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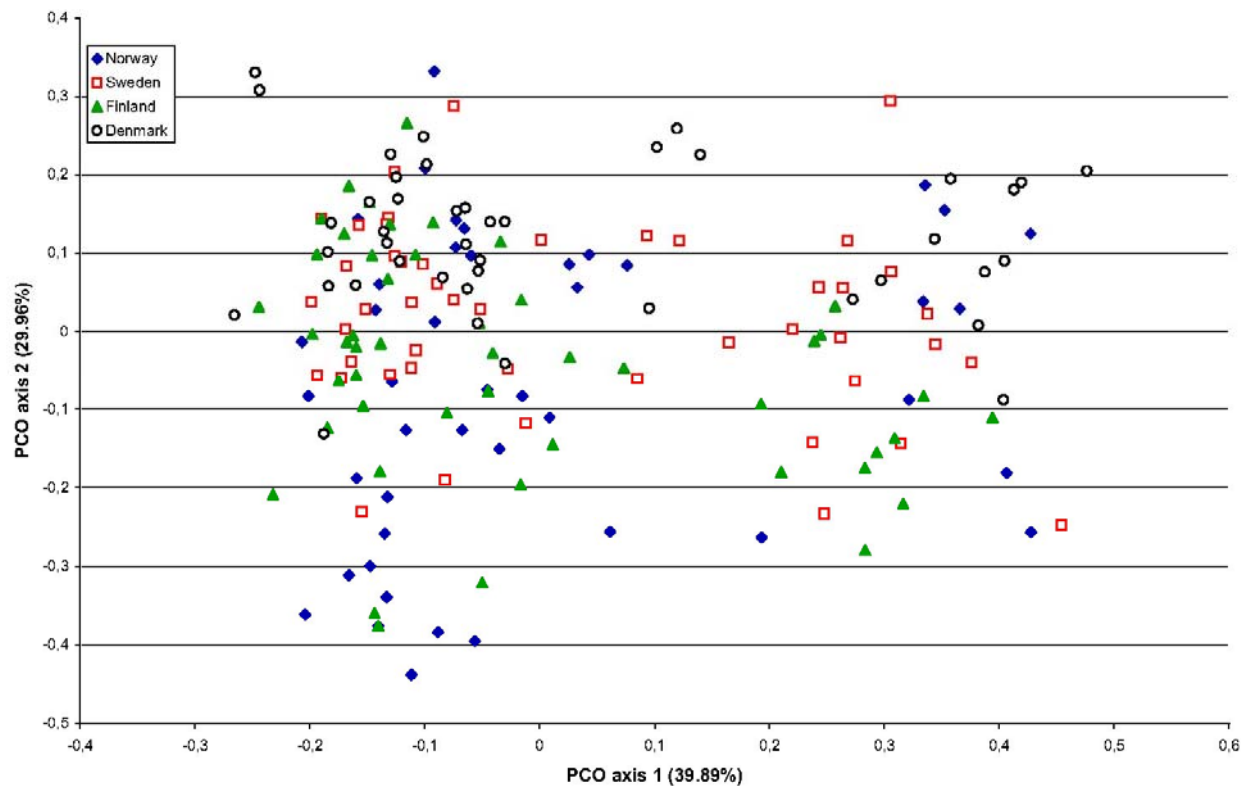
# Estimating pathogen migration and population size

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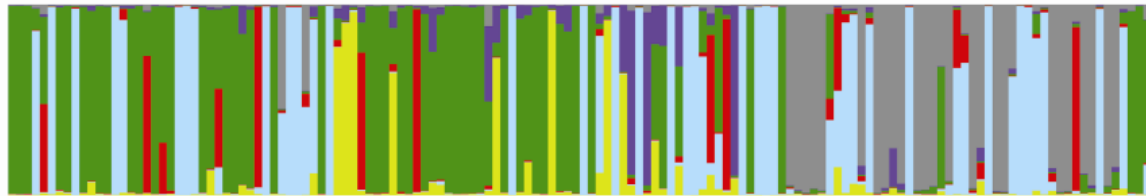
# Nordic populations of *Phytophthora infestans* are extremely variable



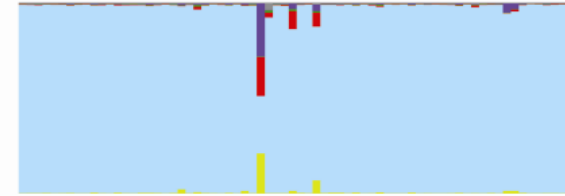
# The program 'Structure' can supply information about some pathogen populations



Barberry



Rye



Oats

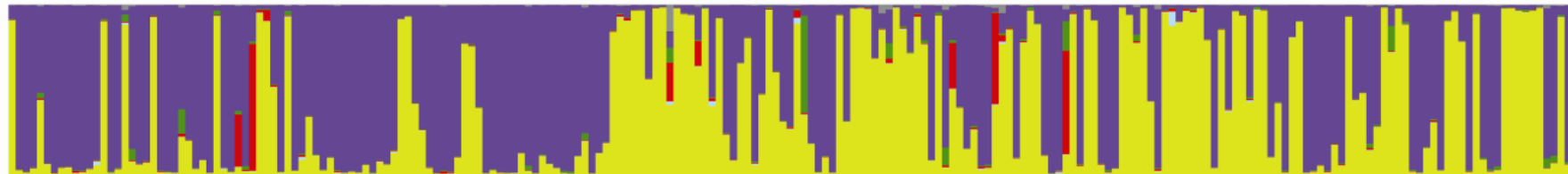


Fig. 3. Inferred ancestry of *Puccinia graminis* samples to six genotypic groups based on 11 simple sequence repeat markers using the program Structure. Each color represents one genotypic group.

But we haven't been successful  
with *P. Infestans*.....

Berlin et al, Phytopathology





# *P. infestans* from two hosts

Ecology and Epidemiology

## Can Weed Hosts Increase Aggressiveness of *Phytophthora infestans* on Potato?

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### ABSTRACT

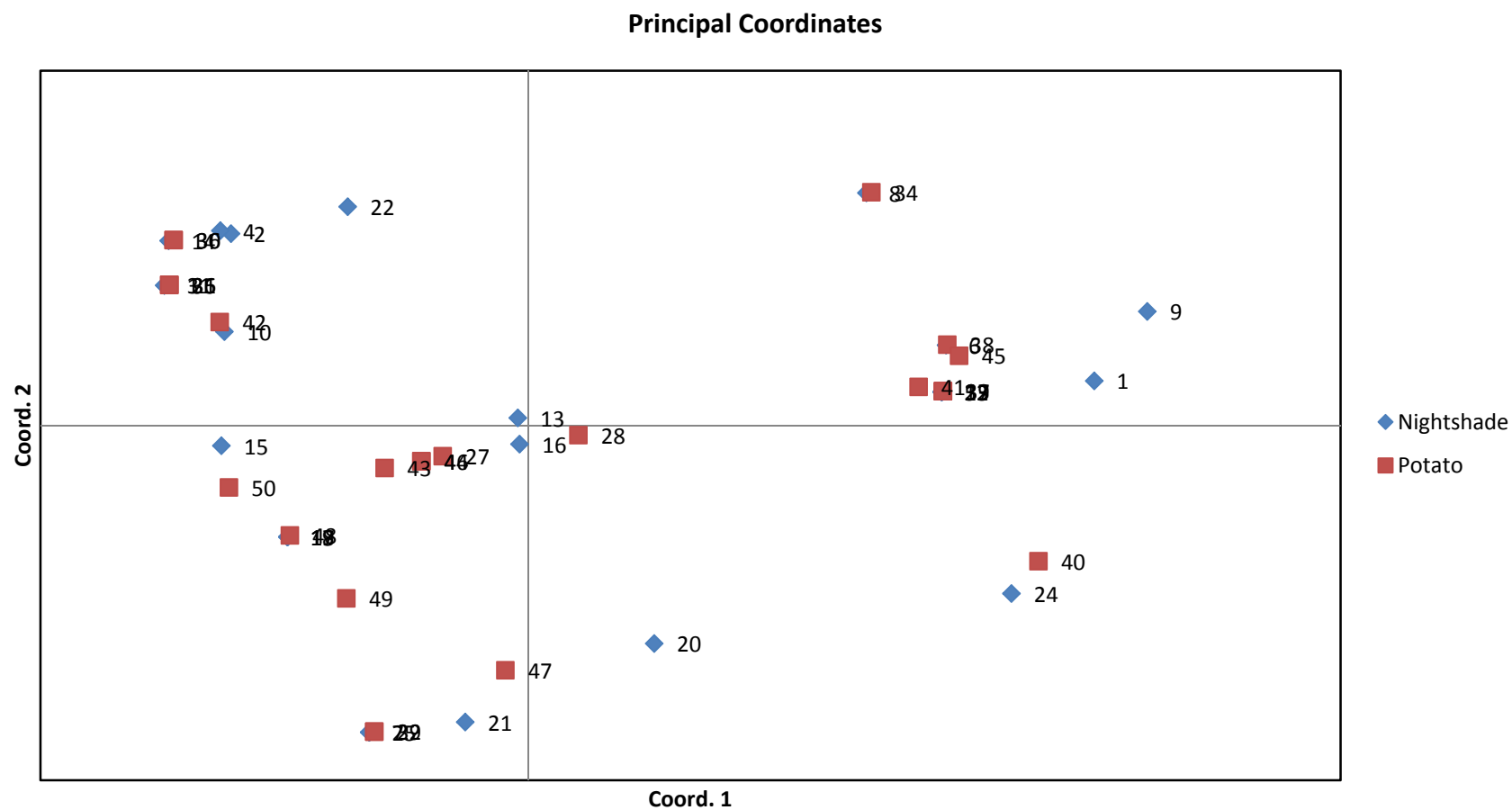
Grönberg, L., Andersson, B., and Yuen, J. 2012. Can weed hosts increase aggressiveness of *Phytophthora infestans* on potato? *Phytopathology* 102:429-433.

Potato late blight, caused by *Phytophthora infestans*, is a major disease in potato production throughout the world. In southern Sweden, hairy nightshade (*Solanum physalifolium*), an alternative non-crop host to the pathogen, is an increasing weed problem. Single-lesion leaves infected by *P. infestans* were collected from potato and hairy nightshade to determine phenotypic and genotypic population differentiation of *P. infestans* between the two hosts. Genotypic variation was estimated using micro-

satellites as markers. The results showed no genotypic differentiation in the samples between the two hosts. Aggressiveness tests were performed using the sampled isolates to cross-inoculate potato and hairy nightshade. The proportion of infected leaves, latency period, lesion growth rate, and sporulation capacity were measured. For isolates from hairy nightshade, the odds of infection were higher on both hosts combined. When tested on potato leaves, isolates from hairy nightshade showed a significantly shorter latency period and higher sporulation capacity compared with isolates from potato. This indicates that an alternative host can filter populations of *P. infestans* toward a higher aggressiveness, which could lead to increasing problems in controlling potato late blight.



# PCA of genotypes



# A second look with the program 'Migrate'

- ▶ Is there differentiation between the nightshade and potato populations (one population or two)
- ▶ What are the relative population sizes and migration rates (if two populations)?

# Migrate-N

- ▶ Estimates population size and migration rates (assuming asymmetric migration models)
- ▶ Can use either maximum likelihood or Bayesian inference
- ▶ Uses different kinds of input data
- ▶ Marginal likelihood can be used to compare different models with Bayes Factors
- ▶ Calculates the probability of the population parameters, given the data ( $\text{Prob}(P|D)$ )
- ▶ Integration via Markov Chain Monte Carlo (MCMC methods)

# Comparison of Models with Bayes Factors

| $2 \log_e(B_{10})$ | $B_{10}$         | Evidence against $H_0$             |
|--------------------|------------------|------------------------------------|
| 0 to 2             | 1 to 3           | Not worth more than a bare mention |
| 2 to 6             | 3 to 20          | Positive                           |
| 6 to 10            | 20 to 150        | Strong                             |
| Greater than 10    | Greater than 150 | Very Strong                        |

$$BF_{12} = \frac{P(D|H_1)}{P(D|H_2)}$$

Kass and Raftery, 1995

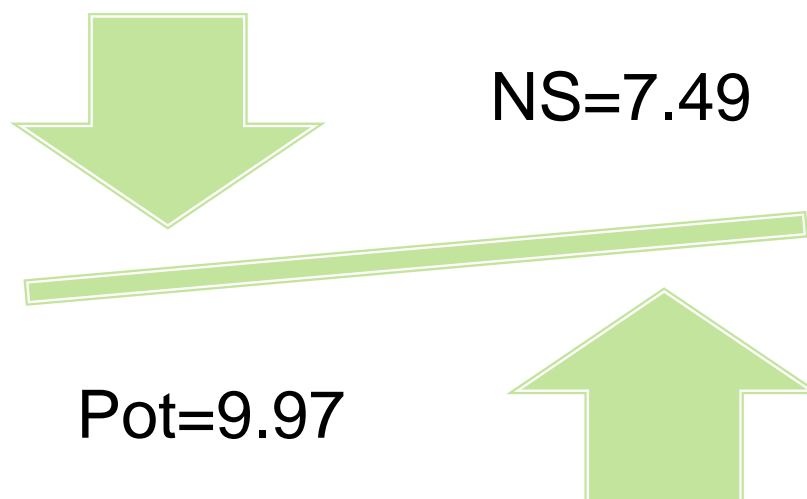


# Analysis of nightshade data using migrate-n

- ▶ Test a 'one population model' against a 'two population model' with migration between the two populations

# Comparison of Models

| Model          | Log Marginal Likelihood | Log (Bayes Factor) |
|----------------|-------------------------|--------------------|
| Full model     | -751.15                 | 0                  |
| One Population | -769.38                 | -18.23             |



# Can we find any population structure in the Nordic *P. infestans* populations?



- ▶ 2008 collection
- ▶ Multiple isolates from each field
- ▶ Genotyping with 6 SSR markers
- ▶ 524 genotypes in 836 samples
- ▶ Is there any population structure here?

# Is there a structure in the Nordic *P. infestans* populations?

| Model                        | Log Marginal Likelihood | Log (Bayes Factor) |
|------------------------------|-------------------------|--------------------|
| Full Model 4 populations     | -2333.54                | 0                  |
| 3 Population (SE+DK, NO, FI) | -2386.72                | -53.185            |
| 2 Population (SE+DK+NO,FI)   | -2736.4                 | -402.76            |
| 1 population                 | -4060.35                | -1726.81           |



# Relative Population Size and Range

| Populations | Relative Size    |
|-------------|------------------|
| Sweden      | 4.28 (2.36-7.43) |
| Finland     | 1.48 (0.43-2.36) |
| Denmark     | 2.22 (0.33-4.66) |
| Norway      | 1.57 (1.30-1.70) |

# Population Migration

|          | Source population |                   |                   |                   |
|----------|-------------------|-------------------|-------------------|-------------------|
| Sink Pop | Sweden            | Finland           | Denmark           | Norway            |
| Sweden   | ...               | 3.17 (0.33-9.00)  | 0.33 (0.33-0.33)  | 3.5 (0.33-6.34)   |
| Finland  | 0.33 (0.33-0.33)  | ...               | 9.67 (0.33-13.00) | 6.17 (0.33-15.67) |
| Denmark  | 0.33 (0.33-0.33)  | 8.17 (0.33-13.67) | ...               | 2.00 (0.33-7)     |
| Norway   | 2.17 (0.33-5.67)  | 1.58 (0.33-5.00)  | 3.50 (0.33-13.00) | ...               |

# Migration patterns in Scandinavia

