KnE Life Sciences
DonAgro
International research conference on Challenges and Advances in Farming, Food Manufacturing, Agricultural Research and Education
Volume 2021

Conference Paper

Comprehensive Assessment of Promising Potato Hybrids of Breeding VSC RAS

Fatima Gerieva[1,2], Viktoria Biryukova[3], and Irina Gazdanova[1]

[1] Vladikavkaz Scientific Center of the Russian Academy of Sciences RAS-Alania, Vladikavkaz, Russia
[2]North Caucasian Research Institute of Mining and Piedmont Agriculture - a branch of Vladikavkaz Scientific Center of the Russian Academy of Sciences, RSA-Alania, Mikhailovskoe, Russia
[3]A.G. Lorkh All-Russian Scientific Research Institute of Potato Farming, Moscow region 140051, p. Kraskovo, Russia

ORCID:
Fatima Gerieva: http://orcid.org/0000-0002-7704-5966

Corresponding Author:
Irina Gazdanova
Gazdanovaira2020@gmail.com

Published: 5 April 2021

Publishing services provided by Knowledge E

Selection and Peer-review under the responsibility of the DonAgro Conference Committee.

Abstract

Using the traditional and marker-assisted selection methods, a comprehensive assessment of promising hybrids from the collection of the All-Russian Scientific Center was carried out. The assessment was conducted in 2018–2019 in the Republic of North Ossetia-Alania. As a result of molecular genetic analysis, hybrids were found with complex resistance to potato nematode, virus Y and X viruses - 2 / V, 5 / V, 6 / V, 17 / V, 40 / V, 43 / V, 46 / V, 54 / V, 124 / V, 9 / VI, 22a / VI, 35 / VI, 130 / VI, 71 / VII and 118 / VIII. Use of these selected forms allows optimal protection of potatoes, limitation of the spread of pathogens and prevention of the emergence of more aggressive pathotypes (races and strains). The hybrids with resistance to potato virus Y (with the presence of R-gene markers - 1/I, 3/I, 10/I, 13/I, 11/II, 15/III, 2/V, 5/V, 6/V, 7/V, 10/V/1140, 17/V, 40/V, 43/V, 46/V, 54/V, 124/V, 9/VI, 22a/VI, 35/VI, 100/VI, 130/VI, 71/VII) are of interest for practical breeding, as well as the hybrids with resistance to *Phytophthora infestans* such as 15/III, 119/IX and the hybrids 15 / III, 35 / VI, 130 / VI and 71 / VII, which have high marketable yield and weight of tuber.

Keywords: potato, interspecific hybrids, marker-assisted breeding, resistance genes

1. Introduction

In recent years in connection with the problem of global climate change, the role of “adaptive” breeding, based on the use of the natural potential of plant organisms to adapt to survival and reproduction in rapidly changing environmental conditions, has significantly increased. The increase in resistance to biotic and abiotic stresses is one of the important areas of plant breeding. The creation of potato varieties with high adaptive potential is especially important for regions with a wide variety of agro-climatic conditions, such as the Republic of North Ossetia-Alania. Testing genotypes in such a

How to cite this article: Fatima Gerieva, Viktoria Biryukova, and Irina Gazdanova, (2021), “Comprehensive Assessment of Promising Potato Hybrids of Breeding VSC RAS” in *International research conference on Challenges and Advances in Farming, Food Manufacturing, Agricultural Research and Education*, KnE Life Sciences, pages 826–836. DOI 10.18502/kls.v0i0.9020

variety of soil and climatic conditions makes it possible to select promising hybrids or varieties of potatoes that are distinguished by a wide range of adaptive ability to growing conditions, high yield potential and high product quality.

In potato, for the control of resistance introgression, as well as for the simultaneous selection of genotypes with several traits, along with traditional methods, molecular markers linked to R-genes (resistance genes) are widely used [1]. Previous studies have shown that marker-assisted breeding of the main dominant genes for resistance to pathogens is effective for combining these traits in breeding lines and potato varieties [2].

Research purpose: the assessment of promising potato hybrids from the collection of the All-Russian Scientific Center using traditional laboratory-field and modern marker-assisted breeding methods

2. Materials and Methods

1. Plant material. The authors studied 44 promising potato hybrids from 12 hybrid combinations: Kolobok x Valentina, Tuleevsky x 128-6, Sarpo Mira x Russian souvenir, Roko x 88/16/20, Alwara x Russian souvenir, Meteor x Violet, Prestige x Sarpo Mira, Nikulinsky x Ausonia, 22.7.26 x Zhukovsky early, Sierra x 99.14 / 99, Sante x Peresvet, Volzhanin x Piedmont. The studies were carried out in the Piedmont zone of North Ossetia at the experimental base of North Caucasian Research Institute of Mining and Piedmont Agriculture of Vladikavkaz Scientific Center of the Russian Academy of Sciences (Prigorodny district, North Ossetia-Alania) in 2018-2019, differing in meteorological conditions.

2018 had a more favorable hydrothermal regime during the growing season at moderate temperatures with sufficient moisture. 2019 year was the most unfavorable, with sharp fluctuations in temperature and excessive precipitation during the period of formation of tubers.

Planting was carried out in the second decade of April with a planting scheme of 70-35 cm. The total area of the plot was 70 m^2; the accounting area was 20 m^2 with 4 times repetition. The soil was represented by leached chernozem with underlying gravel.

2. Laboratory and field assessment. Promising hybrids were studied in laboratory-field conditions on the basis of the All-Russian Scientific Center of the Russian Academy of Sciences for the main economically valuable traits in accordance with the “Methodological recommendations on the technology of the potato breeding process” [3]. The hybrids were assessed according to the morphological characteristics of the tops and tubers, the structure of the yield on a 9-point scale and visual resistance to diseases under conditions of a natural infectious background.

3. Molecular genetic analysis. Screening of promising potato hybrids for the presence of markers of genes for resistance to pathogens was carried out on the basis of Vladikavkaz Scientific Center using an instrumental and hardware line for PCR analysis.

Genomic DNA was determined according to a protocol based on the CTAB method with modifications [4]. Light sprouts of tubers of interspecific hybrids (200–250 mg) were homogenized with 1 ml of 2×-CTAB buffer containing 2% (v / v) 2-mercaptoethanol [5]. For molecular screening of interspecific hybrids, DNA markers were used: resistance to Y potato virus - STS marker YES3-3A closely linked to Ry_{sto} gene [5] and SCAR marker RYSC3 of the Ry_{adg} gene [6], as well as STS marker Ry186 of Ry_{chc} gene [7]; resistance to the golden potato nematode Globodera rostochiensis (Woll.) Behrens - SCAR markers of the H1 gene - TG 689 [8], 57 R [9], N 146 and N 195 [7]; STS marker Gro1-4-1 of the Gro1-4 gene [10]; resistance to the pale potato nematode *Globodera pallida (Stone) Behrens* - STS marker *Gpa2-2* of *Gpa2* gene [10]; resistance to potato virus X - the STS PVX marker of the Rx1 gene [7]. DNA amplification was performed in a PTC-100 thermal cycler (MJ Research, USA).

3. Results and Discussion

Molecular genetic analysis. 35 promising hybrids with the presence of molecular markers were identified out of 44. Among the tested genotypes, potato hybrids with markers TG 689, 57R, N146, N195, Gro1-4-1 and YES3-3A, obtained with the participation of varieties Alwara (Germany), Ausonia (Holland), Roko (Holland), Sante (Holland), early Zhukovsky, Meteor, Kolobok (table 1) prevailed. The *H1* gene is inherited in hybrids through parental forms – the varieties resistant to golden potato nematode - Ausonia, Sante, early Zhukovsky. The Roko variety is the source of three R-genes and the Meteor and Alwara varieties are the source of four R-genes, respectively (table 1). H1 gene markers were detected in 18 hybrids, and the Gro1-4 gene marker was detected in 11 hybrids. In hybrids 50 / X and 65 / IV, N195 marker of the H1 gene was absent (Fig). The presence of “false negative” results (no PCR product) for N195 can possibly be explained by incomplete linkage between the molecular marker loci and H1 gene.

Since the optimal strategy for the creation of potato varieties with long-term resistance to the potato cyst nematode is “pyramidation” or combining several R-genes in one genotype. Potato samples with a combination of molecular markers are of particular

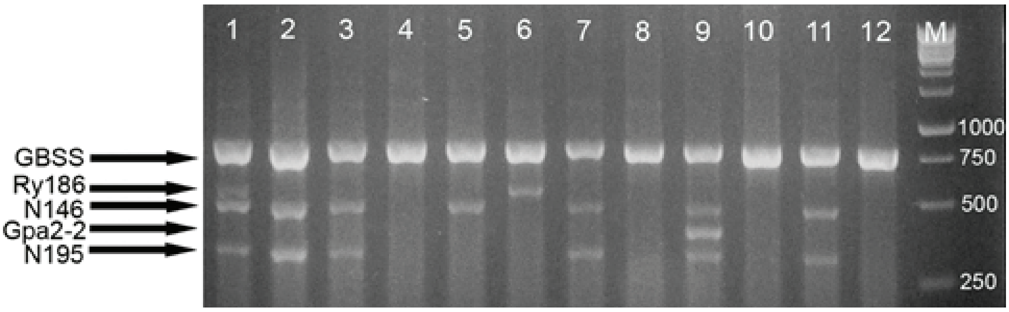

Figure 1: Multiplex PCR analysis for the presence of GBSS, Ry186, N146, Gpa2-2, N195 markers. 1 - potato variety Bashkir (as a positive control, which contains markers Ry186, N146, N195), 2 - variety Ausonia (as a positive control, which contains markers N146, N195), 3 - 124 / V, 4 - 6 / V, 5 - 65 / IV, 6 - 119 / IX, 7 - 17 / V, 8 - 22a / II, 9 - 118 / VIII, 10 - 20 / XI, 11 - 50 / X, 12 - 116 / XII, M - DNA marker - GeneRuler 1 kb DNA Ladder, ready-to-use (Thermo Scientific ^{TM}).

interest for further breeding. As a result of marker-assisted selection, markers of two genes *H1* and *Gro1-4* were identified in hybrids - 4 / V, 43 / V, 46 / V, 52 / V, 54 / V, 124 / V, and the combination of H1 and Gpa2 gene markers - in hybrids - 71 / VII, 118 / VIII, CP 154 / VIII, which are sources of resistance to the pathotypes of both types of potato cyst nematode.

Molecular marker RYSC3 of the Ry$_{adg}$ gene was found in potato hybrid 11 / II, in the origin of which the highly fertile form 128-6 is involved, combining extreme resistance to Y potato virus with field resistance to late blight. Since the optimal strategy for the creation of potato varieties with long-term resistance to potato cyst nematode is “pyramidation” or combination of several R-genes in one genotype, potato samples with a combination of molecular markers are of particular interest for further breeding. As a result of marker-assisted selection, the markers of two genes H1 and Gro1-4 were found in hybrids - 4 / V, 43 / V, 46 / V, 52 / V, 54 / V, 124 / V, and the combination of markers of H1 and Gpa2 genes - in hybrids - 71 / VII, 118 / VIII, CP 154 / VIII, which were the sources of resistance to pathotypes of both types of potato cyst nematode.

Molecular marker RYSC3 of *Ry*$_{adg}$ gene was found in potato hybrid 11 / II, in the origin of which the highly fertile form 128-6 was involved, combining extreme resistance to Y potato virus of with field resistance to late blight.

Promising potato hybrids, which contain the YES3-3A marker of the *Ry*$_{sto}$ gene linked to CMS, were obtained on the basis of the varieties Alwara, Roko, Meteor and Kolobok – the derivatives of *S. stoloniferum* Schltdl. The *Ry*$_{chc}$ gene marker was in the hybrids 15 / III, 119 / IX, obtained with the participation of the Sarpo Mira cultivar (Hungary), in which Ry186 was identified earlier [11]. The PVX marker of the Rx1 gene in potato hybrids 9 / VI, 71 / VII, 118 / VIII, 130 / VI was detected together with the Gpa2-2 marker of the

Gpa2 gene, which confirmed their joint introgression from a single source - sample CPC 1673-20 *S. andigenum* Juz. et Buk.

As a result of marker-assisted selection, the forms with a combination of several R-genes - 2 / V, 5 / V, 6 / V, 17 / V, 40 / V, 43 / V, 46 / V, 54 / V, 124 / V, 9 / VI, 22a / VI, 35 / VI, 130 / VI, 71 / VII, 118 / VIII were chosen among promising hybrids from the collection of the All-Russian Scientific Center which were the sources of group and complex resistance to potato cyst nematode, Y and X potato viruses and represented interest for targeted breeding of potato varieties with long-term protection against pathogens.

Table 1: Molecular markers in promising potato hybrids

Variety / hybrid	Origin	Presence of DNA markers (marker / gene)									
		TG 689	57R	N 195	N 146	Gro1-4	Gpa 2-2	YES3-3A	RYSC3	Ry 186	PVX
		resistance to PCN						resistance to PTY and PVX			
Alwara	290/76 x Desiree	0	0	0	0	**1**	**1**	**1**	0	0	**1**
Roko	Alwara x MA 81-536	**1**	**1**	**1**	**1**	**1**	0	**1**	0	0	0
Meteor	84.19⁄44 x Shurminsky -2	**1**	**1**	**1**	**1**	0	**1**	**1**	0	0	**1**
1/I	Kolobok x Valentine	0	0	0	0	0	0	**1**	0	0	0
3/I	Kolobok x Valentine	0	0	0	0	0	0	**1**	0	0	0
10/I	Kolobok x Valentine	0	0	0	0	0	0	**1**	0	0	0
13/I	Kolobok x Valentine	0	0	0	0	0	0	**1**	0	0	0
11/II	Tulevsky x 128-6	0	0	0	0	0	0	0	**1**	0	0
15/III	Sarpo Mira x Russian souvenir	0	0	0	0	0	0	0	0	**1**	0
44/IV	Nikulinsky x Ausonia	**1**	**1**	**1**	**1**	0	0	0	0	0	0
49/IV	Nikulinsky x Ausonia	**1**	**1**	**1**	**1**	0	0	0	0	0	0
50/IV	Nikulinsky x Ausonia	**1**	**1**	**1**	**1**	0	0	0	0	0	0
65/IV	Nikulinsky x Ausonia	**1**	**1**	**0**	**1**	0	0	0	0	0	0
2/V	Roko x 88.16/20	**1**	**1**	**1**	**1**	0	0	**1**	0	0	0
4/V	Roko x 88.16/20	**1**	**1**	**1**	**1**	**1**	0	0	0	0	0
5/V	Roko x 88.16/20	**1**	**1**	**1**	**1**	0	0	**1**	0	0	0
6/V	Roko x 88.16/20	0	0	0	0	**1**	0	**1**	0	0	0
7/V	Roko x 88.16/20	0	0	0	0	0	0	**1**	0	0	0
10/V/1140	Roko x 88.16/20	0	0	0	0	0	0	**1**	0	0	0
17/V	Roko x 88.16/20	**1**	**1**	**1**	**1**	0	0	**1**	0	0	0
40/V	Roko x 88.16/20	0	0	0	0	**1**	0	**1**	0	0	0
43/V	Roko x 88.16/20	**1**	**1**	**1**	**1**	**1**	0	**1**	0	0	0
46/V	Roko x 88.16/20	**1**	**1**	**1**	**1**	**1**	0	**1**	0	0	0
47/V	Roko x 88.16/20	0	0	0	0	**1**	0	0	0	0	0
52/V	Roko x 88.16/20	**1**	**1**	**1**	**1**	**1**	0	0	0	0	0

Variety / hybrid	Origin	Presence of DNA markers (marker / gene)									
		TG 689	57R	N 195	N 146	Gro1-4	Gpa 2-2	YES3-3A	RYSC3	Ry 186	PVX
		resistance to PCN						resistance to PTY and PVX			
54/V	Roko x 88.16/20	**1**	**1**	**1**	**1**	**1**	0	**1**	0	0	0
124/V	Roko x 88.16/20	**1**	**1**	**1**	**1**	**1**	0	**1**	0	0	0
9/VI	Alwara x Russian souvenir	0	0	0	0	0	**1**	**1**	0	0	**1**
22a/VI	Alwara x Russian souvenir	0	0	0	0	**1**	0	**1**	0	0	0
35/VI	Alwara x Russian souvenir	0	0	0	0	**1**	0	**1**	0	0	0
100/VI	Alwara x Russian souvenir	0	0	0	0	0	0	**1**	0	0	0
130/VI	Alwara x Russian souvenir	0	0	0	0	0	**1**	**1**	0	0	**1**
71/VII	Meteor x Violet	**1**	**1**	**1**	**1**	0	**1**	**1**	0	0	**1**
118/VIII	22.7.26 x early Zhukovsky	**1**	**1**	**1**	**1**	0	**1**	0	0	0	**1**
CP 154/VIII	22.7.26 x early Zhukovsky	**1**	**1**	**1**	**1**	0	**1**	0	0	0	0
119/IX	Prestige x Sarpo Mira	**0**	**0**	**0**	**0**	0	**0**	0	0	1	0
K19/X	Sante x Peresvet	**1**	**1**	**1**	**1**	0	**0**	0	0	0	0
50/X	Sante x Peresvet	**1**	**1**	**0**	**1**	0	**0**	0	0	0	0

*Legend: PCN – potato cyst nematode, YBK – potato virys X Y, PVX – potato virys X, 1/0 – presence / absence of a marker.

TABLE 2: Characteristics of promising hybrids in terms of resistance to diseases and pests (Piedmont zone, average for 2017–2019)

Variety / hybrid	Disease resistance, score (visual assessment in the field)				
	To viruses	to phytophthora	to alternaria	to rhizoctonia	to common scab
Volzhanin (st)	7	7	8	8	8
Predgorny (st)	9	7_-8	9	9	8
1/I	8	7,5-6,5	8	8	8
3/I	8	7,5-6,5	9	9	8
10/I	8	7,5-6,5	8	9	8
13/I	8	7,5-6,5	8	9	8
11/II	9	8,0-6,5	9	9	8
15/III	8	8-9	8	9	8
44/IV	7-9	7,0-5,0	8	8	8
49/IV	7-9	7,0-5,0	9	9	7
50/IV	7-9	7,0-5,0	8	7	7
65/IV	7-9	7,0-5,0	9	9	7
2/V	9	8,5-7,5	9	9	8
4/V	9	8,5-7,5	9	9	8
5/V	9	8,5-7,5	9	9	8
6/V	9	8,5-7,5	9	8	8
7/V	9	8,5-7,5	9	9	8
10/V/1140	9	8,5-7,5	8	9	8
17/V	9	8,5-7,5	9	9	8
40/V	9	8,5-7,5	9	8	8
43/V	8	8,5-7,5	8	8	8
46/V	8	8,5-7,5	8	8	8
47/V	9	8,5-7,5	9	8	7
52/V	8	8,5-7,5	8	8	7
54/V	8	8,5-7,5	8	8	7
124/V	9	8,5-7,5	9	9	8
9/VI	9	8,0-7,5	9	9	8
22a/VI	8	8,0-7,5	8	7	8
35/VI	9	8,0-7,5	9	9	8
100/VI	8	8,0-7,5	8	7	8
130/VI	8	8,0-7,5	8	8	8
71/VII	9	7,0-5,0	9	9	8
118/VIII	7-9	7,5-6,5	8	8	8
CP 154/VIII	7-9	7,5-6,5	8	8	8
119/IX	9	8-9	8	8	7
K19/X	8	8,0-6,0	9	9	8
50/X	8	8,0-6,0	8	9	8

Table 3: Productivity of promising hybrids in the forest-steppe zone of North Ossetia-Alania (average for 2018-2019)

Hybrid	Number of tubers, pcs / bush		Tuber weight, g / bush		Average weight of marketable tuber, g
	marketable	Non-marketable	marketable	Non-marketable	
Volzhanin (st)	6	2	460	50	77
Predgorny (st)	6	8	408	280	68
1/I	8	5	758	148	95
3/I	8	2	688	74	86
10/I	6	4	654	107	109
13/I	7	4	600	136	85
11/II	6	10	920	68	115
15/III	13	4	1321	124	102
44/IV	6	10	400	191	67
49/IV	9	2	1040	49	115
50/IV	6	3	517	99	86
65/IV	6	3	681	87	114
2/V	7	7	581	193	83
4/V	8	1	808	50	101
5/V	7	3	730	76	104
6/V	10	10	900	324	90
7/V	4	7	347	215	87
10/V/1140	9	11	720	269	80
17/V	6	5	523	173	87
40/V	8	2	944	77	118
43/V	7	1	719	28	103
46/V	9	6	847	156	94
47/V	8	7	588	106	74
52/V	9	4	847	147	94
54/V	7	1	744	61	106
124/V	9	4	1125	127	125
9/VI	6	1	749	45	125
22a/VI	8	4	1042	105	130
35/VI	12	4	1343	108	112
100/VI	7	2	850	69	120
130/VI	13	4	1397	118	107
71/VII	12	4	1305	109	132
118/VIII	9	2	1201	39	133
CP 154/VIII	7	2	1233	69	176
119/IX	8	2	944	77	118
K19/X	7	1	719	28	103
50/X	8	1	808	50	101

The assessment of resistance to diseases and pests. According to the results of visual assessment, most of the promising hybrids selected according to the results of marker analysis are characterized by high field resistance to viral diseases (7-9 points), Alternaria (8-9 points), rhizoctonia (8-9 points) (Table 2).

The assessment of the crop structure. The yield accounting (Table 3) of the studied hybrids was carried out in the forest-steppe zone of the Republic of North Ossetia-Alania. During the analysis of the data on the structure of the yield, one of the most important indicators is the number of marketable tubers, the number of which is 8-9 pieces per bush in average. In the conditions of 2018-2019 according to this indicator, promising hybrids were identified - 15 / III, 6 / V, 35 / VI, 130 / VI, 71 / VII, in which 10-13 tubers per bush were found in comparison with the standards of Predgorny (6 tubers) and Volzhanin (6 tubers). In terms of the mass of marketable tuber, the hybrids, with the exception of 44 / IV, significantly exceed the standards. According to commercial productivity, 9 hybrids were determined - 15 / III, 49 / IV, 124 / V, 22a / VI, 35 / VI, 130 / VI, 71 / VII, 118 / VII, CP154 / VIII, the mass of commercial tubers in which exceeded 1000 g / bush.

According to two indicators (the number of commercial tubers and commercial productivity) the hybrids showed a significant excess compared to standard varieties - 15 / III, 35 / VI, 130 / VI, 71 / VII, according to the average weight of commercial tubers - 22a / VI, 71 / VII, 118 / VIII, CP 154 / VIII.

4. Conclusion

A comprehensive assessment of promising potato hybrids from the collection of the All-Russian Scientific Center of the Russian Academy of Sciences, carried out in the conditions of the Republic of North Ossetia-Alania, using traditional and marker-assisted breeding methods, allowed determining the samples with a combination of R-genes for resistance to Y and X potato viruses and potato cyst nematode, characterized by a high commercial yield and the mass of marketable tuber.

Conflict of Interest

The authors have no conflicts of interest regarding the presented results.

Acknowledgments

This research was performed with the support of the Ministry of Science and Education of the Russian Federation.

References

[1] Barone, A. (2004). Molecular Marker-Assisted Selection for Potato Breeding. *American Journal of Potato Research,* vol. 81, pp. 111-117.

[2] Gebhardt, C., *et al*. (2006). Marker-Assisted Combination of Major Genes for Pathogen Resistance in Potato. *Theoretical and Applied Genetics*, vol. 112, pp. 1458-1464.

[3] Simakov, E. A., Sklyarova, N. P. and Yashina, I. M. (2006). Methodical Instructions on the Technology of the Potato Breeding Process. Moscow: Editorial Office of the Journal, p. 72.

[4] Sagai-Maroof, M. A., *et al*. (1984). Ribosomal DNA Spacer-Length Polymorphism in Barley: Mendelian Inheritance, Chromosomal Location, and Population Dynamics. *Proceedings of the National Academy of Sciences,* vol. 81, pp. 8014-8018.

[5] Song, Y. S. and Schwarzfischer, A. (2008). Development of STS Markers for Selection of Extreme Resistance (Rysto) to PVY and Maternal Pedigree Analysis of Extremely Resistant Cultivars. *American Journal of Potato Research.,* vol. 85, pp. 159-170.

[6] Kasai, K., *et al*. (2000). Development of SCAR Markers to the PVY Resistance Gene Ryadg Based on a Common Feature of Plant Disease Resistance Genes. *Genome,* vol. 43, pp. 1-8.

[7] Mori, K., *et al*. (2011). Development of a Multiplex PCR Method for Simultaneous Detection of Diagnostic DNA Markers of Five Disease and Pest Resistance Genes in Potato. *Euphytica,* vol. 180, pp. 347-355.

[8] Galek, R., *et al*. (2011). Application of DNA Markers Linked to the Potato H1 Gene Conferring Resistance to Pathotype Ro1 of Globodera Rostochiensis. *Journal of Applied Genetics*, vol. 52, pp. 407-411.

[9] Schultz, L., *et al*. (2012). Evaluation and Implementation of a Potential Diagnostic Molecular Marker for H1-Conferred Potato Cyst Nematode Resistance in Potato (Solanum tuberosum L). *Plant Breed*, vol. 131, pp. 315-321.

[10] Asano, K. and Tamiya, S. (2013). Development of Rapid Estimation Method for Allele Number of H1 and Selection of Multiplex Lines in Potato. *Ikushugaku kenkyu (Breed. Res.)*, vol. 15, issue 1, p. 53.

[11] Tomczynska, I., *et al*. (2014). Hypersensitive Response to Potato virus Y in Potato Cultivar Sarpo Mira is Conferred by the Ny-Smira Gene Located on the Long Arm of Chromosome IX. *Molecular Breeding*, vol. 34, issue 2, pp. 471-480.