

Phenotypic characteristics of North-Western Russian populations of *Phytophthora infestans* (2003-2008)

N.M. Zoteyeva¹, M.V. Patrikeeva²

¹⁾ All-Russian Institute of Plant Industry (VIR), St. Petersburg

²⁾ All-Russian Institute of Plant Protection (VIZR), St. Petersburg

Phytophthora infestans is the causal agent of late blight, which is the most devastating disease in potato worldwide. In the European Union almost 6 Mha of potatoes are grown representing a value of close to €6,000,000,000. Late blight caused by *P. infestans* causes annual losses (costs of control and damage) estimated at more than €1,000,000,000 (Haverkort et al. 2008). More pathogenic isolates appeared in Europe when the old clonal lineage of *P. infestans* was replaced by a new more diverse population during the 1990s (Goodwin, 1977). The occurrence of A2 mating type led to sexual reproduction of *P. infestans*. Many studies performed in worldwide potato production regions showed a large spectrum of isolates with complex races (Drenth et al. 1994, Flier et al. 2003, Forbes et al. 1997). Both mating types had been detected in *P. infestans* populations in St. Petersburg Region in the late 1990s (Vedenyapina et al., 2002). Analyses of phenotypic structure of *P. infestans* populations in North-Western Russia in two epidemic seasons (1998 and 2003) reflected that the average numbers of virulence genes per isolate has increased much (Zoteyeva, Patrikeeva, 2008). The main goal of evaluation performed is the characterization of *P. infestans* populations from St. Petersburg Region to detect changes in genes for virulence (R1-R11) frequencies. More frequent occurrence of genes for virulence in *P. infestans* populations increases the risk of destruction of potato plants.

In the evaluation of 2003 – 2008 the isolate study for mating types was done in 2003, 2004 and 2007. The isolates of A2 mating type were identified in each of these seasons. Epidemics occurred during the seasons 2003 and 2008. Average number of virulence factors per isolate in epidemic 2008 was 8.1. In all 459 isolates collected during 2003-2008 genes for virulence R1 and R3 were common for 100% of the isolates. Figure 1 (a,b) demonstrates the frequency of genes for virulence R2, R4, R5, R6, R7, R8, R9, R10 and R11 in *P. infestans* isolates collected in this period. Similar frequencies of genes for virulence R2 and R6 had been detected during all years. In a large part of the isolates sampled in 2005 from leaves of variety Newsky genes for virulence R2 and R6 were not detected in similar proportions. In other years both genes had been detected more frequently in similar proportions as well (Figure 2). Data obtained in 2004 and 2005 showed differences in frequency of genes for virulence in isolates sampled from two varieties: Newsky (68 isolates) and Snegir (47 isolates) (Figure 3). AMOVA test showed there was no significant difference between years ($p=0.3640$), but there was significance between varieties ($p<0.001$).

Current evaluation showed that the potato late blight populations from St. Petersburg Region are highly genetically divers. Due to the detection of A2 mating type the sexual reproduction in *P. infestans* populations is very assumed. More frequent genes for virulence occurred in isolates sampled in 2003-2008 in respect to isolates sampled in late 1990s indicates the changes in phenotypic structures of late blight populations in this region. The average number of virulence factors per isolate in 2003-2008 increased in respect to late 1990s from 6.3 to 7.7 in 2003 and to 8.1 in 2008. The least frequent gene for virulence R9 was identified in 11 % of isolates collected in the end of 2008 epidemic season. The schedule of data obtained indicates the similarity in number of genes for virulence R2 and R6 detected in *P. infestans* isolates studied. Probably the functions of these genes are correlated. Due to the differences in genes for virulence frequency in isolates sampled in the same seasons (2004, 2005) from leaves of two cultivars, Snegir and Newsky, it is possible to assume that cultivar Newsky possess the ability for selection by phenotypes in *P. infestans* isolates.

Literature cited:

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Material and methods

Phytophthora infestans isolates were sampled in St-Petersburg Region, North-Western Russia from single lesion on potato leaves into tubers of R-genes free potato variety. The virulence factors in totally 459 *P. infestans* isolated (Table 1) sampled in 2003-2008 have been studied. The genotypes of Black's Differential set each possessing a single R-gene (R1-R11) were used to define genes for virulence. This set was offered by IHAR-Mlochow Research Center (Poland).



Table 1. Number of isolates sampled in 2003-2008

Year	Number of sampled isolates	Sources	Localities
2003	88	14 potato cultivars (p. cvs), 3 interspecific hybrids, 3 potato species	7 (Vyborg, Pushkin, Tosno, Gatzyna, Luga, Vsevolozhsk)
2004	69	7 p. cvs, 3 potato species	3 (Pushkin, Tosno, Gatzyna)
2005	145	4 p. cvs, 1 potato species, 1 tomato cv.	3 (Pushkin, Tosno, Gatzyna)
2006	52	3 p. cvs	4 (Pushkin, Gatzyna, Luga, Vsevolozhsk)
2007	54	2 p. cvs, 1 interspecific hybrid, 1 potato species	3 (Pushkin, Gatzyna, Luga)
2008	51	10 p. cvs	3 (Pushkin, Gatzyna, Luga)

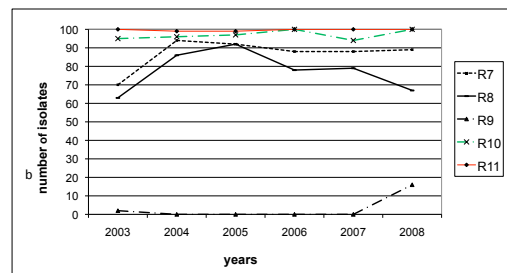
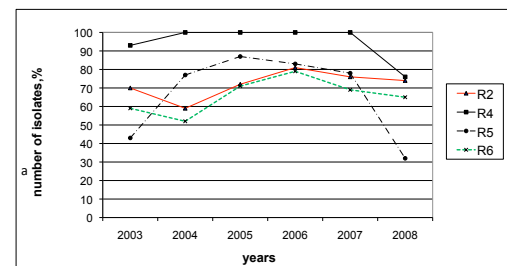


Figure 1 (a,b). Frequency of genes for virulence (R1 – R11) in the isolates of *Phytophthora infestans* sampled in St. Petersburg Region in 2003-2008.

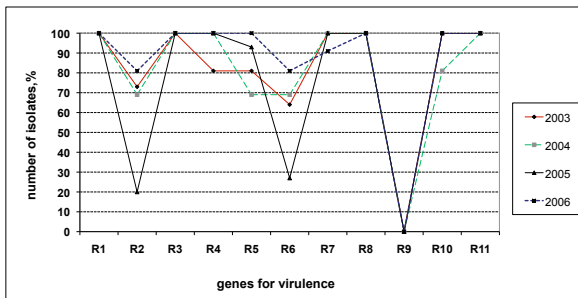


Figure 2. Number (%) of genes for virulence detected in *Phytophthora infestans* isolates sampled from leaves of potato cultivar Newsky in 2003-2006

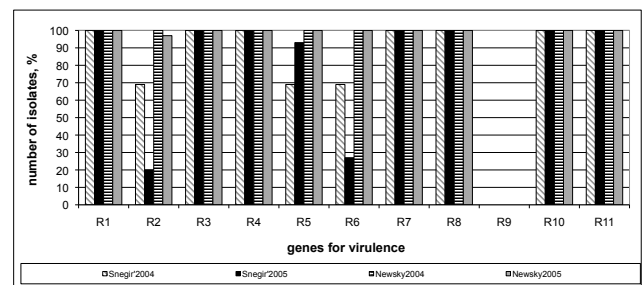


Figure 3. Genes for virulence (R1 – R11) expression in *Phytophthora infestans* isolates sampled from leaves of potato cultivars Newsky and Snegir in 2004, 2005

Amova year/virulence						Amova variety/virulence					
F.V.	SC	gl	CM	F	p-value	F.V.	SC	gl	CM	F	p-value
Model	0.01	1	0.01	0.83	0.3640	Model	0.40	1	0.40	59.41	<0.001
YEAR	0.01	1	0.01	0.83	0.3640	VAR	0.40	1	0.40	59.41	<0.001
Error	0.99	91	0.01			Error	0.61	91	0.01		
Total	1.00	92				Total	1.00	92			