

# Mapping the *H2* Resistance Gene in Potato

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## Introduction



The *H1* gene confers almost complete resistance to pathotype Ro1 of the potato cyst nematode *Globodera rostochiensis* (Bakker *et al*, 2004) and since its discovery it has been integrated into several commercially available cultivars, including Maris Piper. The success of *H1* containing cultivars has inadvertently led to selection for *G. pallida*. Unlike *G. rostochiensis*, no single gene has been discovered which confers complete resistance against all three European *G. pallida* pathotypes. The best method to create broad spectrum, durable resistance is to stack several resistance genes into a single cultivar. The *H2* gene is considered to be a single copy, dominant gene which confers a high level of resistance to *G. pallida* pathotype Pa1 (van der Voort *et al*, 1998), and partial resistance to Pa2/3. The *H2* gene has never before been mapped to the potato genome and here we outline the methods used to determine its location.

## Objectives

- Generate phenotypic data from Pa1 infection of a Picasso x P55/7
- Identify potato material containing the *H2* resistance gene

## Methods

### Plant Material

A cross between susceptible cv Picasso and resistant P55/7 yielded 192 progeny plants. Cuttings were taken and used in the first screening experiment (Summer 2014). Tubers from 154 plants were used for the second screen (Spring 2015).

### Bio Assay Screen

Material was infected with ~15 Pa1 cysts and left to grow for 8 weeks to allow suitable root systems to form and the cysts to hatch and the resultant juveniles to carry out their lifecycle. Experiments were replicated three times, with repeats two and three having randomised plant position. After 8 weeks, root trainers were opened and all visible females were counted.

## Results

The screening experiment was carried out twice due to leaf cutting death/poor growth in Summer 2014, which directly impacted analysis. Repeating using tubers increased survival rate, allowing better analysis of when a plant was either susceptible or resistant. The segregation ratio for the Spring 2015 experiment was 0.8:1 (data not shown) which is close to the 1:1 ratio expected from a cross of this type. This confirms the hypothesis that the *H2* gene is acting in a dominant manner. Figure 1 shows a positive skew in the distribution, suggesting that although the progeny segregated in a 1:1 ratio, multiple genes may be controlling the resistance phenotype. This supports JM Dunnett's (1961) hypothesis that *H2* is not a single resistance gene but multiple genes acting together.

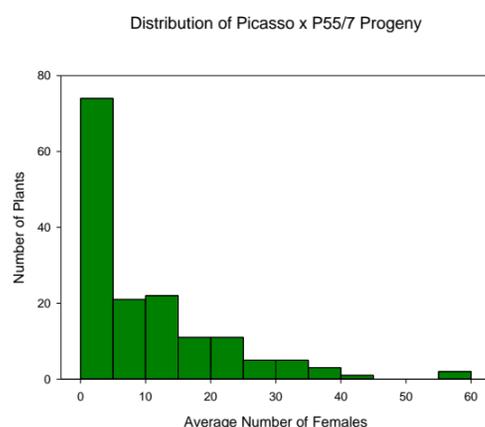


Figure 1: Distribution of females observed on Picasso x P55/7 cross. The results show a positive skew to the left

## Implications for the Industry

The next stage of this research will be to carry out gene enrichment across all 12 chromosomes of potato to try and determine the location of the *H2* gene(s). With the location of the gene, quicker and more efficient work can be carried out in both genetic and breeding screens.

Identification of *H2* will give the industry another gene which can be combined with current resistances against not only parasitic nematodes but other pathogens to help create durable and sustainable cultivars for the future.

### Acknowledgements

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### References

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