A MULTI-OBJECTIVE NSGA-LL APPROACH TO OPTIMISING GENOMIC AND PEDIGREE-BASED POTATO BREEDING

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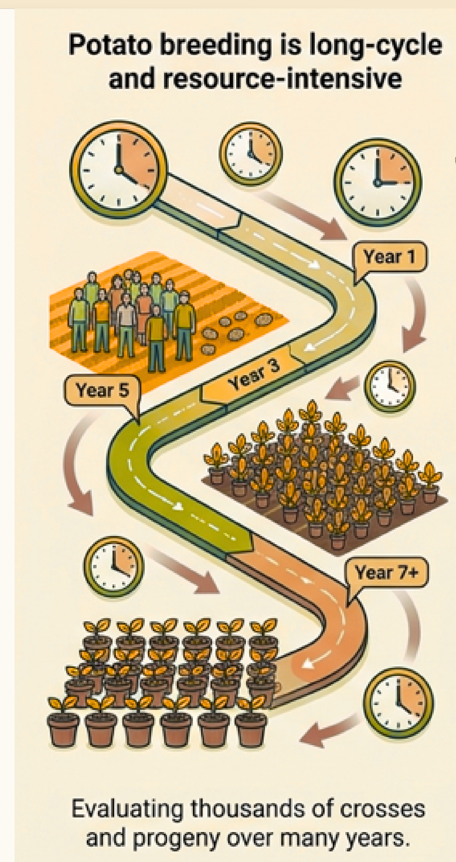
INTRODUCTION

Potato breeding: long-cycle, resource-intensive ·
Thousands of crosses evaluated across multiple seasons ·
Marker-Assisted Selection (MAS): DNA markers identify resistance genes early ·
Teagasc: 2,000+ varieties with MAS, pedigree & phenotypic trial data · AI optimisation enables strategic crossing decisions

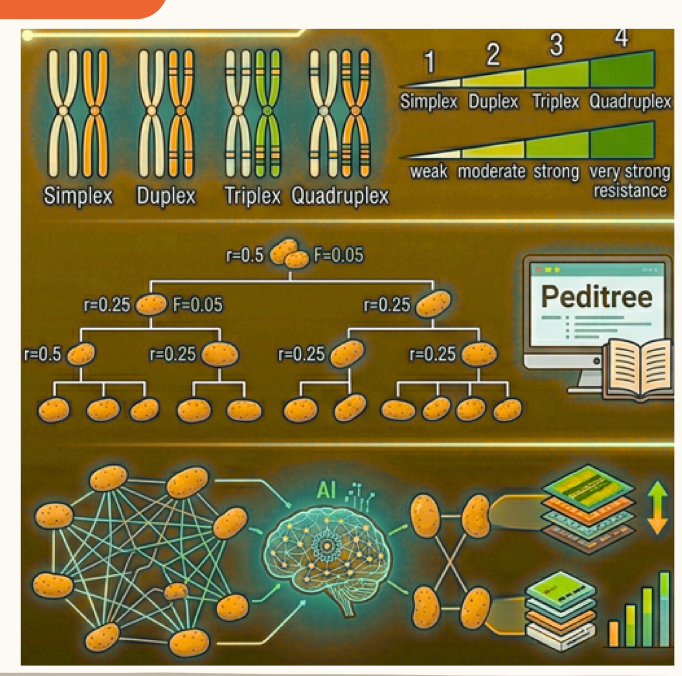


RESEARCH OBJECTIVE

AI-based decision-support system integrating MAS marker data, pedigree-based kinship & phenotypic trial data · Maximise disease resistance stacking · Maintain agronomic performance · Control inbreeding

BACKGROUND AND SIGNIFICANCE

Autotetraploid crop — 4 chromosome copies ·
Peditree quantifies relatedness between breeding lines ·
Genomic markers + pedigree data → efficient resistance gene stacking

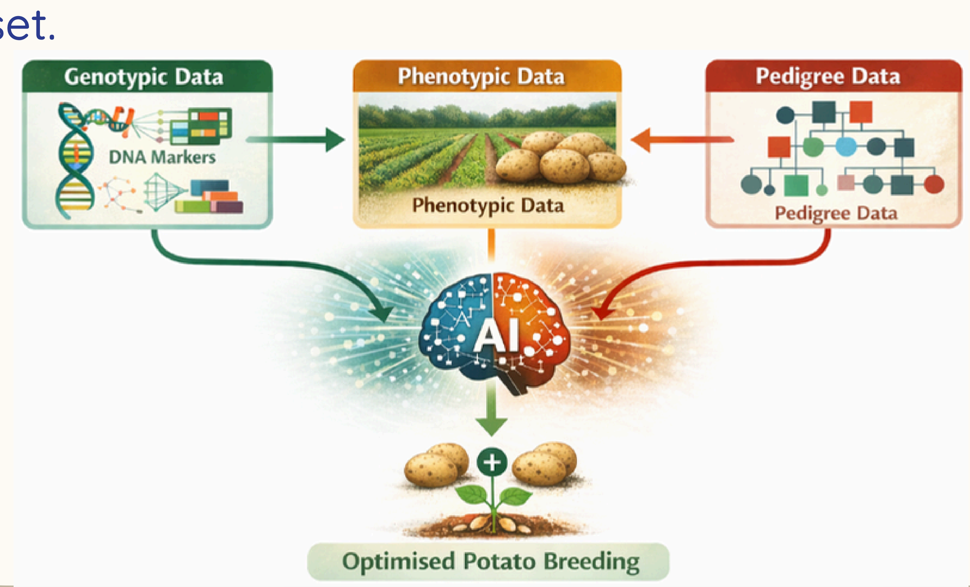


THE DATASET (TEAGASC - CONFIDENTIAL)

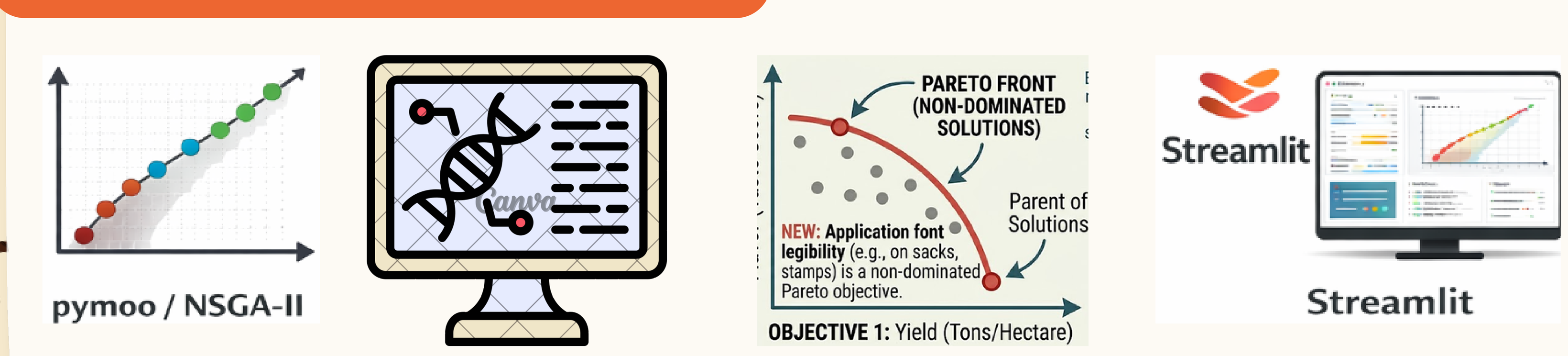
pedigree records from Teagasc's active potato breeding programme — 2,323 varieties.
Allele dosage encoding: 0 = nulliplex (no alleles), 1 = simplex, 2 = duplex, 3 = triplex, 4 = quadruplex (fully resistant)

METHODOLOGY

Dosage encoding 0–4; BLUP normalisation across multi-year trial environments.
Apply Genetic Algorithm using single objective.
NSGA-II Cross Optimisation Each candidate cross encoded as (female, male) — an integer pair indexing the variety dataset.



TECHNOLOGIES



EARLY INDICATIONS & NEXT STEPS

Early Indications:

- Potato encoding 0–4; BLUP normalisation across multi-year trial environments.
- The single-objective GA is also performing strongly, with resistance stacking scores.

Next steps include:

- Expand the model into a full NSGA-II framework using all three objectives.
- Generate a Pareto front of optimal crossing pairs.
- Develop a Streamlit-based explainable prototype to display ranked crosses and marker-wise resistance profiles.
- Compare results with a random baseline using the hypervolume indicator

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