Figure 2. Adult Dingy Cutworm Moth.

800 or more adult Army Cutworm or 200 or more adult Pale Western Cutworm Moths. The final adult Army Cutworm moth numbers for each site are 747 for Senter and 1,202 for Dietrich. The adult Pale Western Cutworm moth numbers for both sites were low, 11 at Senter 11 and 9 at Dietrich.

Recently, Dr. Wenninger asked if I would write a letter of support for a grant proposal on cutworm moths. The grant proposal is a regional one with Dr. Kevin Wanner from Montana State; Dr. Peter J. Landolt, Research Leader at the USDA-ARS in Wapato, Washington; and Dr. Erik Wenninger from the University of Idaho. I hope that this project can provide us with valuable information, which will be beneficial to our growers in the future.

DNA FINGERPRINTING OF SUGARBEET VARIETIES TO TRACK ROOT ROT

Imad Eujayl and Carl Strausbaugh
USDA-ARS, NWISRL, 3793 N. 3600 E., Kimberly, ID 83341
E-mail: imad.eujayl@ars.usda.gov

The sugar beet industry is continuously undertaking major efforts to reduce postharvest sucrose losses. In Idaho sugarbeet roots may be stored indoors or outdoors for up to five months. Sugarbeet variety genetic make-up, pre-harvest field conditions, harvest practices, and post-harvest storage conditions can affect storability significantly. Physical root conditions and root health before delivery to the pile contribute to the magnitude of sucrose losses.

Growers chose different varieties for a certain season and may plant more than one variety in a field. This practice renders it difficult to collect information on the exact location of varieties in the field and storage piles. Additionally, it's a daunting task to physically tag samples starting in the field until delivered to the pile, as well as, it is difficult to locate these samples after a storage period of a few months.

In an effort to advance knowledge of varietal effect on storability, DNA fingerprinting was used to track varietal postharvest performance. In general DNA markers are used routinely in marker-assisted breeding of many crops including sugarbeet. For example, in genetic mapping studies, if a DNA marker was found genetically linked to a disease resistance gene(s), it can be used to screen specific targets in pre-breeding germplasm in the laboratory to expedite advancement of breeding lines and allowing for repeated cycles of screening in the early stages of breeding before final field screening.

The objective of this study was to develop a DNA fingerprinting database to trace variety performance during storage. The performance data was collected from different storage piles and roots were sampled. DNA was isolated from root samples and fingerprinted using database markers to identify unknown varieties.

Eighty-seven varieties including conventional and Roundup® ready varieties that were approved by the Snake River Sugar company for seasons 2007 to 2010 were analyzed in this study. Seeds were provided by Amalgamated Co. Seedlings were grown in the greenhouse and DNA was isolated from healthy leaves and roots using standard DNA isolation kits. The experiment was designed to identify useful markers by elimination of markers that generate redundant alleles. Seventy DNA markers, known as Simple Sequence Repeats (SSR) or microsatellites, were used for fin-

gerprinting of all varieties. For each of these 70 SSR markers a primer pair was used to amplify DNA samples from leaf and root using Polymerase Chain Reaction (PCR). The PCR analysis involved 1680 reactions and the PCR product was visualized using capillary electrophoresis. Primer pairs that produced a DNA pattern that was unique by itself or in combination with other primer pair patterns were selected to be used for variety identity tests (Fig. 1). The analysis revealed 4 SSR markers that generated 19 allelic variants which are capable of uniquely identifying a variety from the pool of 24 varieties approved for Idaho for seasons 2010 and 2011. These are specific short DNA fragments that are highly variable in certain regions of sugarbeet genome. These markers are ready to be deployed to trace variety postharvest performance. Root samples were collected from storage piles throughout locations in Idaho based on their storability. Data on the incidence of root rot in recently harvested roots entering storage piles (Table 1) was provided to Amalgamated to allow specific growing areas to be targeted for better root rot management. The fields that feed approximately one third of the piling grounds in the sampled area were in need of better root rot management. The four SSR markers will be used routinely to reveal varieties performance in these areas. In conclusion, this study resulted in a DNA fingerprinting database for all varieties and experimental hybrids that were approved to be grown in Idaho in seasons 2010 and 2011.

	Number of piling grounds with this root rot incidence		
Location	High	Intermediate	Low
Treasure Valley	6	1	6
Magic Valley	2	1	14
Total	8	2	20

Table 1. Incidence of root rot in recently harvested roots entering 30 piling grounds in Amalgamated Co. growing area.

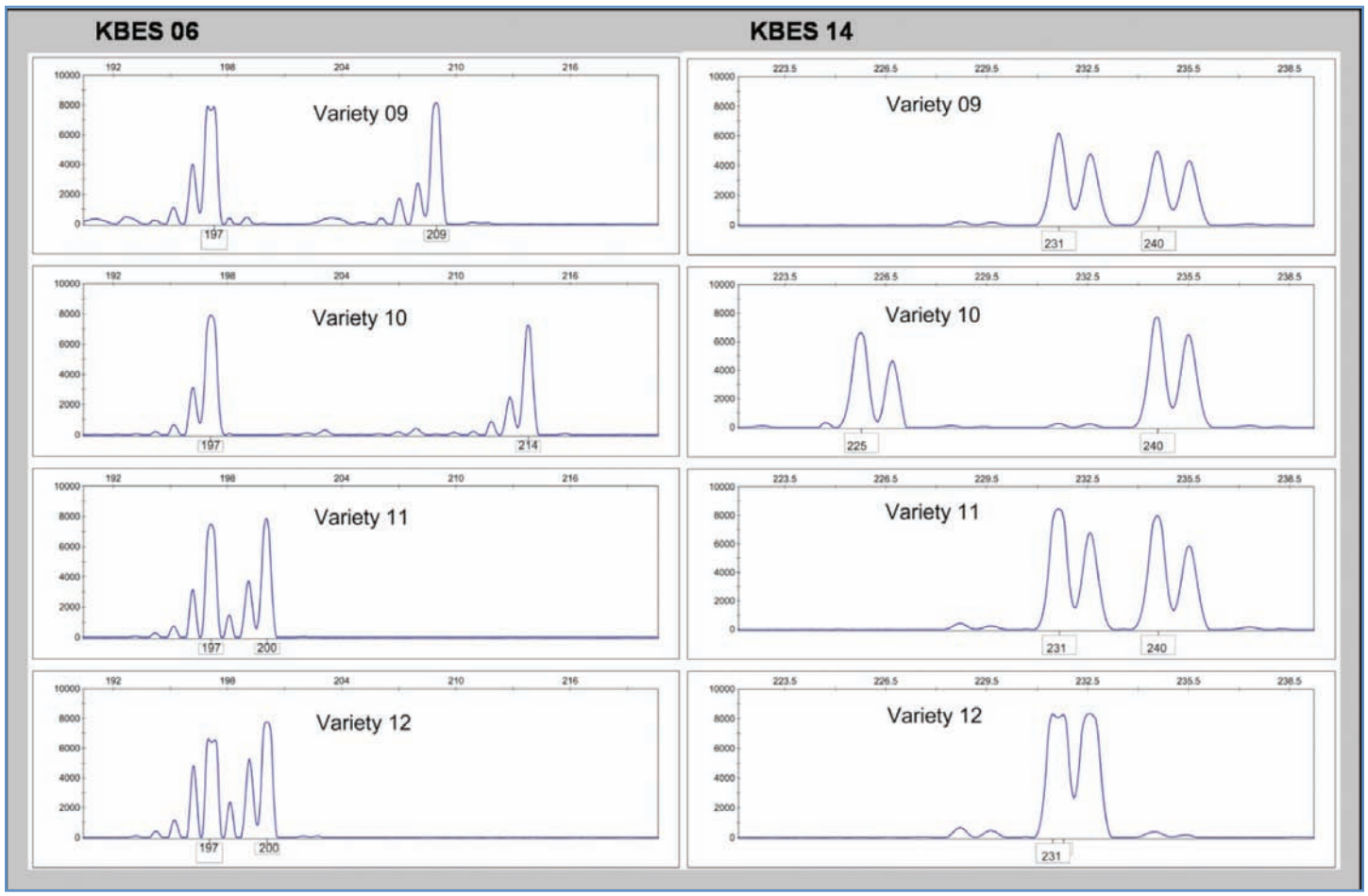

Fig. 1. Example of two SSR markers that produced unique pattern (KBES14) or in combination (KBES06). Each peak base is a representative of a DNA fragment from a variety (ABI 3100 capillary electrophoresis image).