

**Pest Resistance**

Trait	At present	Next 5 years
PVY	<ul style="list-style-type: none"> <li>*Extreme resistance (R<sub>yadg</sub>) already present in many chip clones; clones are screened with DNA marker in FY3</li> </ul>	<ul style="list-style-type: none"> <li>*Move PVY-resistance from chips to reds and russets by crossing and selection with marker</li> <li>*Use Japanese clones with R<sub>y<sub>chc</sub></sub> to stack resistance; DNA marker is already available</li> </ul>
Late Blight	<ul style="list-style-type: none"> <li>*We have a few chip clones with the R8 gene, which is effective against US-8</li> <li>*In 2018 we created DNA marker for R8</li> <li>*We have a few russets with same resistance as Defender &amp; Palisade</li> <li>*Crossing with K41 to introduce RB gene into current germplasm</li> </ul>	<ul style="list-style-type: none"> <li>*Increase frequency of R8 gene in chip germplasm through marker-assisted selection</li> <li>*Move R8 into russet background through crossing</li> <li>*Develop and apply DNA marker for Palisade resistance</li> <li>*Stack late blight resistance genes through crossing and marker-assisted selection</li> </ul>
Golden nematode	<ul style="list-style-type: none"> <li>*H1 gene for resistance to pathotype 1 is present in many chip clones; clones are screened with DNA marker in FY3</li> </ul>	
<i>G. pallida</i> nematode	<ul style="list-style-type: none"> <li>*Crossing with two resistant clones from Europe</li> </ul>	<ul style="list-style-type: none"> <li>*Use published DNA markers to select for resistance</li> </ul>
Common scab	<ul style="list-style-type: none"> <li>*There are no validated R genes</li> <li>*Collaborating with Felix Navarro to screen clones beginning FY3</li> </ul>	<ul style="list-style-type: none"> <li>*Identify new sources of resistance</li> <li>*Use genomic prediction model</li> </ul>
Verticillium wilt	<ul style="list-style-type: none"> <li>*There are no validated R genes</li> <li>*Select based on natural disease pressure at Hancock and Rhineland (in fumigated fields)</li> <li>*Few clones per year evaluated in disease nursery by Jansky group</li> </ul>	<ul style="list-style-type: none"> <li>*Screen clones earlier in the selection process (FY4?) in dedicated disease nursery</li> </ul>

### Agronomics & End-Use Quality

Trait	At present	Next 5 years
Yield & size distribution	*Hancock Ag-Ray used to calculate total yield, size fractions, and tubers per plant starting FY3	*Use genomic prediction model
Maturity	*Vine maturity rating in early August *Early trial (vine kill 90 DAP) to measure tuber bulking starting FY4 *Skin set scored visually on grader	*Use aerial imaging to characterize canopy development over entire season *Use genomic prediction model
Water & N use efficiency		*Use aerial imaging to characterize
Hollow heart	*Measure in 20 tubers starting FY3	
Tuber Dormancy	*Measured starting FY3	*Develop DNA markers
Blackspot bruise	*Collaborating with Hancock SRF to measure in FY4 russets	*Extend to FY4 chips
Tuber appearance	*Scored visually on grader	*Investigate genetics of netting/russeting, develop markers *Develop germplasm with "second skin" = pigmented phelloderm *Measure changes in red skin color during storage
Lenticels		*Develop flooding stress test to measure lenticel size
Specific gravity	*Underwater weight measured in bulk sample	*Investigate genetics of dry matter distribution within tuber *Use genomic prediction model
Fry color & defects	*Chip clones fried beginning FY2 *Russet clones fried beginning FY4 in collaboration with Hancock SRF	*Lower storage temp for chips to 45F to improve selection for cold-sweetening resistance *Use genomic prediction model
Taste & Texture	*Informal tasting by program staff; chef evaluation with Dawson group *Clones in NFPT undergo sensory evaluation by processors	