Accelerated potato breeding using genomics

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Amanpreet Kaur [1,2], Drummond Todd[3], Vanessa Young[3], Xinwei Chen[1], Ingo Hein[1,4]

1. James Hutton Institute, Dundee
2. International Potato Center, Peru
3. James Hutton Limited, Dundee
4. University of Dundee, Dundee

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Introduction

Disease-related crop losses threaten UK potato production, with £50 million spent annually controlling late blight alone. Potato cyst nematodes further endanger the seed industry. Genomic tools, particularly diagnostic Resistance gene enrichment Sequencing (dRenSeq), have transformed resistance breeding. Our research generated high-resolution disease resistance gene profiles for 1043 samples including varieties, wild species and breeding clones worldwide. This resource informs parental selection, enables strategic stacking of disease resistance genes against major pests and diseases, and accelerates marker development. Critically, it has shortened the breeding cycle from 10 – 12 years to as little as 7 years, expediting delivery of resistant, high-performing potato varieties to growers.

Methods

1. The Commonwealth Potato Collection (CPC) is screened for resistance against major potato diseases including late blight, potato cyst nematodes and viruses.
2. DNA from resistant plants is isolated and enriched using state-of-the-art techniques such as Resistance gene Enrichment and Sequencing (RenSeq) to identify underlying resistance sources.
3. Diagnostic RenSeq (dRenSeq) enables presence/absence profiling of novel resistance genes.
4. This information is integrated into breeding programmes to guide parental selection.
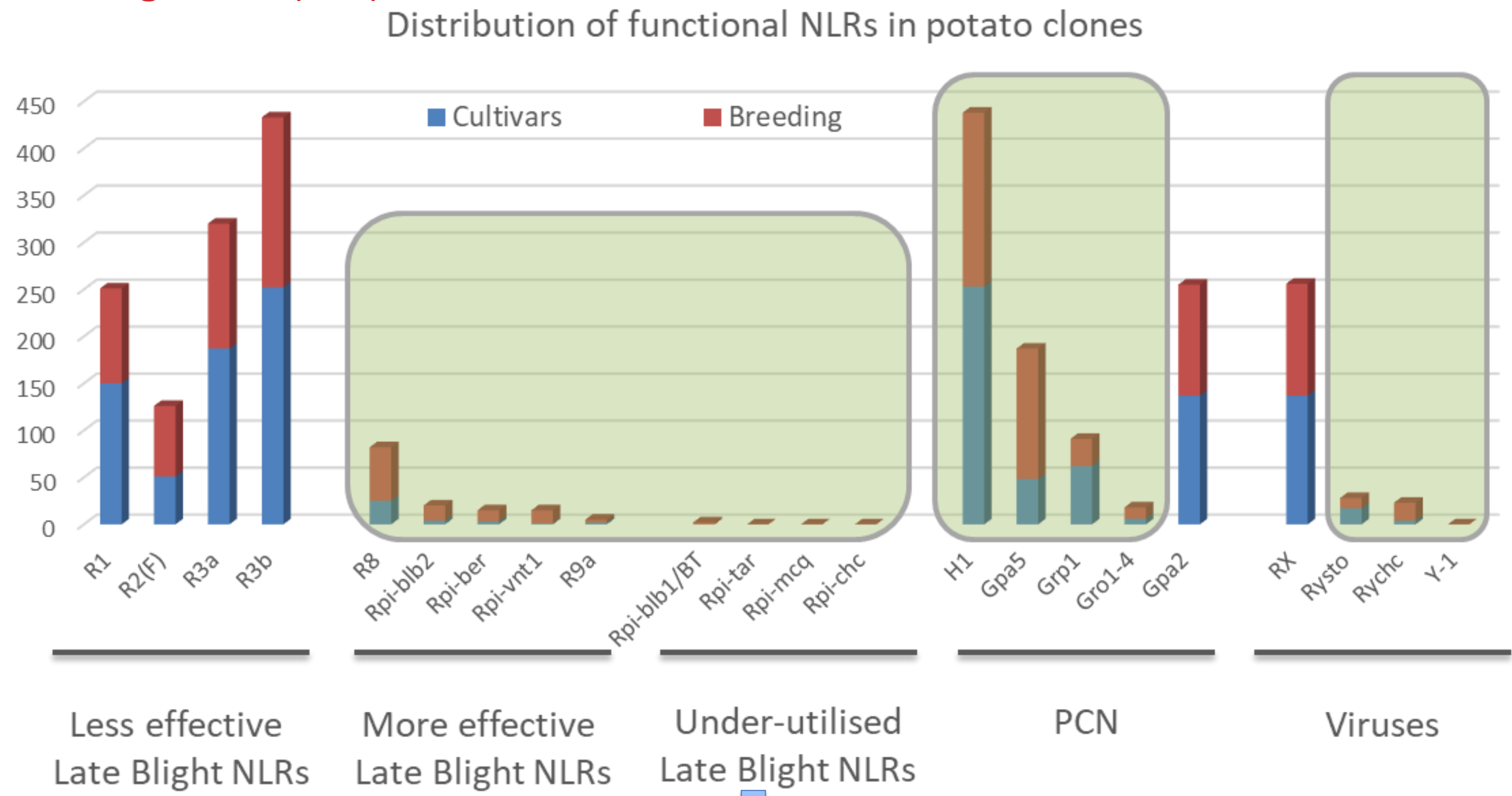
Figure 1 – Accelerated potato breeding pipeline from the Commonwealth Potato Collection through genomics (dRenSeq) to breeding, enabling informed selection of parents and accelerating resistant cultivar development from 12 to 7 years

CPC diversity   Genomics/genetics   Breeding

Results

Evaluation of 1,043 samples for the presence or absence of functional resistance genes against major potato diseases (late blight, potato cyst nematodes, and viruses) revealed that currently grown cultivars and available breeding lines are dominated by resistance genes that are no longer effective.

Figure 2 : Distribution of Functional NLRs in 1043 Samples Varieties (626) and Breeding clones (417)

Distribution of functional NLRs in potato clones

Less effective Late Blight NLRs | More effective Late Blight NLRs | Under-utilised Late Blight NLRs | PCN | Viruses

This advanced genomic information has been integrated into potato breeding programmes, along with off-season LED seedling production and marker selection in year 2, to accelerate parental selection and reduce the breeding cycle from 12 years to 7 years.

Two disease resistant varieties developed in only 7 years at JHL from the parental breeding clone 18_WC_1A23 are currently included in the National Trials list

Conclusions

1. We have reduced the time required for potato breeding from 12 to 7 years by integrating genomic tools to guide parental selection.
2. Using dRenSeq outcomes, two new late blight-resistant varieties (from initial crosses established in 2018) are set to complete National List Trials in 2025.
3. New parental material is being developed at JHL through resistance gene stacking, enabling the creation of potato varieties with enhanced and more durable disease resistance against multiple pathogens.
4. Leveraging the developed datasets, we are creating a high-throughput diagnostic genotyping platform (MAXY-ID) to accelerate seedling selection in the second year of breeding programmes.

References

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sefari.scot   info@sefari.scot   @SEFARIscot

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