

Proteomics-based biomarkers for seed potato physiological age

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KEY POINTS

- Tuber ageing accelerate above 4° storage temperature
- Seed tuber physiological ageing is reflected in the proteome.
- PCA confirms structured, reproducible proteomic variation with storage time.
- Candidate proteins show progressive ageing-associated trajectories.
- Cross-season and treatment validation is ongoing.

Why this research?

Physiological age (p-age) of seed potato tubers strongly influences plant vigour, canopy development, tuber size, and total yield. Current methods for assessing p-age rely on visible traits such as sprouting behaviour and storage conditions; however, these methods are slow requiring >1 month, cultivar dependent, and impractical for pre-planting decisions. As a result, a fast and reliable method to quantify p-age is still lacking. Advances in proteomics offer a promising alternative, as it has been successfully employed in other crops for biomarker discovery. These approaches have strong potential to identify protein biomarkers linked to physiological status of seed tubers. Storage temperature is a key driver of potato p-age, with higher temperatures accelerating metabolic activity, dormancy release, and sprout development.

Objective

To identify the key proteins that could serve as a biomarker for p-age using proteomics analysis.

Experimental approach

Potato seed tubers (RBV from two locations) were artificially aged using heat treatment (32°C for 3 weeks), which was applied to half of each seed batch. Heat-treated seed tubers were then transferred to 4°C for storage, along with control tubers, which did not undergo heat treatment. Samples were collected every month for proteomics analysis.

Protein profiles were analysed using untargeted proteomic techniques (LC-MS/MS) to identify potential protein biomarkers associated with p-age.

Candidate biomarkers were identified and evaluated for consistency across treatments, and promising markers will be used to develop a rapid and simple assay.

Results

- Quantitative proteomic analysis of Y1 heat-treated seed tubers revealed distinct protein abundance patterns associated with p-age (Figure 1).
- LC-MS/MS based proteomic profiling detected reproducible, storage-time-dependent changes in a subset of proteins over storage time (Figure 2).
- Differential abundance analysis identified a panel of candidate proteins that show progressive changes with increasing p-age, which are being prioritized for further validation.
- These preliminary results support proteomics as a biomarker discovery tool for seed tuber p-age, with ongoing validation aimed at developing a rapid, practical and industry-ready assay.

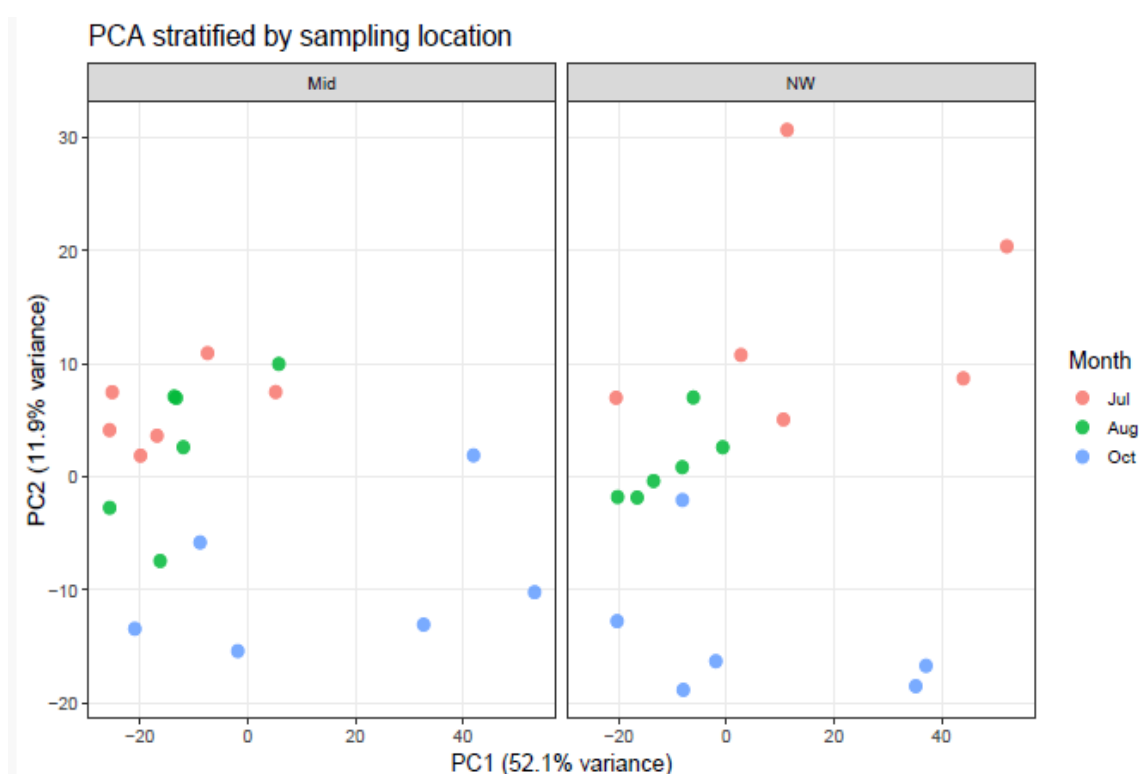


Figure 1.. Principal component analysis (PCA) stratified by sampling location reveals clearer ageing associated clustering. This shows that samples from the same location and storage time cluster more closely, indicating location affects ageing-related proteomic patterns.

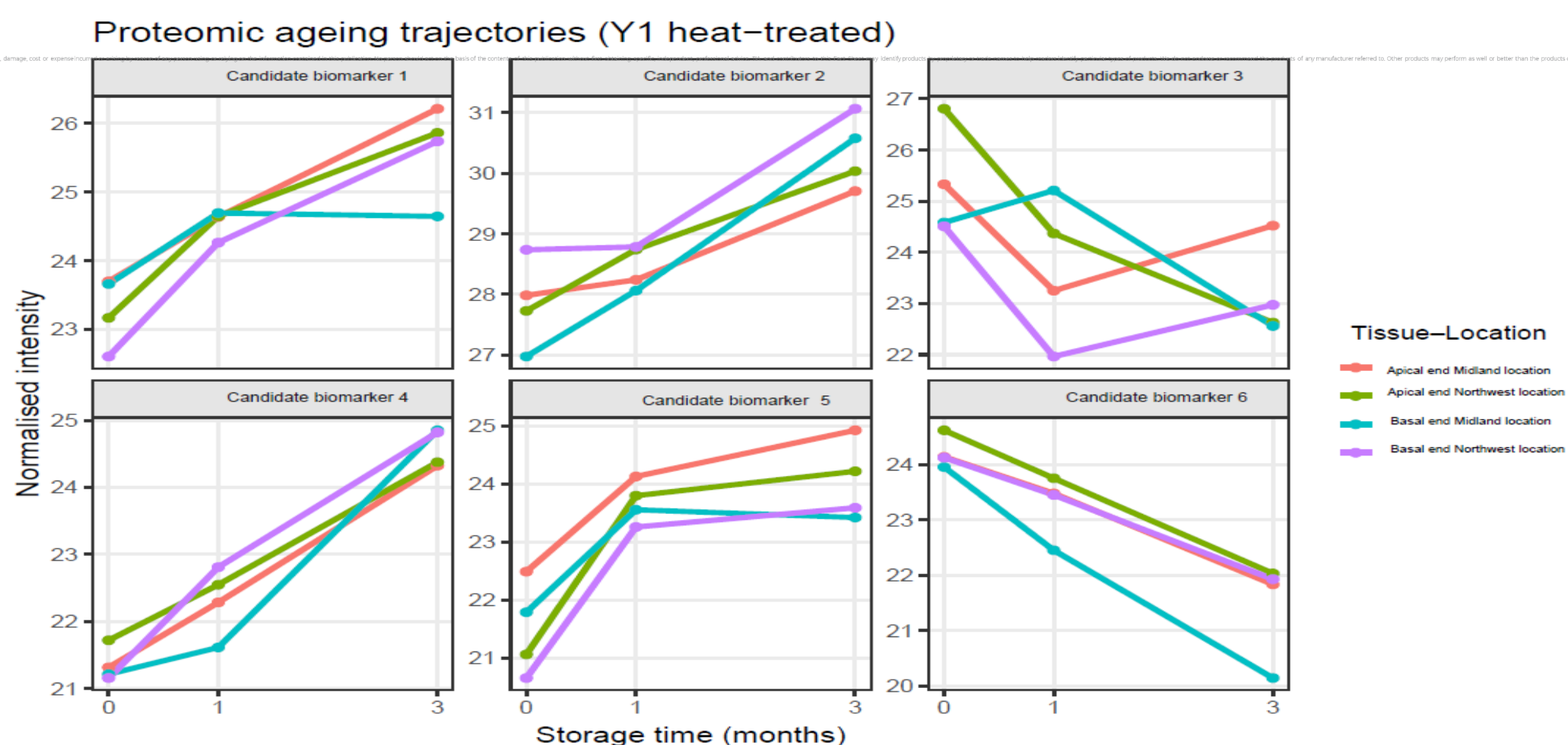


Figure 2. . Proteomic ageing trajectories in Y1 heat-treated seed potato tubers. Storage time is shown as months of storage (0=July, 1= August, 3= October). Lines represent mean normalised protein abundance for each tissue-location combination across two locations. Progressive increases or decreases in protein levels over time indicate systematic ageing patterns, supporting them as candidate ageing markers, with some modulation by tissue and seed location.

What's next?

The proteins in graph shown are natural molecules in seed tubers that change consistently as tubers age in storage. These progressive patterns reflect p-age rather than short term stress. Measuring a small group of these proteins together could enable a rapid, objective test to assess tuber age earlier and more reliably than traditional methods.