

Eucablight – pathogen database update



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- **Eucablight project summary**
- **Data updates**
- **New version of P.exe**
- **Updates on SSR methodology**
- **Future plans & Funding**
 - **Main challenges – expansion, momentum, relevance, funding & publications**

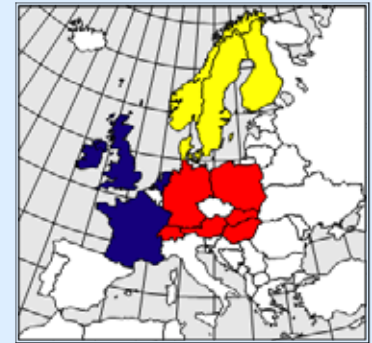


WP1

'... establish a **comprehensive network** on the population biology of *P. infestans* across Europe'

WP2

Collect and collate data (pheno and genotype) on existing/past *P. infestans* collections



WP4

4.1 Collate and review existing methods for assessing variation in *P. infestans* populations and to test, standardise and publish these methods in a www database

4.2 To create a **European isolate database** detailing existing data on isolate variation using new data as assessed by the methods developed in Objective 4.1

4.3 Training course on agreed and adopted methods

4.4 Pan-European **interpretation** of changing population structure in *P. infestans*

WP5

Integration of all derived data to benefit of control strategies



1. Where, when and how blight infection starts

- primary inoculum

2. Rate of infection and spread

- foliar
- tuber

3. Control options

- fungicide efficacy
- host resistance stability
- DSS

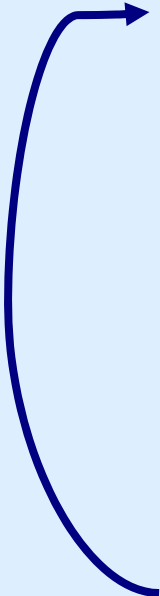
4. Survival

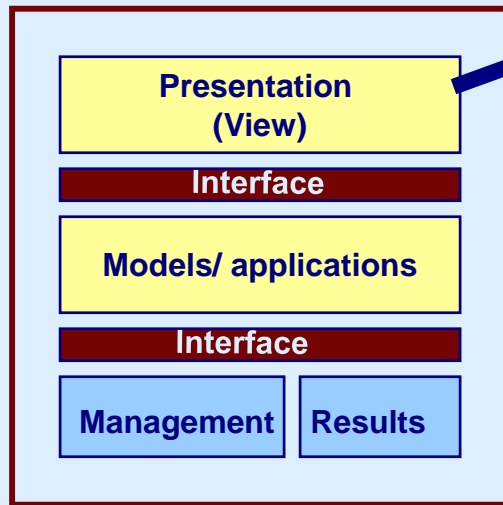
- cull piles/seed
- volunteers
- solanaceous weeds
- soil - oospores

5. Changing pathogen population

- Immigration
- Evolution – mutation & recombination

Integration of all data into practical management advice





Graphic analysis



$$H = -\sum_{i=1}^S p_i \ln(p_i)$$

Genotype analysis

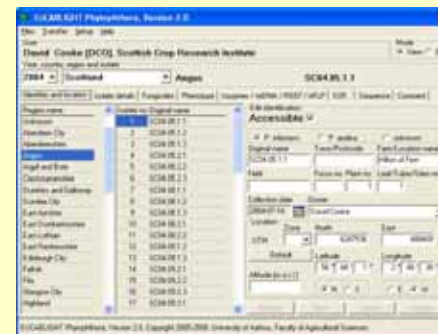


Allele frequencies



50+ database fields behind each isolate entered into the database = wealth of data to be mined.

Pathogen data



Phytophthora.exe





03-06 Project funded (i.e. no € Jan 06 onwards)

Apr 07 Discussed revisions needed for P.exe in S. America

Merging of Eucablight and EU.ICP.NET to Euroblight

May 07 Bologna – planned new version of P.exe

July 07 Shut down P.exe 1.3 until version 2.0 launched

Feb 08 Launch of P.exe 2.0 for Europe & S & C America
improved data transfer, expandable to other regions, additional features such as DNA sequence data, more user friendly

Mar 08 P.exe training course and presentation at GILB meeting in Beijing – general support for system
“CIP’s directors recognize the power of such an approach and support the expansion of the system”

Oct 08 Training in Chile – agreement for data entry



Tallinn
Oct 2005 12,300

Rennes
Jan 2006 13,600

Bologna
May 2007 15,500

Hamar
Oct 2008 19,200

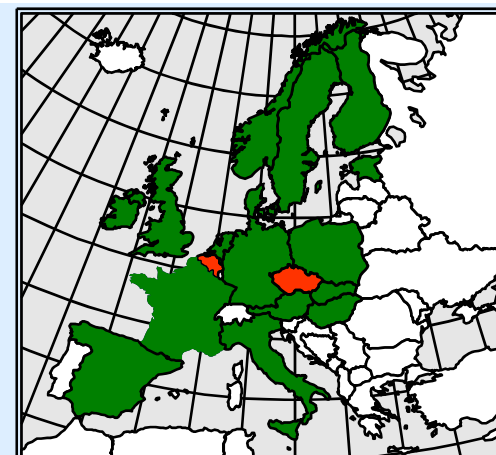
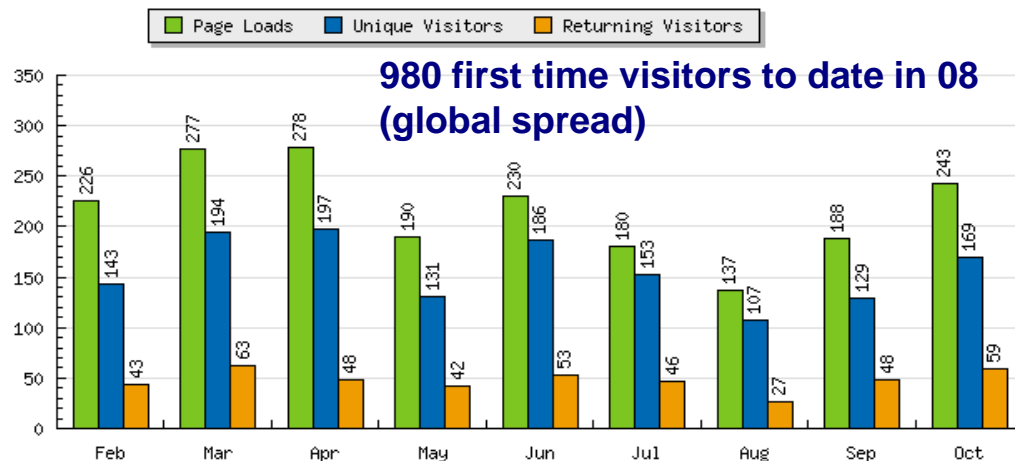
Pathogen overview

Select one or more traits and press the show button. [Help](#)

Mating type Metalaxyl resistance Aggressiveness Virulence mtDNA AFLP Isozyme SSR All

Show

Country	AT	BE	CZ	DE	DK	EE	EN	ES	FI	FR	HU	IE	IT	MA	ND	NL	NO	PE	PL	SC	SE	SK	WA	All countries
2008							117								1					48		23		189
2007				46			822								578				45	94		75		1660
2006			80			103	801		87		56	1			20				105	135		110		1498
2005			177			103					67				54		21		93					515
2004			64			144									24	25	115		46	456		26		900
2003			31		65	84			234	7					40	109	331	36	22	216	88	26		1289
2002	100					89				75	93				58				30			26		471
2001						83		210	112	27					38				149	8	277	36		940
2000				7		13		675	84	3				42	26	481	197		155	4	163			1850
1999						12		457	216					25	35		269	66	149		258			1487
1998		46					336	538	73	36					78		678	5	256	22	263	25		2356
1997							630	602	86	5					53		167	112	147	215		48		2065
1996							143	10	16	156	1	147	10	7	195	353	493	1	189	171		97		1989
1995							26	12	1	135					114	383	1	1	152			16		841
1994								12	117	87				1	64	278			1					560
1993									3	69	1				60	41								174
1992									15	83					4									102
1991										56	1		1											58
1990										35														35
1989										22														22
1988										4														4
All years	100	46	352	53	65	631	2875	34	2955	1300	290	148	11	75	1442	1670	2272	220	1388	1521	1049	114	394	19005



SSR data critical and more needed to fill in details



Pathogen overview



Select one or more traits and press the show button. [Help](#)

Mating type
 Metalaxyl resistance
 Aggressiveness
 Virulence
 mtDNA
 AFLP
 Isozyme
 SSR
 All

Show

Country	AT	BE	CZ	DE	DK	EE	EN	ES	FI	FR	HU	IE	IT	MA	ND	NL	NO	PE	PL	SC	SE	SK	WA	All countries
Year																								
2008							715																	748
2007				33			753				14												90	984
2006											63				10	24			43		127			116
2005						71									24	24			14	3	434			567
2004																		21	3	216				240
2003											93				47				4					144
2002											27				3				3	4	61			98
2001											3				3				2	1				9
2000											3				3									16
1999															2			13	1					95
1998		30					51				12				1								1	177
1997							122				1							9	1	27			17	177
1996							29				1										33		14	77
1995																					40			40
1994																								
1993											1													1
1992																								
1991											1													1
1990																								
1989																								
1988																								
All years		30		33		71	1670				216				90	24		43	71	882	61	122		3313



SSR alleles – Current SCRI panels



Panel 1 Pi02			Panel 1 Pi89			Panel 1 Pi4B			Panel 2 G11			Panel 2 Pi04			Panel 2 Pi70			Panel 2 Pi56			Panel 2 Pi63			Panel 3 D13			Panel 3 Pi16			Panel 3 Pi33						
Peak size	Allele name and colour	Comment	Peak size	Allele name and colour	Comment	Peak size	Allele name and colour	Comment	Peak size	Allele name and colour	Comment	Peak size	Allele name and colour	Comment	Peak size	Allele name and colour	Comment	Peak size	Allele name and colour	Comment	Peak size	Allele name and colour	Comment	Peak size	Allele name and colour	Comment	Peak size	Allele name and colour	Comment	Peak size	Allele name and colour	Comment				
	142	nordic		175.7	177	mex & ec		203	nordic	128.5	128	ec	162.4	160	nordic	187.3	189	US-1	253.4	174	widespread	269.8	143	widespread	99.1	100	widespread		160	nordic	189.8	191	possible GB			
	150	nordic		177.9	179	widespread		206.6	206	widespread	130.3	130	ec		162	nordic	180.3	192	widespread	255.3	176	widespread	272.8	151	widespread		106	nordic		166	nordic	201.5	203	widespread		
151.2	152	widespread		179.9	181	widespread		210.5	209	rare	132.3	132	mex	167.5	166	widespread	193.1	195	widespread				278.7	157	widespread	106.2	108	US-8	167.4	168	nordic_mex	204.3	206	widespread		
	156	nordic		181.8	183	ec		212.5	211	mex	136.0	136	mex	169.8	168	rare	196.0	198	bolivia?							108.2	110	ec mex	171.4	172	nordic_mex		173.2	174	rare	
157.5	158	ec&hu			186	ec		214.7	213	widespread	138.5	138	NL_00	171.9	170	widespread										110.0	112	hu	173.2	174	rare					
159.8	160	widespread			187	ec		218.6	217	widespread	140.5	140	widespread	173.7	172	nordic											114.2	116	rare	175.2	176	widespread				
161.9	162	widespread		190.9	191	mex		222.6	221	rare		142	nordic													116.3	118	widespread	177.2	178	widespread					
163.8	164	rare		192.8	193	BPC		226.7	226	hu&us8	146.0	146	BPC_06												119.0	120	UD	179.2	180	mex						
166.0	166	rare		195.0	195	BPC			235	ec	147.1	148													120.9	122	rare	181.1	182	ec&mex						
168.0	168	rare		196.8	197	BPC			243	ec	148.4	149	ec&nordic												123.1	124	ex& hu	184.4	186	ec						
170.0	170	mex		198.7	199	BPC			247	ec	151.4	152	widespread												125.1	126	rare									
				200.7	201	BPC			256	ec	153.6	154	widespread												127.1	128	rare									
				202.7	203	BPC			263	ec	156.4	156	widespread												128.8	130	widespread									
				204.8	205	mex			267	ec	157.5	158	widespread												130.6	132	widespread									
				208.6	209	mex			269	ec	159.6	160	widespread												132.6	134	widespread									
				210.5	211	mex			271	ec	161.5	162	widespread												134.8	136	widespread									
									273	ec	163.3	164	widespread												136.6	138	widespread									
									277	ec	166.3	166	widespread												138.9	140	widespread									
									281	ec	167.6	168	widespread												141.1	142	rare									
									283	ec	169.2	170	ec & GC06											143.3	144	ec mex										
									285	ec	171.7	172	?											146.6	146	ec										
									289	ec	196.3	198	ec											147.8	148	ecGB										
									293	ec	196.3	200												150.2	150	rare										
									295	ec	200.2	202												152.3	152	ec&hu										
									299	ec	202.4	204	widespread											154.3	154	widespread										
									etc	ec	204.1	206	widespread											156.4	155	widespread										
											206.8	208	widespread											158.6	158	widespread										
											207.9	210												160.8	160	gp 07										
											209.9	212												162.4	162	rare										
											213.6	216												164.4	164	rare										
																								166.6	166	hu										
																								168.4	168	rare										
																								170.4	170	rare										
																								172.5	172	rare										
																								174.4	174	rare										
																								176.6	176	mex										
																								210.8	210	Kent_2007										

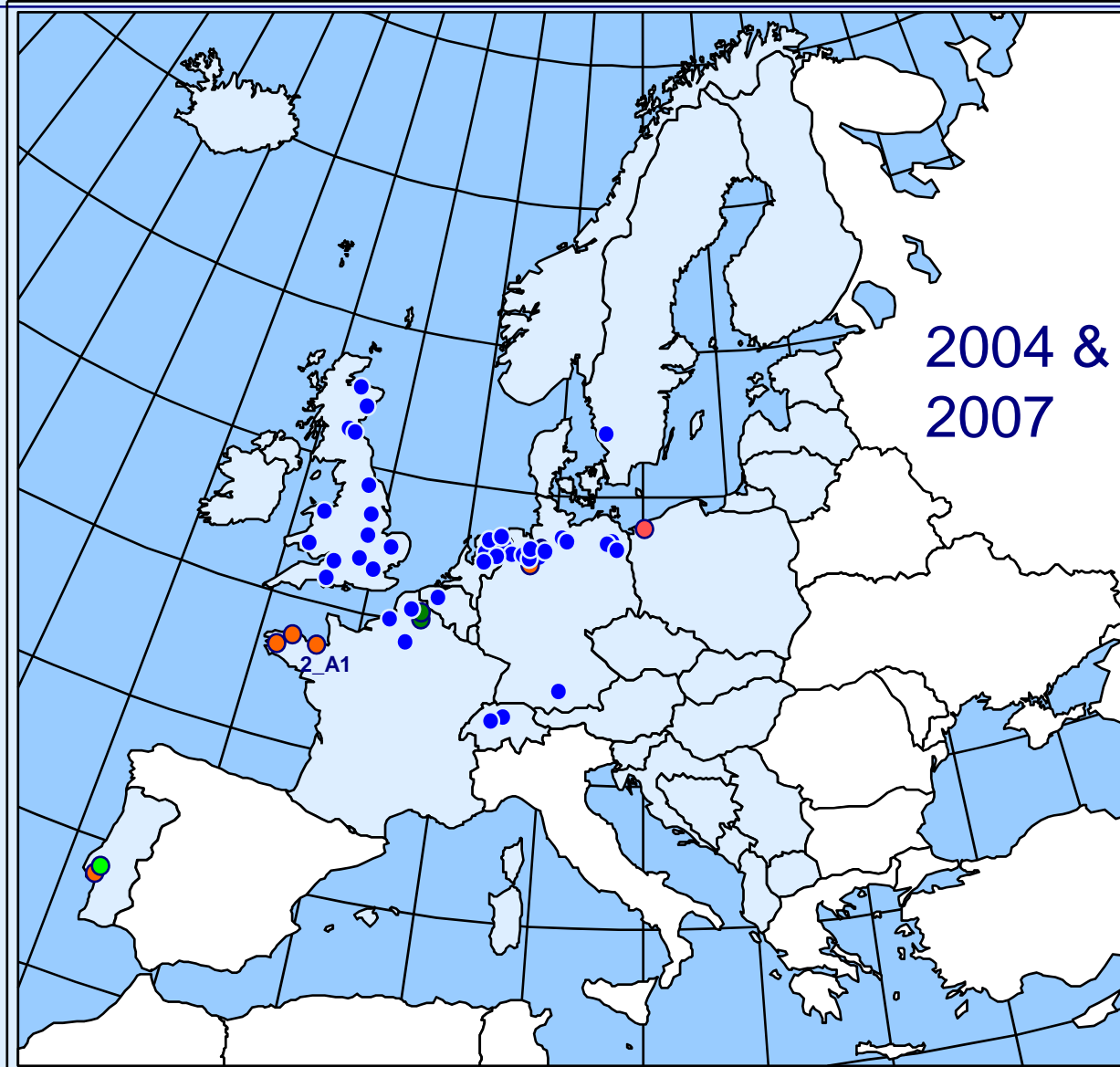
SSR allele information sheet indicating, for each locus: a) the actual peak size when run on an ABI 3730 according to the euca blight protocol b) the allele names used in the euca blight database and colour codes used by D. Cooke at SCRI and c) an indication of the frequency in the comment column that is based largely on GB populations. Additional notes are made under circumstances where a particular allele is associated with a country or clonal lineage.
see www.euca blight.org for protocol

Note this is a working document - comments can be passed back to david.cooke@scri.ac.uk

note a drift in size versus name from small to large alleles

SSR harmonisation

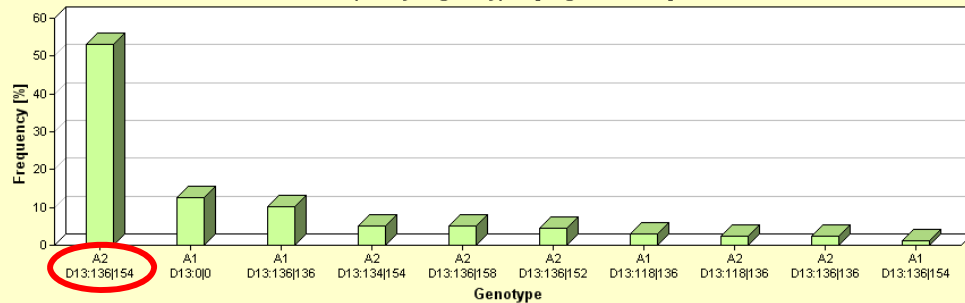
- **SCRI** (Pi02, Pi04, Pi16, Pi26, Pi33, Pi56, Pi63, Pi66, Pi70, Pi89)
- **UW Bangor** (D13)
- **Syngenta** (Pi4B, PiG11, Pi4G, Pi1D, Pi2D, Pi2H)
- **PRI** (SSR1-8)
- Theo van der Lee and David Cooke working on a revised set of the best 12 markers
- Markers and alleles already built into P.exe
- Existing SCRI system and allele images on Eucablight website



- European samples indicate '13_A2' present in NL and DE in 2004 & 2007
- 2007 French samples high frequency of A2 (Detourne et al., 2007)
- EUCABLIGHT data suggests this shift to A2 not universal: 2006 % A2 data (CZ 10, EE 12, HU <10, FI 40)
- Updates in SSR data needed
- Thanks to Bayer and Syngenta

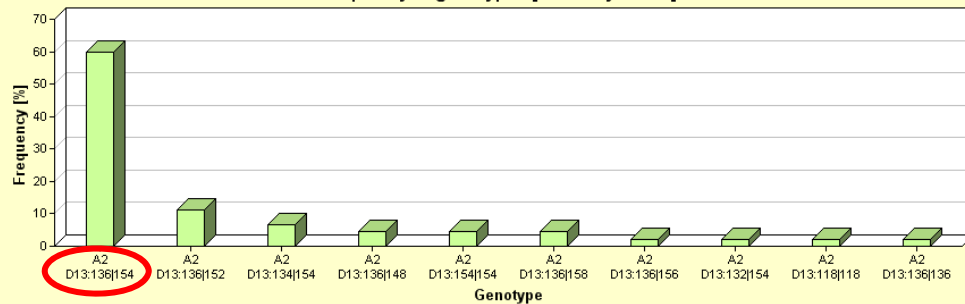


Frequency of genotypes [England - 2007]

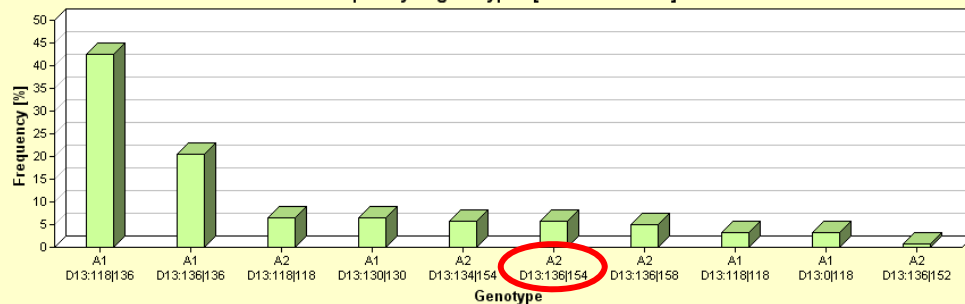


Number of isolates: 672 | Number of genotypes: 26
 Shannon index: 1,90 | Shannon Equitability J: 0,58 | Shannon Equitability E: 0,26
 Simpson's index of diversity: 0,72

Frequency of genotypes [Germany - 2007]



Frequency of genotypes [Scotland - 2006]



Number of isolates: 126 | Number of genotypes: 14
 Shannon index: 1,91 | Shannon Equitability J: 0,73 | Shannon Equitability E: 0,48
 Simpson's index of diversity: 0,77

	IE	IT	MA	ND	NL	NO	PE	PL	SC	SE	SK	WA
									5,6			21,3
				0,0	58,3				0,0			
							0,0		0,0			
				0,0					0,0	0,0		
				0,0					0,0			
				0,0			0,0					0,0
				0,0					0,0			0,0
				0,0					0,0			0,0
				0,0					0,0			0,0



Tracking type 13_A2 in the database

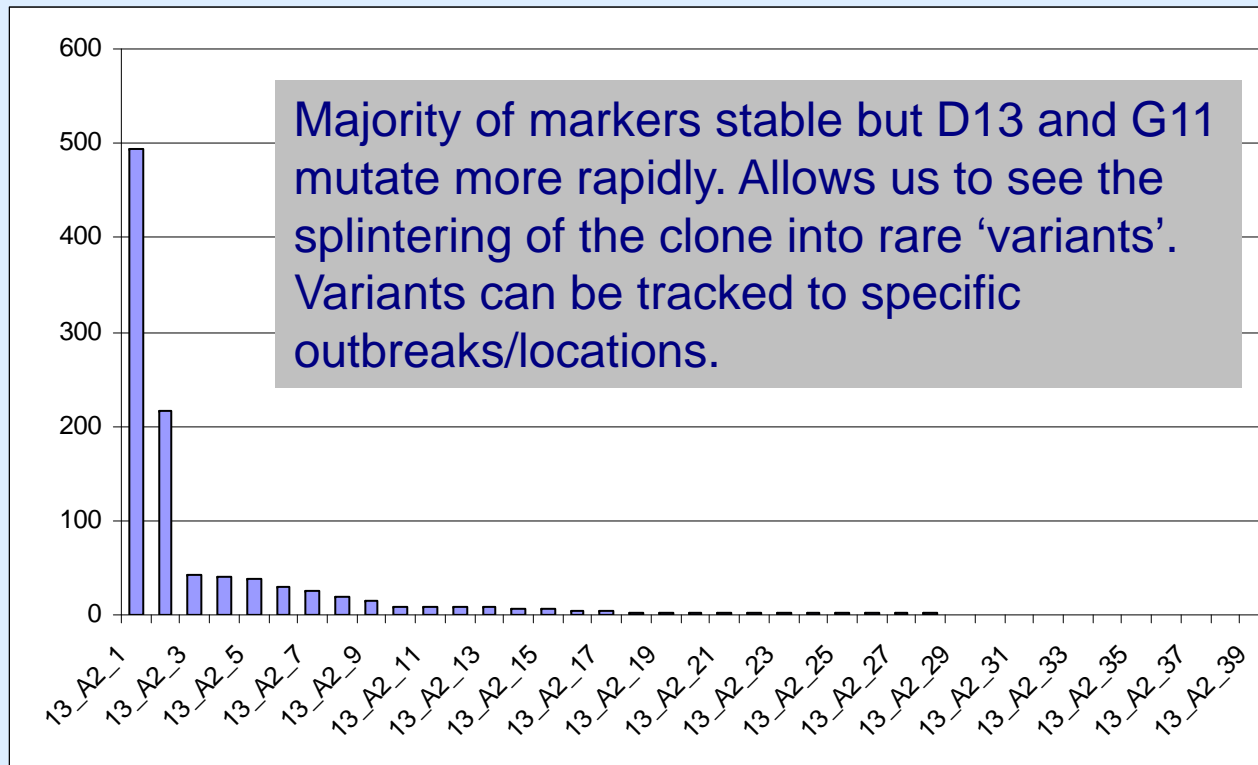


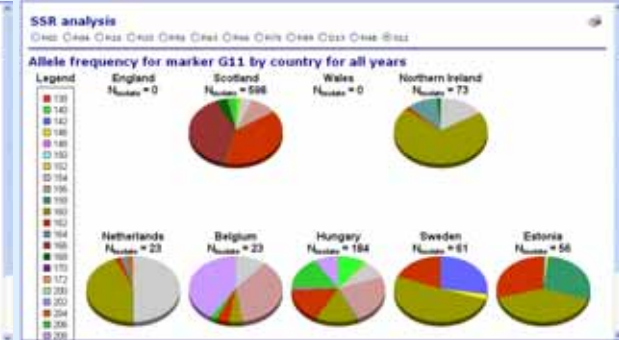
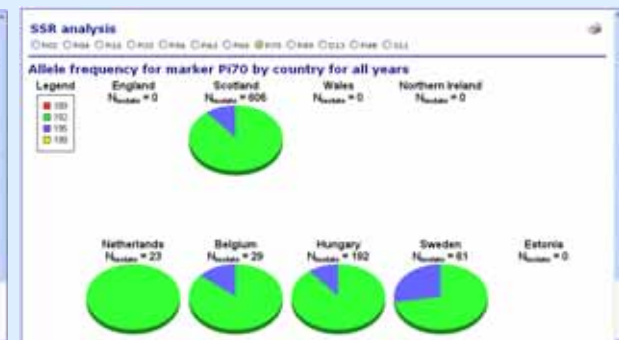
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162	162	0	118	136	0	203	203	160	168	213	217	178	178	154	154	0	176	176	0	0	0	0	0	0	
162	162	0	118	136	0	203	206	166	170	205	213	178	178	162	162	0	174	176	157	157	192	192	179	181	
162	162	0	118	136	0	203	206	166	170	205	217	176	178	160	160	0	176	176	151	157	192	192	179	181	
0	0	0	118	118	0	203	206	166	170	205	217	176	178	166	166	0	176	176	151	157	192	192	179	181	
160	162	0	118	118	0	203	206	166	170	205	217	176	178	162	162	0	176	176	151	157	192	192	179	181	
162	162	0	136	136	0	203	203	166	170	213	217	178	178	162	206	0	174	176	157	157	192	192	179	179	
162	162	0	136	136	0	203	203	166	170	213	217	178	178	162	203	0	176	176	151	157	0	0	181	181	
162	162	0	118	118	0	203	203	166	170	213	217	176	178	154	166	160	176	176	157	157	192	195	179	179	
162	162	0	136	150	0	203	203	166	170	213	217	178	178	154	166	0	176	176	148	157	192	195	179	199	
162	162	0	136	136	0	203	203	166	170	213	217	176	178	140	156	162	174	176	151	157	192	195	179	181	

900
13_A2
isolates
(stable)

13_A2 →

other GB
genotypes







Refined tools needed to:

Track changing allele frequencies over time and space

Genotype identification and naming

Plot relationships between genotypes

Search for specific genotypes

Relate phenotype to genotype

Map diversity – GIS systems





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- EU Framework 7 bid – Jan 08
 - USDA Biosecurity bid - June 08
 - Support of GILB/CIP

 - Need to build Eucablight database development into other funding bids
 - Sponsorship – other ideas?



- Unique resource to help understand pathogen population change on a range of scales
(thanks to all data submitters and DIAS)
- *P. infestans* population diverse
- Association between factors observed (e.g. fungicide resistance and mating type)
- Dramatic shift in many regions

- Database updates and more interpretation at local and EU scale required -2009 timescale
- Need to link data on population change with the cause of that change. Identify factors that 'push' or 'pull' population change (e.g. increased aggressiveness and fitness – need better links to fundamental research on effectors and R-genes)
- Better exploitation of host resistance (GM-based?) – will only work if we understand pathogen population
- Continue expansion beyond Europe - setting context of EU populations