



ISSN: 2075-6240

# Genetic variation of morphological and yield-related traits in backcrossed and selfed population of maize

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## ABSTRACT

The number of genes controlling the morphological and yield-related traits and their mode of action plays a vital role in selecting traits and favourable progenies in a segregating population. In this study, we analysed the skewness and kurtosis in the backcrossed and selfed populations of SC11-2×UMI1230β1<sup>+</sup>. Negative skewness refers to redundant gene activity, positive skewness is connected to complementary gene action. Positive kurtosis suggests the existence of gene activity controlled by a smaller number of genes. Negative kurtosis shows a lack of gene activity and is controlled by a large number of genes. The BC<sub>2</sub>F<sub>2</sub> population of plant height and single plant yield showed positive skewness and platykurtic distribution, suggesting that the genes were governed by complementary gene action and controlled by the large number of genes. This implied need for rigorous selection to achieve a genetic gain in later generations. Cob length and kernel weight showed a duplicate gene action which implied that mild selection can fix these traits and accelerate genetic gain.

**Keywords:** backcross population, gene action, skewness, kurtosis, selection.

**Received:** May 23, 2022  
**Revised:** September 02, 2022  
**Accepted:** September 03, 2022  
**Published:** September 21, 2022

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## INTRODUCTION

*Zea mays* L. *saccharata*, known as sweet corn, is one of the most consumed vegetables in nations like the United States and Canada. It has also gained popularity in the urban market of India and other Asian nations. Sweet corn is consumed as a fresh and processed vegetable due to its sweet taste, tender nature, easy digestibility, and nutritional values (Mehta *et al.*, 2017). Fresh sweet corn was first produced in the USA and has since been exported to several nations, where it has gained appeal as a preferred vegetable (Revilla *et al.*, 2021). Corn is processed to lengthen its shelf life, but as a result, leaching or heat degradation might result in a large loss of nutrients (Singh *et al.*, 2014). Corn gained the worldwide lead among the most significant grains produced, with a production output of 1.2 billion metric tonnes. The production volume of corn produced in India during 2021 was 30 million metric tonnes. This decreased compared to the previous year when

the production volume of corn was about 32 million metric tonnes.

The critical analysis of distribution properties by third-order statistics such as skewness and kurtosis, which are more important than first and second-order statistics that reveal only the interaction effects, is usually used to determine the nature of gene action and the number of genes controlling the trait (Rani *et al.*, 2016). The frequency distribution is a graphical depiction of the number of individuals in each category on a measurement scale (Gravetter *et al.*, 2020). The skewness is used to indicate the nature of gene action and to quantify the symmetry of the population, or more precisely, the lack of symmetry (Fisher *et al.*, 1932). Kurtosis identifies the number of genes that control the feature and whether the data is left- or right-tailed in comparison to its normal distribution (Robson, 1956). The non-additive gene activity will be dominant, and the genotype affects the skewness of the distribution. Positive skewness is associated with

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complementary gene activity, while negative skewness is related to duplicate gene action. Kapur (1980) classified kurtosis into three types: (i) leptokurtic (positive kurtosis), (ii) platykurtic (negative kurtosis), and (iii) mesokurtic (Zero kurtosis). Several studies have investigated the diversity and frequency distribution of maize lines that have improved nutritional content (Lal & Singh, 2014; Chandana, 2018; Nagalakshmi et al., 2018; Pukalenty et al., 2018; Sarankumar et al., 2019).

The present study focuses on estimations of the descriptive statistics of the improved sweet corn inbred lines of SC11-2. The current research sought to investigate backcross populations ( $BC_1F_1$ ,  $BC_2F_1$ , and  $BC_2F_2$ ) of SC11-2  $\times$  UMI 1230 $\beta_1^+$  for descriptive statistics, frequency distribution patterns based on skewness and kurtosis and to obtain beneficial individuals with high yield coupled with adequate agronomical features.

## MATERIALS AND METHODS

### Plant Genetic Materials

A sweet corn inbred SC11-2, developed at the Department of Millets, Tamil Nadu Agricultural University, Coimbatore, India, was selected as their current parent. UMI1230 $\beta_1^+$ , a provitamin A biofortified maize, developed at the Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore, India was chosen as the donor parent. All the studies were carried out at the Eastern block farm, Tamil Nadu Agricultural University, Coimbatore, India, during 2019-2020.

### Generation of Backcross and Selfed Progenies

The backcross population of SC11-2  $\times$  UMI1230 $\beta_1^+$  was developed to introgress the crtRB1 favourable allele into the sweet corn inbred from the donor parent to enhance the

provitamin A concentration. A single cross between SC11-2 and UMI1230 $\beta_1^+$  was made in Rabi 2019 and the  $F_1$ 's were evaluated in Kharif 2020. The  $F_1$  progenies were backcrossed with the recurrent parent in Kharif 2020 to generate  $BC_1F_1$ . The  $BC_1F_1$  progenies were considered in Rabi 2020. The selected plants in  $BC_1F_1$  were backcrossed in Rabi 2020 to generate the  $BC_2F_1$  generation. The  $BC_1F_1$  generation was grown in the Summer 2021, and the selected plants were selfed to produce  $BC_2F_2$  cobs. The  $BC_2F_2$  was raised in field and evaluated in Kharif 2021.

### Evaluation of Biometrical Traits

Fourteen biometrical traits, viz., days to tasselling (days), days to silking (days), plant height (cm), ear height (cm), tassel length (cm), number of tassel branches (Nos.), leaf length (cm), leaf breadth (cm), cob length (cm), cob girth (cm), number of kernel rows per cob (Nos), number of kernels per row (Nos), 100-grain weight (g) and single plant yield (g) (Sarankumar et al., 2019) were recorded in the backcrossed ( $BC_1F_1$  and  $BC_2F_1$ ) and selfed ( $BC_2F_2$ ) progenies. The mean values of the morphological and yield-related traits were used to calculate descriptive statistics using SPSS 28.0.1.1. Mean, standard deviation, variance, skewness, and kurtosis were used to find the nature of gene action.

## RESULT

The frequency distribution of the 14 morphological and yield-related traits was studied for SC11-2  $\times$  UMI 1230 $\beta_1^+$  in  $BC_1F_1$ ,  $BC_2F_1$ , and  $BC_2F_2$  generations. Among the traits, plant height, ear height, 100 kernel weight, and single plant yield showed a wide range of variation. The frequency distribution graphs were represented in Figure 1. The cob length variation was represented in Figure 2. The statistical data of range, standard deviation, and variance were presented in Table 1. Skewness and kurtosis were presented in Table 2.

**Table 1: Estimation of range, mean, standard deviation and variance in backcrossed and selfed populations of SC11-2  $\times$  UMI 1230 $\beta_1^+$**

Traits	$BC_1F_1$				$BC_2F_1$				$BC_2F_2$						
	Range		Mean	Standard Deviation	Variance	Range		Mean	Standard Deviation	Variance	Range		Mean	Standard Deviation	Variance
	Min	Max				Min	Max				Min	Max			
DT	50	55	52.49	1.23	1.53	55.00	61.00	57.86	1.68	2.82	52.00	60.00	55.74	1.70	2.89
DS	53	57	54.11	5.11	26.14	58.00	63.00	60.50	1.69	3.06	54.00	62.00	57.73	1.84	3.40
PH	98.5	126	111.21	7.47	55.75	162.00	178.00	170.37	4.68	25.50	175.00	191.00	181.03	3.89	15.11
EH	58	78	66.88	4.56	20.81	54.00	70.00	61.38	4.67	23.99	82.00	102.00	87.59	4.43	19.58
TL	24	31	27.13	1.40	1.97	23.00	33.00	28.01	2.99	10.80	22.50	31.00	26.37	1.99	3.97
NTB	9	13	10.95	1.19	1.42	8.00	13.00	10.52	1.73	2.99	8.00	12.00	8.90	0.90	0.81
LL	48	59	52.76	2.80	7.84	48.00	58.00	52.77	3.12	10.62	51.00	59.50	54.57	2.02	4.07
LB	6	10	7.87	0.84	0.70	5.00	10.00	7.46	1.75	3.58	6.00	9.00	7.02	0.70	0.49
CL	14	19	16.40	1.29	1.68	9.00	18.00	13.70	2.88	9.67	9.50	14.50	11.51	1.36	1.84
CG	11.5	15.5	13.93	0.87	0.76	9.00	15.00	12.03	1.98	4.14	9.00	12.00	10.40	0.95	0.90
NKRC	11	14	12.37	0.81	0.66	11.00	15.00	13.07	1.50	2.03	10.00	13.00	10.97	0.70	0.49
NKR	11	19	15.04	1.41	2.00	11.00	18.00	14.38	2.30	4.68	12.00	16.00	13.96	0.95	0.90
100KW	19	25	22.29	1.65	2.73	18.00	26.00	22.01	2.58	7.13	19.00	25.00	21.79	1.34	1.81
SPY	71	77	74.50	1.16	1.34	67.00	76.00	70.95	2.82	7.96	65.00	75.00	69.21	2.16	4.65

DT- Days to tasselling, DS- Days to silking, PH- Plant height, EH- Ear height, TL- Tassel length, NTB- Number of tassel branches, LL- Leaf length, LB- Leaf breadth, CL- Cob length, CG- Cob girth, NKRC- Number of kernel rows per cob, NKR- Number of kernel rows, 100KW- 100 kernel weight, and SPY- Single plant yield

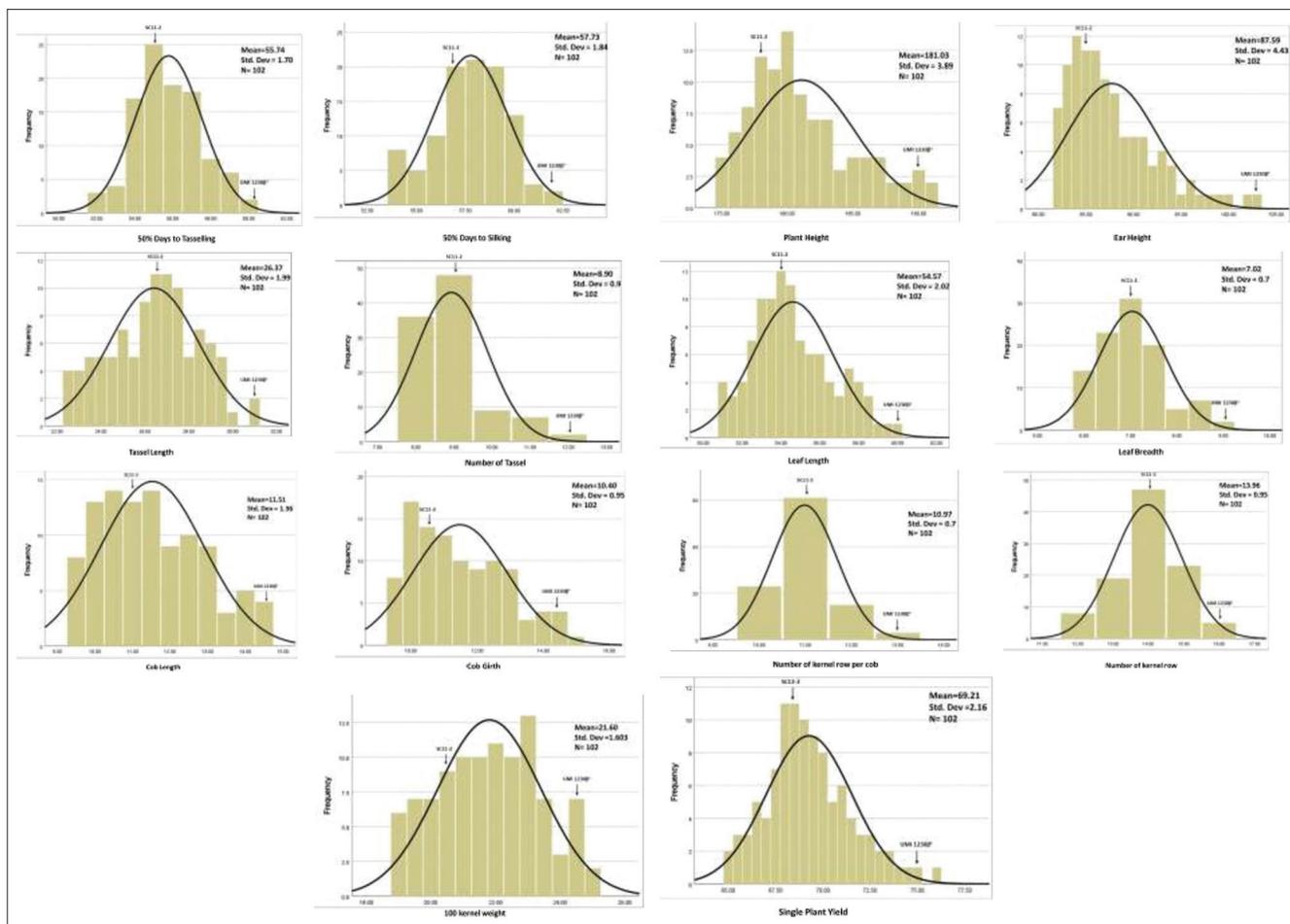


Figure 1: Frequency distribution the morphological and yield related traits of BC<sub>2</sub>F<sub>2</sub> population of SC11-2 × UMI 1230β1<sup>+</sup>



Figure 2: Cob length variation in BC<sub>2</sub>F<sub>2</sub> population of SC11-2 × UMI 1230β1<sup>+</sup>

### BC<sub>1</sub>F<sub>1</sub> Generation

In BC<sub>1</sub>F<sub>1</sub>, the plant height ranged from 98.5 cm to 126 cm, with a mean of 111.21 cm. The skewness and kurtosis were 0.18 and -0.89, respectively. The ear height ranged from 58 cm to 78 cm, averaging 66.88 cm. Skewness for this trait was 0.26 and -0.38, respectively. The weight of 100 kernels varied from 19 gm to 25 gm in this generation, with an average of 22.29 gm, skewness of -0.22, and kurtosis of -0.61. Single plant yield also varied from 71 to 77 gm, with an average of 74.50 gm in this generation. Skewness was calculated at -0.75, and kurtosis was 0.40.

Table 2: Estimation of skewness and kurtosis in the BC<sub>1</sub>F<sub>1</sub>, BC<sub>2</sub>F<sub>1</sub>, and BC<sub>2</sub>F<sub>2</sub> of SC11-2 × UMI 1230β1<sup>+</sup>

Traits	BC <sub>1</sub> F <sub>1</sub>		BC <sub>2</sub> F <sub>1</sub>		BC <sub>2</sub> F <sub>2</sub>	
	Skewness	Kurtosis	Skewness	Kurtosis	Skewness	Kurtosis
DT	0.07	-0.39	-1.10	-0.23	0.15	-0.28
DS	-0.33	-0.28	-1.28	0.01	-0.32	-0.36
PH	0.18	-0.89	-1.16	-0.18	0.69	-0.18
EH	0.26	-0.38	-1.12	0.16	1.04	0.76
TL	0.01	-0.39	-1.18	-0.05	-0.14	-0.70
NTB	-0.01	-0.76	-1.34	-0.03	1.10	1.16
LL	0.27	-0.59	-1.14	0.16	0.39	-0.49
LB	0.04	-0.62	-1.38	0.06	0.55	-0.02
CL	0.44	-0.60	-1.19	-0.13	0.44	-0.63
CG	-0.01	-0.49	-1.18	-0.05	0.02	-1.24
NKRC	0.14	-0.42	-1.43	-0.01	0.57	0.74
NKR	-0.03	0.21	-1.20	0.08	-0.20	-0.09
100KW	-0.22	-0.61	-1.17	-0.09	-0.15	-0.41
SPY	-0.75	0.40	-1.06	0.29	0.39	-0.07

DT- Days to tasseling, DS- Days to silking, PH- Plant height, EH- Ear height, TL- Tassel length, NTB- Number of tassel branches, 7LL- Leaf length, LB- Leaf breadth, CL- Cob length, CG- Cob girth, NKRC- Number of kernel rows per cob, NKR- Number of kernel rows, 100KW- 100 kernel weight, and SPY- Single plant yield

### BC<sub>2</sub>F<sub>1</sub> Generation

In BC<sub>2</sub>F<sub>1</sub>, plant height ranged from 162 cm to 178 cm, with a mean of 170.37 cm. The skewness calculated was -1.16, while

that of kurtosis was -0.18. Ear height also showed a wide range of variation from 54 cm to 70 cm. The average ear height recorded was 61.38 cm with skewness of -1.12 and kurtosis of 0.16. 100 kernel weight varied from 18 gm to 26 gm, averaging 22.01 gm. The calculated skewness was -1.17, and kurtosis was -0.09. A wide variation of 67 gm to 76 gm with an average of 70.95 gm was recorded for single plant yield. Skewness was recorded at -1.06 and kurtosis of 0.29.

### BC<sub>2</sub>F<sub>2</sub> Generation

In BC<sub>2</sub>F<sub>2</sub> generation, plant height varied from 175 cm to 191 cm with an average height of 181.03 cm. The skewness for plant height was 0.69, and kurtosis was 0.18. The ear height varied from 82 cm to 102 cm, with an average ear height of 87.59. Calculated skewness was 1.04, and that of kurtosis was 0.76. In this generation, weight of 100 kernels varied from 19 gm to 25 gm and had an average weight of 21.79 gm. Skewness for the trait was calculated to be -0.15, and kurtosis was -0.41. Single plant yield varied from 65 gm to 75 gm, and the average yield was recorded as 69.21 gm per plant. The skewness was 0.39, and kurtosis was -0.07. Cob length varied from 9.50 cm to 14.50 cm, averaging 11.51 cm. Cob length had a skewness of 0.44 and kurtosis of -0.63.

### DISCUSSION

Skewness and kurtosis are the descriptive statistics used to study the nature of gene action and the number of genes responsible for controlling the traits. Skewness defines the cluster of deviations across the central tendency. Skewness also describes the positive or negative extend of individuals in the population. Positive skewness is associated with complementary gene action, while negative skewness describes duplicate gene action. Kurtosis is the measure of peakedness over the population. Positive kurtosis indicates the presence of gene action, which is controlled by the lesser number of genes. Negative kurtosis indicates the absence of gene action and is controlled by many genes (Pooni *et al.*, 1977).

The backcrossed and selfed population showed a wide variation among the morphological and yield-related traits. The variations can be attributed to segregations of background alleles of the genes in consecutive generations. Positive skewness and platykurtic distribution were observed in the case of plant height and ear height, indicating that the genes were governed by dominant × dominant based complementary gene action and controlled by a large number of genes (Neelima *et al.*, 2020). The weight of kernels exhibited negatively skewed platykurtic distribution, which suggests that the genes show duplicate gene action controlled by a large number of genes. Single plant yield showed negative skewness and platykurtic distribution in the BC<sub>1</sub>F<sub>1</sub> generation. This suggests duplicate gene action controlled by many genes (Sarankumar *et al.*, 2019, Neelima *et al.*, 2020). Cob length is also governed by a large number of genes showing complimentary effects, which contradicts the results reported by Pukalenty *et al.* (2018). This difference can be attributed to the diverse background of the parents, sweet

corn, and normal maize used in the crossing programme. This study indicates that the traits controlled by complementary gene action have to be selected in the later generations. For traits controlled by duplicate gene action, selection should be practiced in the early generations of the breeding programme.

### CONCLUSION

Precise selection of morphological and yield traits is important for the success of plant breeding programmes. Statistical parameters like skewness and kurtosis explain the gene interaction and their number responsible for governing the traits. This study examined the frequency distribution and statistical analysis of morphological and yield-related traits in the backcrossed and selfed populations of SC11-2 × UM11230β1<sup>+</sup>. The study suggested that the plant height and single plant yield were governed by complimentary gene action of several genes. Cob length and kernel weight were determined by duplicate gene action of few genes—this facilitated understanding the selection criteria for these traits in breeding programmes.

### ACKNOWLEDGMENT

Financial support from the Department of Biotechnology (DBT), Government of India (GOI), through the project entitled “Incorporation of *crtRBI* Allele into sweet corn inbreds and north eastern landraces for development of biofortified sweet corn” (BT/PR42333/NER/95/1866/2021 dt. 18.2.2022) is acknowledged. The funders had no role in the work design, data collection, and analysis, or decision and preparation of the manuscript.

### REFERENCES

- Chandana, A. S., John, J. A., Ravikesavan, R., & Uma, D. (2018). Genetic variability and correlation studies of yield and phytic acid in F<sub>2</sub> populations of maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, 9(4), 1469-1475. <https://doi.org/10.5958/0975-928x.2018.00182.5>
- Fisher, R. A., Immer, F. R., & Tedin, G. (1932). The genetical interpretation of statistics of the third degree in the study of quantitative inheritance. *Genetics*, 17(2), 107-124. <https://doi.org/10.1093/genetics/17.2.107>
- Gravetter, F. J., Wallnau, L. B., Forzano, L. A. B., & Witnauer, J. E. (2020). *Essentials of statistics for the behavioral sciences*. (10<sup>th</sup> ed.). Massachusetts, US: Cengage Learning.
- Kapur, S. K. (1980). *Elements of Practical Statistics*. New Delhi, India: Oxford and IBH Publishing Co. Pvt. Ltd.
- Lal, M., & Singh, D. (2014). Studies of variability using morphological and quality traits in quality protein maize (*Zea mays* L.). *Electronic Journal of Plant Breeding*, 5(3), 526-530.
- Mehta, B., Hossain, F., Muthusamy, V., Baveja, A., Zunjare, R., Jha, S. K., & Gupta, H. S. (2017). Microsatellite-based genetic diversity analyses of sugary1-, shrunken2- and double mutant-sweet corn inbreds for their utilization in breeding programme. *Physiology and Molecular Biology of Plants*, 23, 411-420. <https://doi.org/10.1007/s12298-017-0431-1>
- Nagalakshmi, R. M., Ravikesavan, R., Paraniharan, V., Manivannan, N., Firoz, H., Vignesh, M., & Senthil, N. (2018). Frequency distribution analysis in maize (*Zea mays* L.) backcross populations. *Research Journal of Agricultural Sciences*, 9(6), 1270-1274.
- Neelima, C., Sarankumar, C., Sudha, M., Ganesan, K. N., Ravikesavan, R., & Senthil, N. (2020). Estimation of variability, heritability, genetic advance and assessment of frequency distribution for morphological traits in intercross population of maize. *Electronic Journal of Plant Breeding*, 11(2), 574-580.
- Pooni, H. S., Jinks, J. L., & Cornish, M. A. (1977). The causes and

- consequences of non-normality in predicting the properties of recombinant inbred lines. *Heredity*, *38*, 329-338. <https://doi.org/10.1038/hdy.1977.95>
- Pukalenty, B., Manickam, D., Adhimoolum, K., Arunachalam, K., Ganapathyswamy, H., Chocklingam, V., & Natesan, S. (2018). Studies on Frequency Distribution of Backcross Populations in Maize (*Zea mays* L.). *Research Journal of Agricultural Sciences*, *9*(6), 1340-1344.
- Rani, C., Anandakumar, C., Raveendran, M., Subramanian, K., & Robin. (2016). Genetic variability studies and multivariate analysis in F2 segregating populations involving medicinal rice (*Oryza sativa* L.) Cultivar Kavuni. *International Journal of Agriculture Sciences*, *8*(35), 1733-1735.
- Revilla, P., Anibas, C. M., & Tracy, W. F. (2021). Sweet corn research around the world 2015–2020. *Agronomy*, *11*(3), 534. <https://doi.org/10.3390/agronomy11030534>
- Robson, D. S. (1956). Applications of the  $k_x$  statistic to genetic variance component analyses. *Agronomy*, *12*(4), 433-444. <https://doi.org/10.2307/3001682>
- Sarankumar, C., Dhasarathan, M., Kavithamani, D., Vanniarajan, C., Kokiladevi, E., Ravikesavan, R., & Senthil, N. (2019). Assessment of genetic variability, heritability and genetic advance in backcross population of BC1F1, BC2F1 and BC2F2 in maize. *Electronic Journal of Plant Breeding*, *10*(2), 576-584. <https://doi.org/10.5958/0975-928X.2019.00073.5>
- Singh, I., Langyan, S., & Yadava, P. (2014). Sweet corn and corn-based sweeteners. *Sugar tech*, *16*, 144-149. <https://doi.org/10.1007/s12355-014-0305-6>