	Mean(℃)	Max(℃)	Mean(℃)
1	23.9	21.9	39.3	32	30.7	25.3
2	28	23	38.1	32	29.9	25.1
3	33.5	26.5	37.6	32	28.5	24.3
4	32.3	26.4	35	30.2	29.3	23.8
5	30.8	25.7	34.3	29.7	29	23.6
6	27.5	24.3	34.8	29.8	28.8	23.1
7	29.6	24.3	36.4	30.5	25.4	21.4
8	28.2	23.3	36	30.2	28.2	21.3
9	23.6	21.1	34.1	29.4	28.3	21.2
10	27.9	24.7	37	31.2	28	23
11	30.9	27.2	35.6	30.6	25.7	21.4
12	31.1	27.4	35.6	30.3	27.6	22.5
13	32.4	27.3	36.7	31	28	23.5
14	32.8	27.9	37.1	31.8	25.1	23.1
15	34	27.9	39.2	32.4	23.6	21.7
16	33.7	27.8	35.9	30	25.4	21.9
17	32.4	27.2	32.5	26.9	27.8	21.8
18	33.4	27.6	32.1	25.8	26.9	21.3
19	33.4	27.6	33.8	27.1	26.9	21.4
20	34	28.5	32.8	28.3	20.3	19
21	36.7	29.3	30.1	25.6	22.1	19.2
22	37.5	31.1	37.2	30.6	26.5	20.2
23	36	31.2	33.2	29.5	25.7	19
24	36.5	30.6	28	24.7	23.3	17.1
25	33.9	29.6	29.6	24.7	24.1	17.3
26	34.2	29.4	25.9	21.7	24.8	18.9
27	35.7	29.8	24.6	22.4	24.8	18.5
28	34.9	28.9	25.4	23.5	21.3	17.7
29	35.9	30.9	29.6	26.1	27	19.6
30	36.3	31.6	31.4	26.7	22.4	17.2
31	37.5	31.9	30	24.7		

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초록

온대 자포니카 벼에서의 윤기와 취사액 성분 간의 관계

식미는 쌀에 있어 육종목표 중의 한 가지로, 최근 쌀의 품질에 있어 중요한 형질이다. 토요식미측정기는 시험취사된 밥에 여러 전자파를 쏘아 그 반사와 투과 패턴을 분석하여 토요값을 제시하며, 이런 특성으로 인해 이른바 쌀밥의 “윤기”를 측정하는 기계로 알려져 있다. 관능검사와 토요식미측정기를 병행하여 사용한 선행연구들에서 관능검사 결과와 토요값이 유의하면서 강한 정의 상관관계를 보이는 점에 착안하여, 윤기를 측정하는 토요값에 기여하는 물질을 탐색하고자 하였다. HPLC/MS/MS 를 실시하여 얻은 데이터로 대사체 프로파일링을 수행하여 Toyo value 에 의해 분류된 고식미군과 저식미군 간 유의한 intensity 차이를 보이는 물질을 탐색한 결과, positive mode 에서 25 개, negative mode 에서 20 개의 물질이 발견되었다. Positive mode 에서 고식미군에 더 많은 양이 있는 물질은 15 개, 저식미군에 더 많은 양이 있는 물질은 10 개였으며, negative mode 에서는 고식미군에 더 많은 양이 있는 물질과 저식미군에 더 많은 양이 있는 물질은 각각 10 개씩이었다. 탐색된 물질들은 벼 육종 프로그램에서 식미를 증진시키고자 할 때 유용하게 쓰일 수 있을 것이다.

주요어 : 식미, 윤기, 토요식미측정기, 대사체 프로파일링

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감사의 글

가장 먼저, 식품생명공학전공의 제가 일반적인 컨택의 과정을 거치지 않고 작물생명과학전공의 대학원을 오고자 하였을 때, 예상치 못한 인원임에도 저를 받아 연구의 기회를 주신 고희종 지도교수님께 감사드립니다. 연구에 있어서 재료를 확보하는 것 자체부터 상당한 과제였는데, 제 연구 주제를 들으신 후 각별히 신경을 더 써주시고 초행에 혹시나 무언가 빼먹을까 염려해주신 김홍열 연구관님과 강미경 여사님에게 감사드리며, 저를 포함한 식미팀의 재료가 많은 탓에 여러 번 발 벗고 나서준 진우에게 언제나 고마운 마음입니다. 각자의 연구의 결이 조금씩 다름에도, 작물분자육종연구실의 모든 식구들은 부족한 저의 물음에 항상 풍족한 답과 이야기를 들려주었습니다. 분석 실험에서 많은 피드백을 주신 이춘석 박사님, 편하면서도 연구자의 모습을 몸소 보여주신 김백기 박사님, 연구실의 심장 · 척추 · 허리를 동시에 맡고 있으신 은별 누나께 감사드립니다. 항상 최신 연구 동향과 번뜩이는 아이디어를 갖고 있으신 정환이 형과 장수 형, 타지에서 육아와 공부를 병행하느라 바빠 많은 얘기를 나누지 못하지만 언제나 밝게 맞이해주는 서우 형, 생물정보학 문제로 많은 얘기를 나누는 탁이 형, 연구 선배로서 같은 식미팀에서 갖은 고생을 하면서도 연구를 알려준 윤경이, 말은 악의지만 실제는 없는 동기 유석이에게도 깊은 감사의 말을 전합니다. 작년에 들어와 식미팀의 쏟아지는 물량을 같이 감내하게 된 퓨퓨마웅 누나와 승영 ‘씨’ (?)에게는 미안하고 또 고맙습니다. 지금은 연구실을 떠났지만, 같이 있는 시간 동안 동령이 형, 요예 누나, 소명 누나, 혜경 누나, 태준이가 나누어 준 마음이 저를 여기까지 올 수 있게 해주었습니다. 마지막으로 상당히 늦은 때에도 저를 믿고 대학원 생활을 할 수 있게 해준 부모님과 동생, 제 가족에게 고개 숙여 감사드립니다. 비록 지금의 논문은 초라하지만, 어떠한 형태이든 연구를 하면서 살아가고자 하는 저의 의지를 담은 첫 발걸음이라고 생각하며 끝까지 나갈 수 있도록 하겠습니다.