

## Genetic variability of *Phytophthora infestans* in Nordic countries

May Bente Brurberg<sup>1)</sup>, Arne Hermansen<sup>1)</sup>, Elameen Abdelhamed<sup>1)</sup>, Vinh Hong Le<sup>1)</sup>, Björn Andersson<sup>2)</sup>, Asko Hannukkala<sup>3)</sup>, Bent Nielsen<sup>4)</sup>, Jens Grønbech Hansen<sup>4)</sup> & Jonathan Yuen<sup>2)</sup>

<sup>1)</sup>Bioforsk- Plant Health and Plant Protection Division

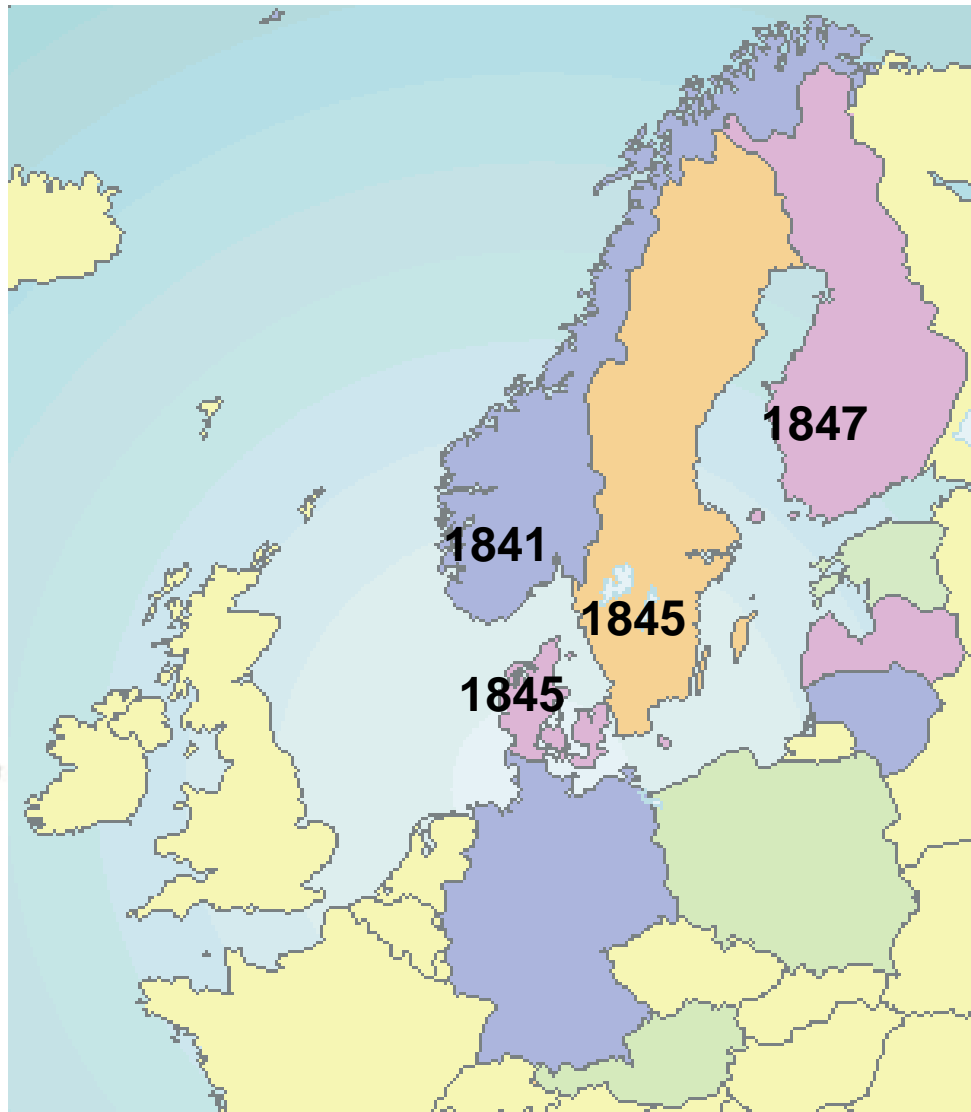
<sup>2)</sup>Swedish University of Agricultural Sciences

<sup>3)</sup>MTT, Agrifood Research Finland

<sup>4)</sup>University of Aarhus, Faculty of Agricultural Sciences



# When did late blight arrive in the Nordic countries?



Norway 1841  
(Svensen, 1852)

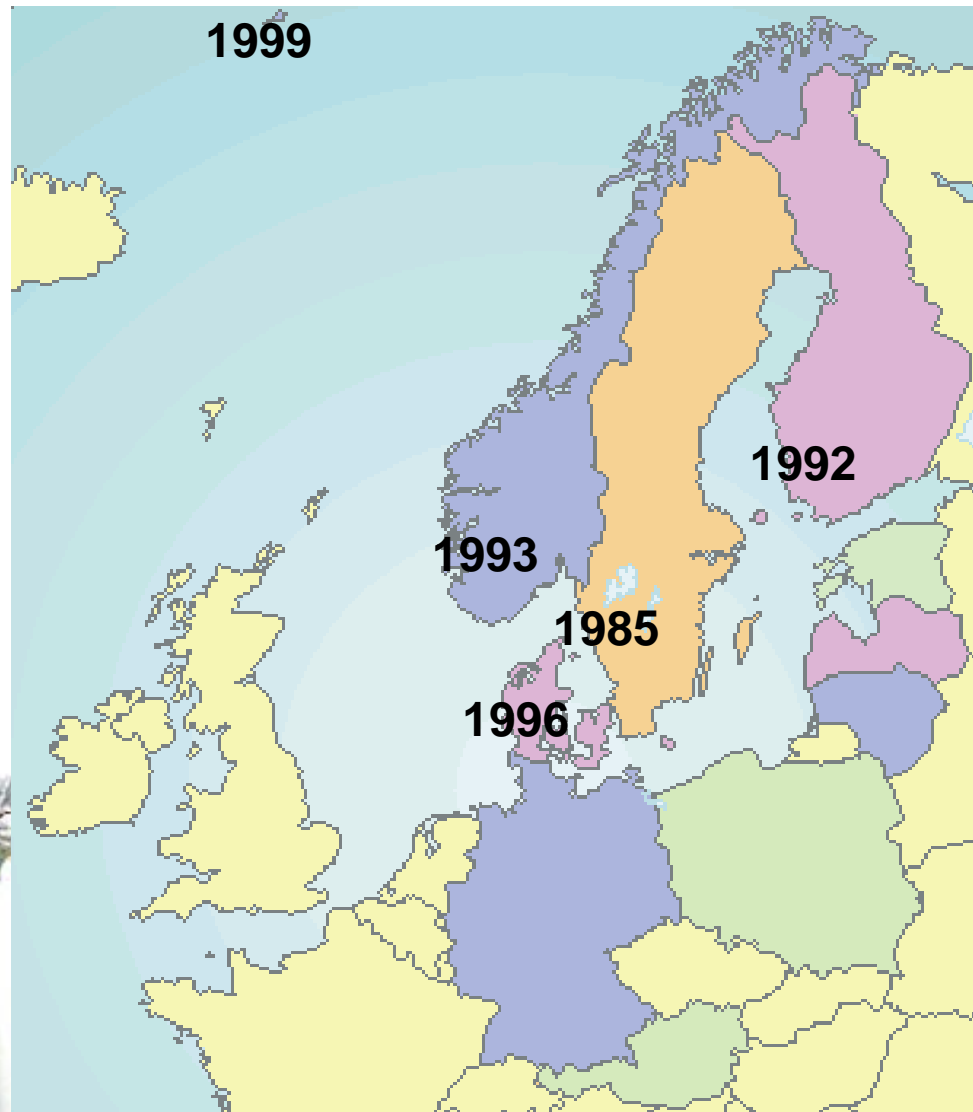
Sweden 1845  
(Wahlberg, 1847)

Denmark 1845  
(Brøndegaard ?)

Finland 1847  
(Mäkelä 1966)



# When was mating type A2 first found in the Nordic countries?



Sweden 1985  
(Kadir & Umaerus, 1987)

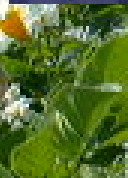
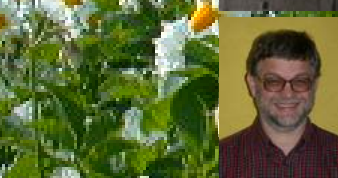
Finland 1992  
Norway 1993  
(Hermansen et al. 2000)

Denmark 1996  
(Bødker et al. 1998)

Iceland 1999  
(Olafsson & Hermansen 2001)



# NorPhyt 2003-2006: Studies on the new Nordic populations of *P. infestans* to improve potato late blight forecasting and control



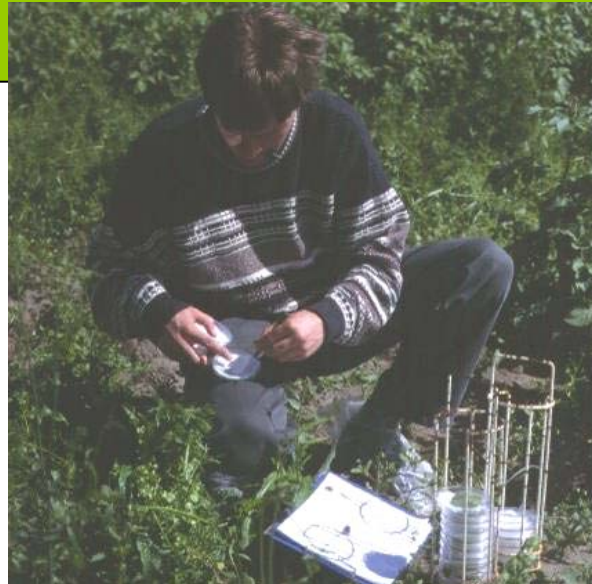
## Norphyt - main objectives

- Evaluate and quantify epidemiological parameters of the "new" population (s) of *Phytophthora infestans* in the Nordic countries
- Obtained results will be implemented in existing and new forecasting - and decision support systems for late blight control





# NorPhyt (2003-2006)



## More information about the isolate collection

- Sampling in the early portion of the epidemic to try to maintain diversity in the material and to reduce the selection for more aggressive isolates that takes place during the growing season
- Material was collected from both conventional and organic potato production fields
- Isolation was done by labs in each of the four countries



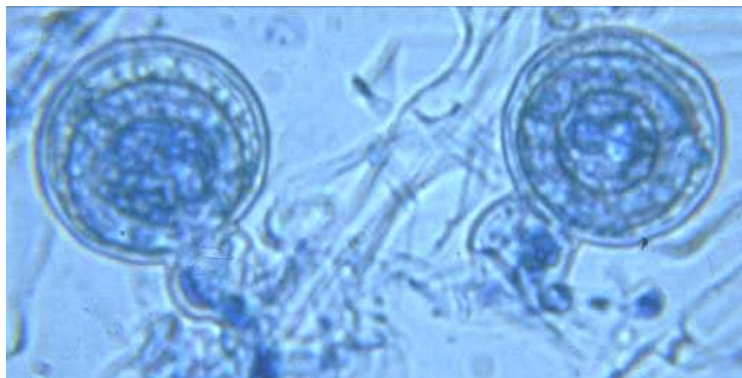
## WP 1.2. Characterization of the isolates

- Mating type
- Fungicide resistance
- Virulence
- Aggressiveness
- SSR

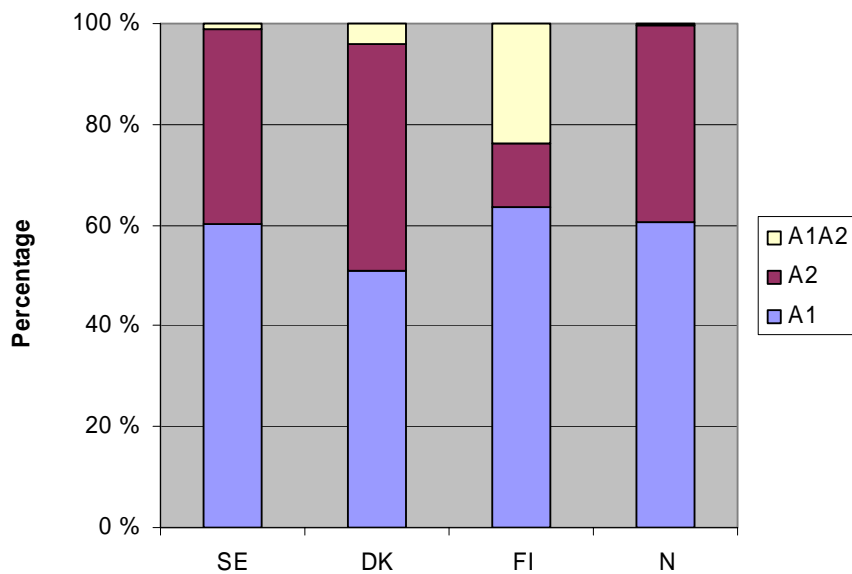




# Mating types

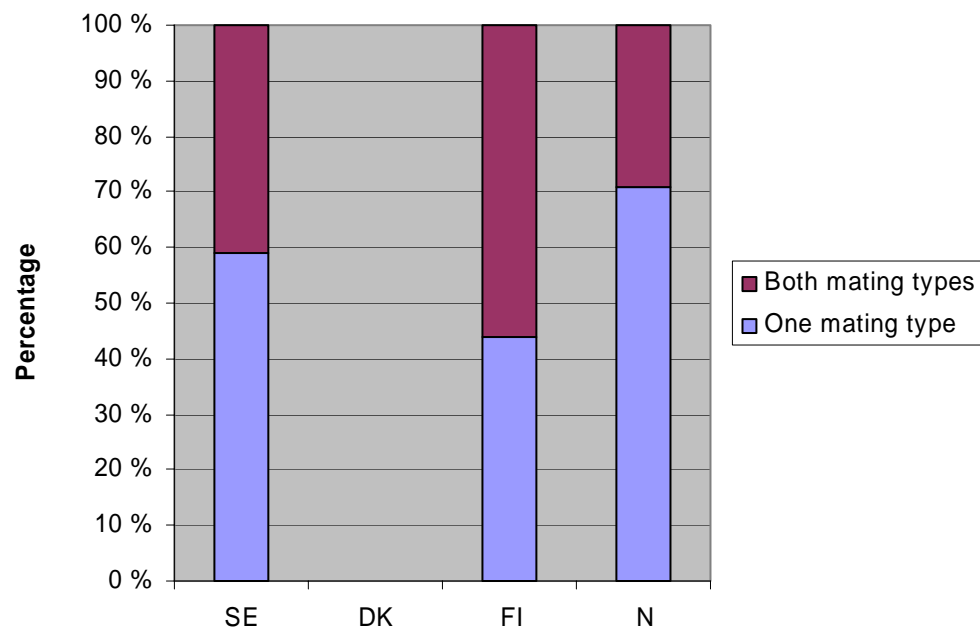


Mating type ratio among isolates



682 isolates

Mating types in the fields



190 fields

## Why use SSR instead of AFLP ?

- SSR have the advantage of being co-dominant, whereas AFLP markers are dominant
- *P. infestans* is a diploid organism, the use of micro satellites greatly increased the power of the genetic analyses
- SSR analysis is more reproducible between labs



## SSR analysis

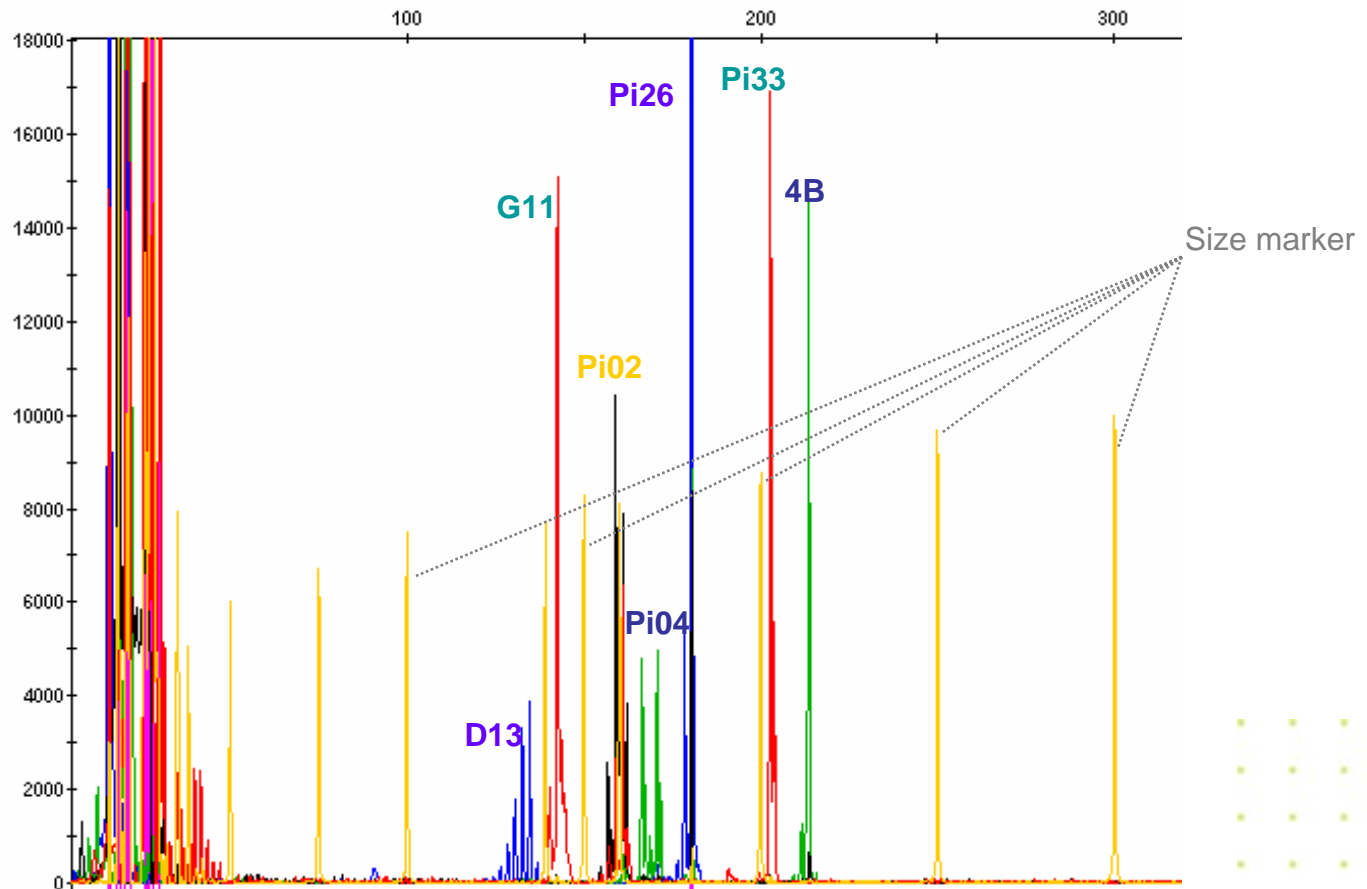
- 200 Nordic isolates selected for genotyping with SSR  
50 from each country (N, S, Fi, Dk)
- SSR markers used:  
Pi4B, Pi4G, PiG11 (Knapova & Gisi)  
Pi02, Pi04, Pi16, Pi26, Pi33 (Lees & Cooke)  
D13 (Pipe & Shaw)
- ABI 3730 DNA Analyzer (cappillary system) for fragment separation  
Software  
Data Collection v 2.0  
GeneMapper v 3.0  
Used 10 of SCRI's control isolates to fine tune the system



# Example of electropherogram

Isolate N29

Markers: Pi02, Pi04, Pi26, Pi33, D13, 4B, G11



# SSR analysis

## Alleles found in the Nordic population

Marker	Allele size										
Pi02	142	150	152	156	158	160	162	164	166		
Pi04	160	162	166	168	170	172					
Pi16	160	166	168	172	176	178					
Pi26	171	173	177	179	181	183	185	187			
Pi33	203	206	209								
D13	106	108	116	118	132	134	136	142			
4B	203	205	213	217							
4G	160	162	164	166	168	170	174	176			
G11	140	142	148	150	152	154	156	158	160	162	166

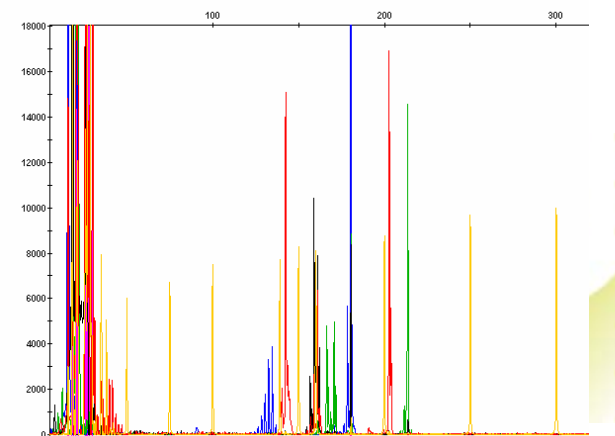




## Genetic variation using SSR markers

- 192 of 200 isolates gave results for seven or more markers
- 181 genotypes occurred
- 2 genotype occurred twice
- 2 genotypes occurred tree times
- 1 genotype occurred six times

(4 N, 2 Fi)

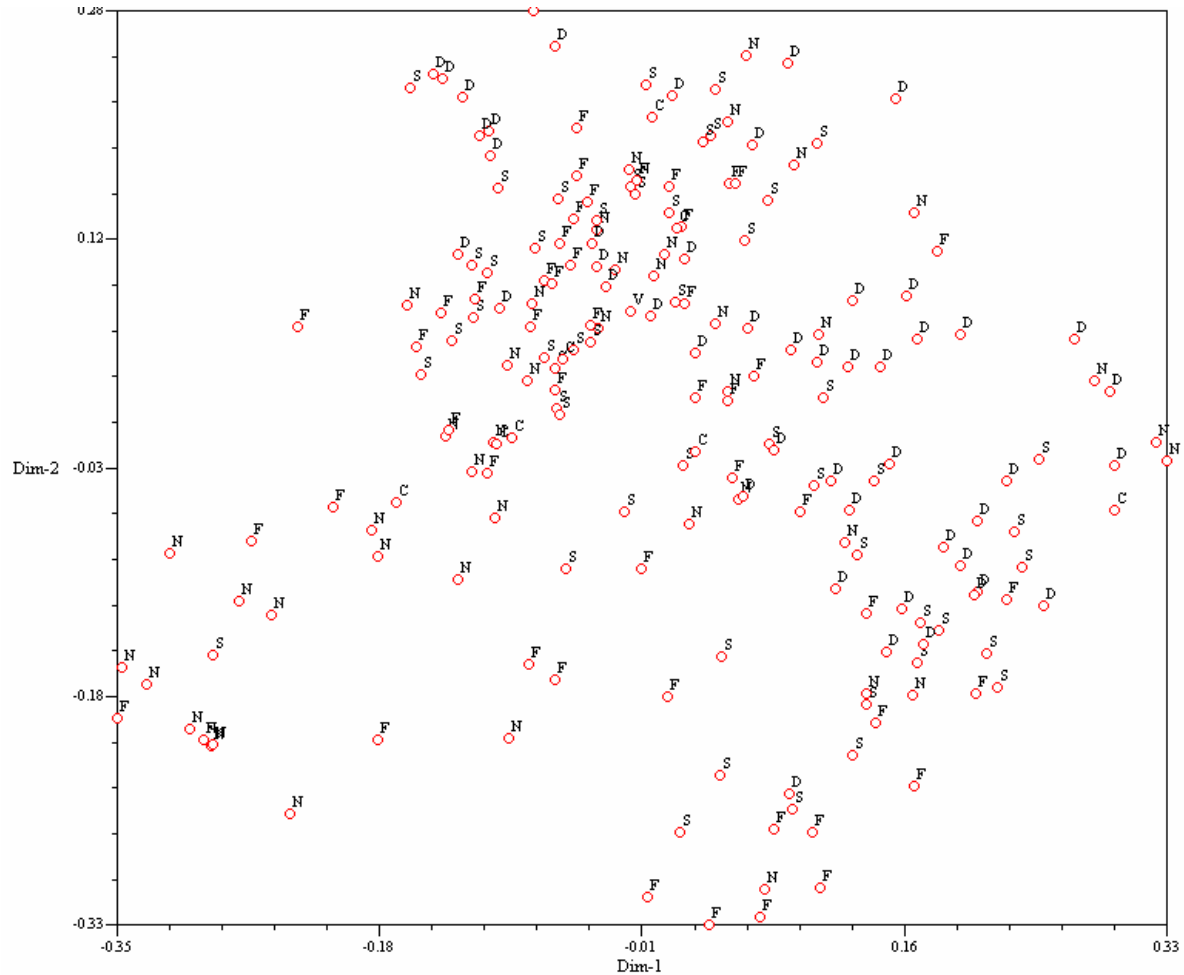


# Characteristics for the 6 isolates with identical SSR-genotype

Isolate code	District	Mating type	Met. sensit.	Prop. sensit.	Pathotype	SSR alleles (8 markers)
F38		A1	100	100	1,3,4,7,10,11	Pi4B 205, 217 Pi26 180, 180 Pi04 166, 170
F40		A1A2	100	100	1,3,4,5,7,10,11	Pi02 160, 160 PI33 203, 206 G11 156, 156
N07	Solør	A1	10	100	1,3,4,7,10,11	Pi4G 163, 163 Pi16 174, 176
N08	Toten	A1	10	10	1,3,4,7,10,11	
N42	Solør	A1	0	10	1,3,4,7,10,11	
N34	Vestfold	A2	1	100	1,3,4,7,10,11	



# Principle coordinate analysis



## Source of the discovered genetic variation

- Different seed potato sources ?
- Alternative hosts ?
- Cull piles ?
- Oospores ?



## Conclusions

- Both mating types common in all Nordic countries - close to 50/50 of A1/A2
- The populations show high genetic variation (SSR-data) indicating sexual reproduction

