N.I.Vavilov Research Institute of Plant Industry

Sunflower genetic resources at VIR

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Status of oil and fibre crop collections of the N.I. Vavilov Institute of Plant Industry (VIR)

№ п/п	Crops	Number of accessions			
		Total	Permanent Catalogue	Temporary Catalogue	
1	Sunflower	2800	2220	580	
2	Flax	6120	5772	348	
3	Groundnut, Sesame, Safflower	3778	3580	198	
4	Rapeseed, Turnip	1484	1459	25	
5	Mustard	1523	1512	11	
6	Cotton	6495	6360	135	
7	Poppy	1846	888	958	
8	Castor	1176	1176	-	
9	Hemp and other fibre crops	1584	1584	-	
10	Other oil crops	582	565	17	
11	Kok-saghyz	128	128	-	
	Total	27517	25244	2273	

Strategy of working with Genetic Resourses of Sunflower

The sunflower collection at VIR numbers 2230 accessions of cultivated sunflower and 580 wild accessions belonging to 24 species.

The accessions are maintained in the field and kipping at storage active (+4° C) and long-term (-10° C) collections

The study of sunflower genetic diversity in the field and laboratory

Disease Resistance

Confection forms

CMS & Rf Lines

Interspecific hybrids

Genetic and molecular studies,
Genetic collection

Breeding

VIR Sunflower Collection at the Kuban Experiment Station

The accessions with different plant height

Plant height 180-220 cm

Variety Peredovik

10 dwarf lines below 70 cm

45 tall accessions above 350 cm

Lines with plant height 80-200 cm

Line VIR 434

Line VIR 358

Variety Gigant k 549

Lines with different shape and colour of leaf blade

Variety Peredovik

Line VIR 130 *vs*

κ- 2239, Bulgaria

Line VIR 340 y

Line VIR 283

Line from hybrid
NS 310, Rumania

κ- 2354, Canada

Line VIR 253
Gr 1 *Gr* 2

Lines with different colour and shape of the ray and tubular flowers

Variety Peredovik

Line VIR 456
genes *Bf1 Bf2*

Line VIR 446
*Genes Cfh*1*Cfh2*

Line VIR 536
gene *bl*

Line VIR 445
gene *A1A2*

Line VIR 531
gene *la*

Line VIR 905

Line VIR 728
gene *wp*

Donskoi krupnoplodnyi

40 large-fruited forms

k-2215, Russia

k-1589, Armenia

k-3578, Ukraine

k-2044, France

k-2676, Ukraine

k-3633, China

k-2835, Russia

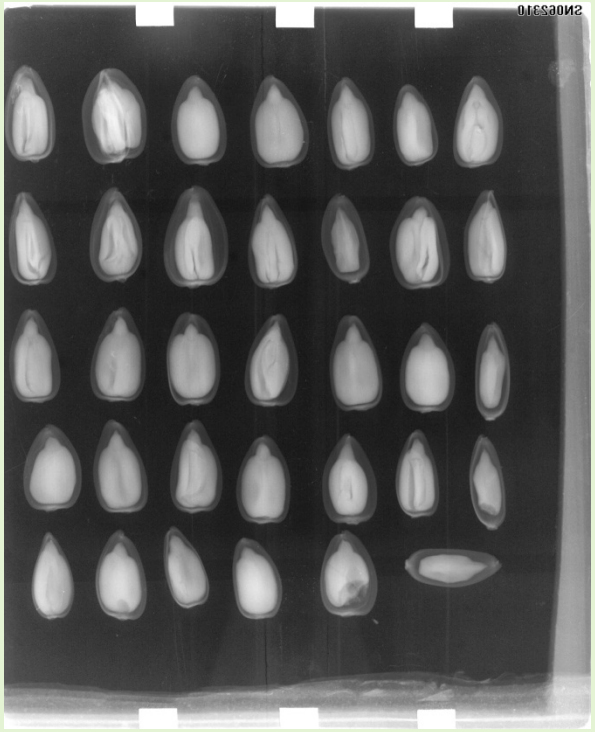
k-3619, USA

k-1898, Russia

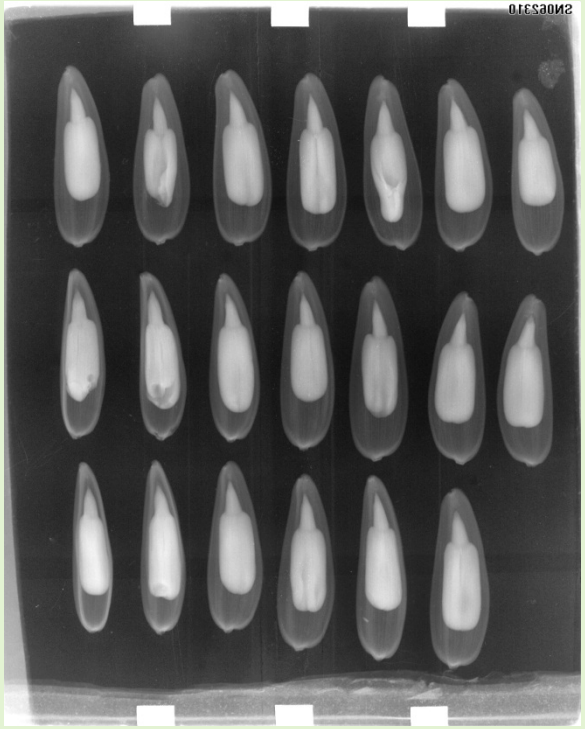
Characterization of confectionary accessions

п/п	№ каталога ВИР	Название	Происхождение	Масса 1000 семян			
				годы			Среднее
				2008	2009	2010	
1	1589	Гяр-гяр	Армения	131	95	110	112±10,4
2	2006	Местный	Приморский край	122	96	91	103±9,6
3	2642	Стадион	Болгария	101	103	97	100±1,7
4	2843	Местный	Приморский край	96	100	89	95±3,2
5	2832	Местный	Приморский край	112	82	-	97±15,0
6	3426	СПК	Россия, ВНИИМК	113	114	118	115±1,5
7	3583	Местный	Аргентина	138	100	95	111±13,5
8	3516	Запорожский кондитерский	Украина	149	110	113	124±12,5
9	3573	Бородинский	Россия	134	108	133	125±8,5
10	3586	Хейлундзянский	Китай	152	135	132	139±6,2
11	3633	с.03002	Китай	247	171	133	183±33,5
12	3683	ВИР 846	США	171	140	138	149±10,6

Fluoroscopy sunflower achenes



Seeds of cv. Rodnik



Seeds of cv. Heylundzyanski

Characterization of confectionary accessions

№	Accenumb	Accename	Country of origin	Vegetation period, days*	Yield per plant, g*	1000-seed weight, g*	Height, cm*	Successibility to phomopsis, %*	Occurrence of the *Rf1* gene, %
1	2835	Local variety	Russia	84	20	112	140	0	0
2	3516	Zaporozhskii konditerskii	Russia	87	83	113	209	12	0
3	3510	Donskoi krupnoplodnyi	Russia	102	109	114	212	0	50
4	3526	Lakomka	Russia	96	116	123	196	10	33,3
5	3573	Borodinskii	Russia	100	50	133	147	18	50
6	3633	03002	China	114	20	133	261	9	90,9
7	3619	Local variety	USA	96	40	138	116	0	90,9
8	3426	Konditerskii	Russia	92	44	161	166	6	0
9	3553	Master	Russia	99	82	71	203	4	-

Resistance to downy mildew (*Plasmopara halstedii* (Farl.) Berl. and de Toni)

- **13** lines with genes for resistance to one race 330 (RHA 297, 299, Do 164, k 3258(USA), Line VIR: 260, 263, 369,370-378 Odessky 113, Line X: 2000, 2004, 2009)
- **1** variety (Lider) with genes for resistance to one race 710
- **1** sample (k 2315) with genes for resistance to one race 730

- **19** lines with genes for resistance to two races (330 and 730)
- **12** lines with genes for resistance to three races (330, 710 and 730) - kk: 2644, Spain; 2793, Russia; 3362, Australia; 3532, USA; line VIR: 247, 387, 435, 581, 632 , 635, 702; RHA 278; *H. annuus* x *H. giganteus*

Ivebor M.V., Antonova T.S. Population of sunflower downy mildew pathogen in Northen Caucasus // Modern Problems of Scientific Support for Sunflower Production. Proc. Int. Sci. Practical Conf., Krasnodar: VNIIMK, 2006

Появление новых патогенов

Фомопсис – возбудитель *Phomopsis helianthi* Munt.

Источники устойчивости: *Helianthus giganteus, H. mollis, H.salicifolius, H.tuberosus*

Линия ВИР 130

Межвидовые гибриды и линии из них

62 accessions resistant to *Phomopsis helianthi* Munt.-Cvet.

Подготовлены семена для питомника источников устойчивости к фомопсису образцов (в количестве 27), выделенных в условиях естественной эпифитотии этого патогена. В состав этого питомника включены 5 образцов, показывающих стабильную устойчивость к фомопсису в течение многих лет: сорт Зеленка (к-552); линии: ВИР 365 (к-3326), ВИР 249 (к-3469), ВИР 449 (к-3527), ВИР 448 (к-3487). По результатам изучения 2006 года включены выделившиеся по устойчивости межвидовой гибрид ВИР 114 × H.gigantheus, 9 сублиний ВИР 130 и 11 линий французской селекции: и-598115, и-598059, L 244/3, L 261/1, L 265/1, L 270/1, L 342/1, L 350/1, L 369/1, L 368/1, L 227/1.

В качестве контроля высеваются 3 сильно поражаемых образца: к-358 из Краснодарского края, к-2019 их Хабаровского края и линия селекции ВНИИМК ВК-571 (к-3511).

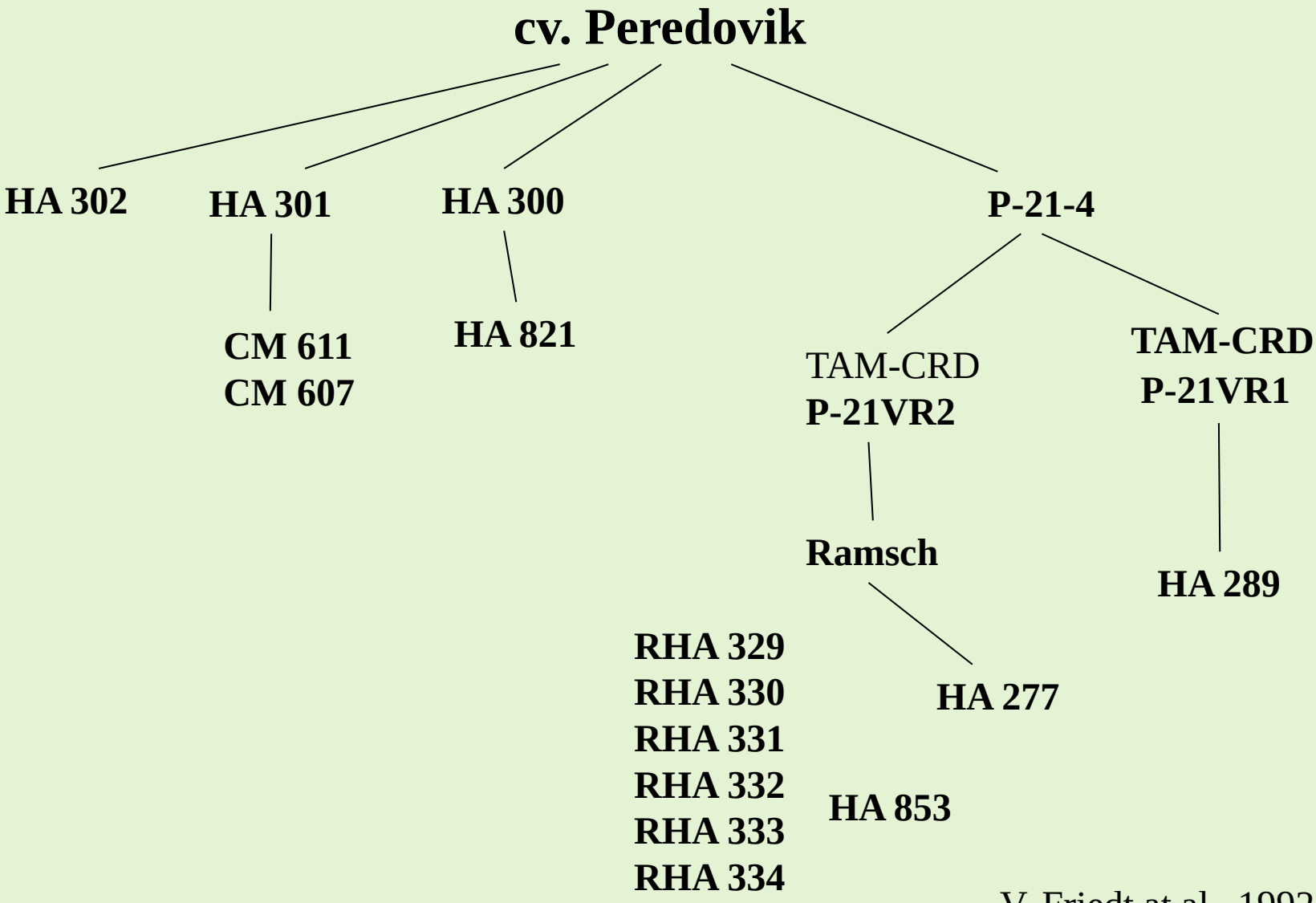
The best accessions tolerant to phomopsis during ten years of field observations (Kuban Station, 2000-2010)

№	Accenumb	Accename	Country of origin	Status
1	358	Zelenka № 106	Russia, Belgorod region	landrce
2	552	Zelenka	Russia, Belgorod region	landrce
3	2019	local	Russia, Habarovsk region	local
4	3326	VIR 365	KES VIR	line
5	3469	VIR 249	KES VIR	line
6	3487	VIR 448	KES VIR	line
7	3527	VIR 449	KES VIR	line
8	3595	VIR 130	KES VIR	line

The best accessions tolerant to phomopsis and Resistance to downy mildew (Kuban Station, 2000-2010)

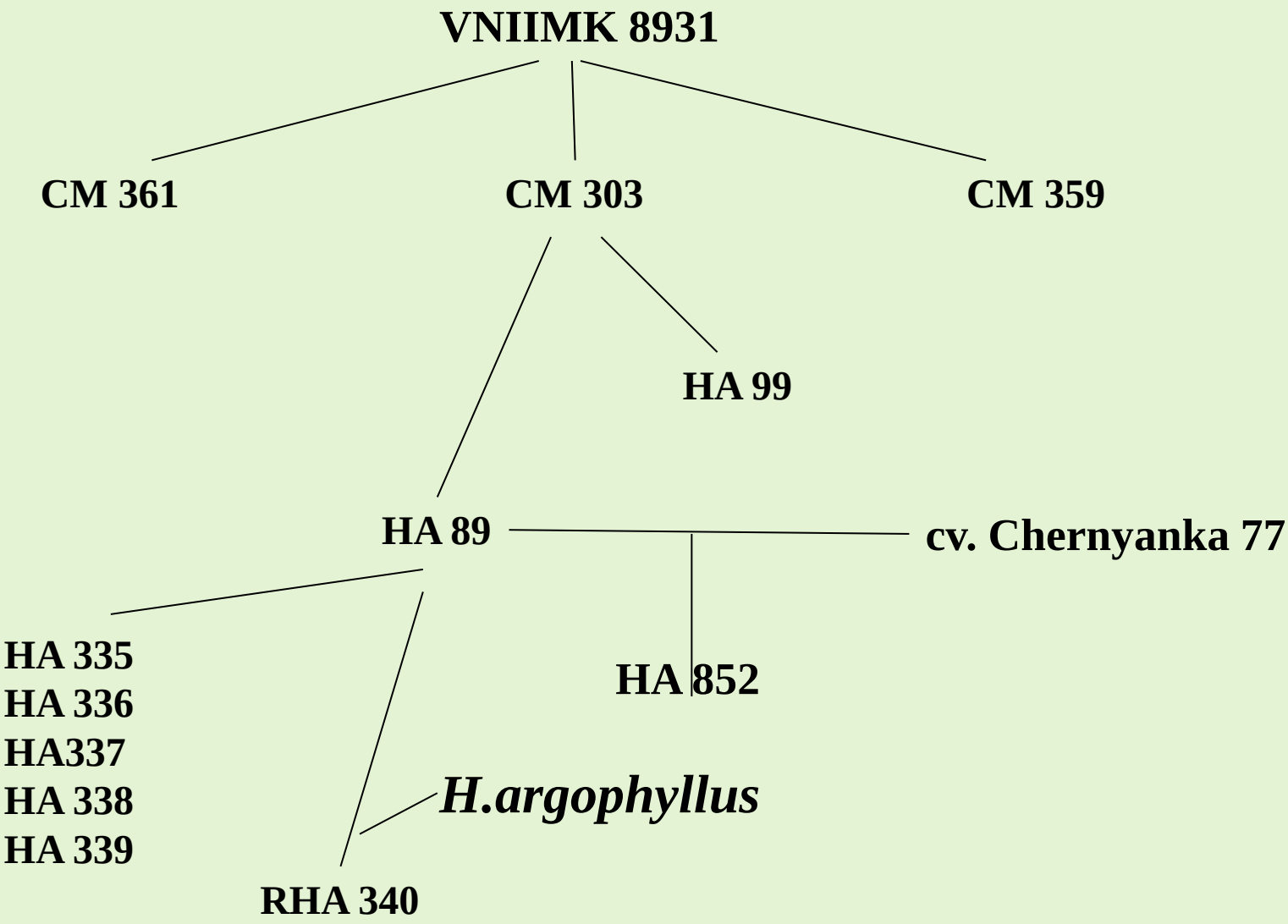
Accename	Accenumb	Sprouting to ripening (days)	Height of plant, см	Diametr of head, см	Phomopsis infestation, %
VIR 172	2793	92	104	18	0
Local	3362	105	167	17	0
VIR 581	3338	102	119	11	0
VIR 435	3467	106	146	16	0
НА - 89	3532	101	122	15	0
VIR 635	б/к	97	125	10	0
RHA - 278	б/к	10	149	13	0
Control, VK - 571	3511	88	111	15	98

Genealogy lines derived from Soviet varieties breeding



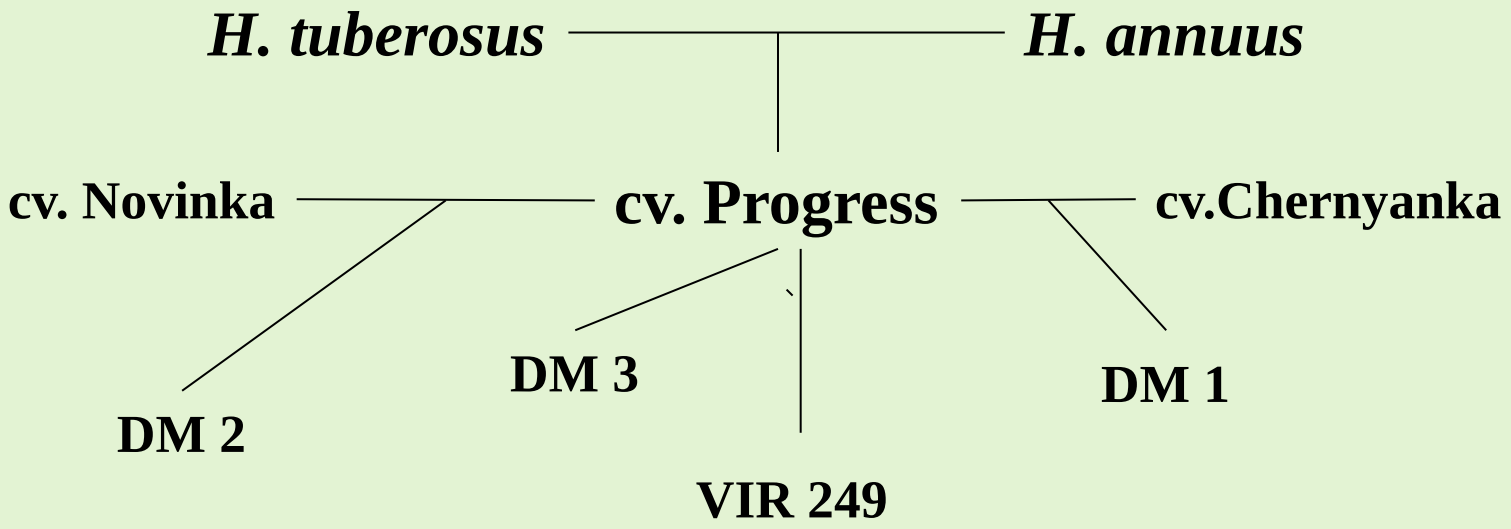
V. Friedt at al., 1992

Genealogy lines derived from Soviet varieties breeding



V. Friedt at al., 1992

Genealogy lines derived from Soviet varieties breeding



Rf, Pl
Tolerace to
Phomopsis

V. Friedt at al., 1992
V.Gavrilova at al., 2015

Genealogy lines derived from Soviet varieties breeding

CMS PET
(from Leclercq)

cv. Armavirsky 1813

VIR 100
VIR 101
VIR 104
VIR 106
VIR 376
VIR 377
VIR 378

CMS lines in the VIR collection

Line	Catalogue No.	Pedigree
VIR100	3443	cv. Armavirsky 1813, Russia
VIR101	3445	cv. Armavirsky 1813, Russia
VIR106	3447	cv. Armavirsky 1813, Russia
VIR109	2509	hybrid HS 52, Romania
VIR114	3453	cv. Sputnik, Russia
VIR116	3455	cv. Vympel, Russia
VIR117	2517	cv. G-22, Russia
VIR129	2310	ZhS-17, Russia
VIR130	3595	k-2266, Germany
VIR137	3459	cv. Sputnik, Russia
VIR138	3461	cv. Vympel, Russia
VIR151	3463	k-2184, South Africa
VIR172	2793	k-705, Uzbekistan
VIR215	3295	VIR 111 x k-2266, Russia
VIR229	3304	hybrid VPBS-211, Yugoslavia
VIR340	3513	k-1933, Hungary

CMS PET1 pollen fertility restorer lines in the VIR collection

No.	Line	Catalogue No.	Origin	Branching
1	VIR183	3280	i-473670, Argentina	No
2	VIR185	3285	k-2222, Armenia (local variety)	No
3	VIR196	3286	SL 3376, Bulgaria	No
4	VIR 218	3297	VIR 113 (VIR 113 from Sputnik), Russia	No
5	VIR 220	3299	Yugoslavia, VPBS-211 (1981)	Lower
6	VIR 249	3469	Progress, Russia	No
7	VIR 260	3318	VIR 113, Russia	No
8	VIR 343	3477	ZhS-17 M, Russia	No
9	VIR 349	3503	VIR 113, Russia	Upper
10	VIR 358	3504	ZhS-17, Russia	Entire stem
11	VIR 364	3480	VIR 161, Russia	From mid-stem
12	VIR 365	3326	Progress x k-2699, Russia	No
13	VIR 376	3331	VIR 104, from Armavirsky 1813, Russia	Lower arched
14	VIR 377	3332	VIR 104 (from Armavirsky 1813), Russia	Lower

Pollen fertility restorer lines (118)

- The ability of these lines to restore pollen fertility of the *cms* forms at the phenotypical level has been compared with the data from the molecular analysis that employed SCAR markers (Horn et al. 2003) linked with the *Rf1* gene.

with total branching

Line without branching

with middle branching

Межвидовая гибридизация

Схема создания и использования межвидовых гибридов подсолнечника

Линия ЦМС культурного подсолнечника (ВИР 114)

x

Многолетний дикорастущий вид (*H.giganteus*)

F1 (ВИР 114 x *H.giganteus*)

расщепление по фенотипу

F2 (ВИР 114 x *H.giganteus*)

нет расщепления по фенотипу

ВИР 114 (ЦМС) x F7 (ВИР 114 x H.giganteus)

BC [ВИР 114 x (ВИР 114 x *H.giganteus*)]

гетерозисный гибрид культурного типа

Схема скрещивания

Родительские формы

Линия ЦМС ВИР 114

x

Многолетний вид

F1

Pollen fertility restorer lines from the VIR collection obtained by interspecific hybridization

No.	Line	Catalogue No.	Origin	Branching
1	VIR 756	3566	HA 232 x *H.laetifolius*	Upper
2	VIR 758	3554	VIR 129 x *H.floridanus*	Entire stem, compact
3	VIR 759	3555	HA 232 x *H.maximiliani*	Entire stem, compact
4		3557	HA 232 x *H.strumosus*	Upper
5	VIR 767	3560	VIR 151x *H.trachelifolius*	Lower
6		3561	HA 232 x *H.mollis*	Upper
7	VIR 768	3568	VIR 151 x *H.maximiliani*	Entire stem, compact
8	VIR 770	3564	VIR 114 x *H.tomentosus*	No
9	VIR 777	3557	HA 232 x *H. strumosus*	No
10	VIR 800	3570	VIR 114 x *H.giganteus*	Upper
11	RIL 80	3598	83 HR4 x RHA345	Entire stem, spreading
12	RIL 130	3599	83 HR4 x RHA345	Entire stem, spreading

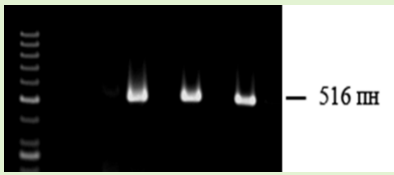
CMS lines and their fertile analogues

Three types of *cms* are represented in the VIR collection,

- the traditional PET1 (17 lines)
- RIG0 on the basis of wild *H. rigidus* (Cass.) Desf. (2 lines)
- PEF on the basis of *H. petiolaris ssp fallax* (1 line)

Sterile analogues of VIR109 and VIR151 lines have been created on the basis of PET1 and RIG0.

The use of *orfH522*, an mtDNA marker characteristic of *cms* PET1 (U. Schnabel et al., 2008) made it possible to genetically identify lines with different *cms* types.



Lines with different manifestation of morphological traits

The Mendelian genetic analysis was applied to study genetic control of short stem

Line VIR 434 *d1d2*

Plant heigt 62±1,8 cm
Internode length 1,4±0,04
Number of leaf 43±2,4
Veg.period 108 days

Line VIR 648 *sd1 sd2 sd3 as1 as2*

Plant heigt 53±0,7 cm
Internode length 2,4±0,03
Number of leaf 23±1,7
Veg.period 80 days

Line VIR 253 *sht1 sht2*

Plant heigt 86±0,7 cm
Internode length 3,2±0,04
Number of leaf 27±2,4
Veg.period 88 days

Lines with different manifestation of morphological traits

sd1 sd2 sd3 as1 as2

The Mendelian genetic analysis was applied to study genetic control of short stem, upper, middle and basal and top branching

Линии ВИР 304
b1

ВИР 635
b3

ВИР 364

Basal branching

ВИР 767
Br3 Br4 Br5

The sunflower character & genetic collection includes

- **62 accessions – source of resistant to *Phomopsis helianthi* Munt.-Cvet.**
- **46 lines with genes for resistance to races (330, 710 and 730) of downy mildew (Plasmopara halstedii (Farl.) Berl. and de Toni)**
- **120 pollen fertility restorer lines**
- **20 cms lines and their fertile analogues**
- **40 large-fruited forms (confectionery forms)**
- **55 forms differing in plant height**
  - **10 dwarf lines below 70 cm**
  - **45 tall accessions above 250 cm**
- **20 lines of ornamental sunflower**

Lines of ornamental sunflower


THANK YOU FOR ATTENTION