Inheritance of potato processing traits in a half-diallel breeding population segregating for Columbia root-knot nematode resistance

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Abstract

The Columbia root-knot nematode (*Meloidogyne chitwoodi*) is a destructive soil borne pest that can cause serious economic damage to potato tubers within infected, unfumigated fields. There are very few known sources of genetic resistance to root-knot nematodes and no released potato cultivars exhibit this trait. Literature indicates that nematode resistance introgressed from Solanum bulbocastanum is dominantly inherited across many genetic backgrounds. We generated a 32 family half-diallel progeny test population utilizing 3 root-knot nematode resistant clones (female) and 11 clones (male) with russet skin type (1,600 clones, between 25 – 60 clones per family). In 2023, 1,200 progeny were evaluated relative to 6 control varieties planted at high replication at the Washington State University Experiment Station in Othello, WA. A scale, RGB-D imaging conveyor, and index scoring system was used to record: total yield, the number of tubers per plant, tuber size distribution, aspect ratio, skin color, starch content, and defect severity from all samples within this population. The distribution of phenotypic values observed from the progeny suggest that choice of parent is a highly significant factor that influences almost all traits evaluated. The phenotyping strategy utilized by our team is inexpensive, expandable, and flexible enough to be adopted by many different types of vegetable breeding programs. Data from this experiment is being used to develop potato tuber defect classification models and assess the utility of adopting genomic selection within our potato breeding program.



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BodyText:

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