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Spotted Lantern Fly: Wisconsin Cranberries Less at Risk Than Other Crops/Locations

By Christelle Guédot, PJ Liesch, Allison Jonjak

The Spotted Lantern Fly (SLF) is an invasive planthopper native to Asia, which was first detected in the US (Pennsylvania) in 2014. Its highly invasive nature warrants education and outreach to protect vulnerable crops, but given current information, cranberries are not topping the 'risk list'.

- SLF is known to feed on over 100 different types of plants, but cranberries are not currently included on these lists. Blueberries are listed in host-plant papers (see Worldwide Feeding Host Plants of Spotted Lanternfly, With Significant Additions From North America linked below), but not cranberries. We can be cautiously optimistic that it could be good news for cranberry growers, but folks should still keep a close eye out as it's possible that SLF simply hasn't been reported from cranberry yet. However, with the heavy SLF presence out east, I'd suspect that if there were any problems in cranberries in states like New Jersey, we would have heard reports by now.
- Some more good news for cranberry growers: given the location of cranberry production in Wisconsin, overall SLF risk may be low. Based on the modeling study The Establishment Risk of Lycorma delicatula (Hemiptera: Fulgoridae) in the United States and Globally, central and northern Wisconsin were deemed to have low suitability for SLF or were unsuitable. Things could always change over time, but Wisconsin doesn't appear to be great SLF habitat compared to other Midwestern states.

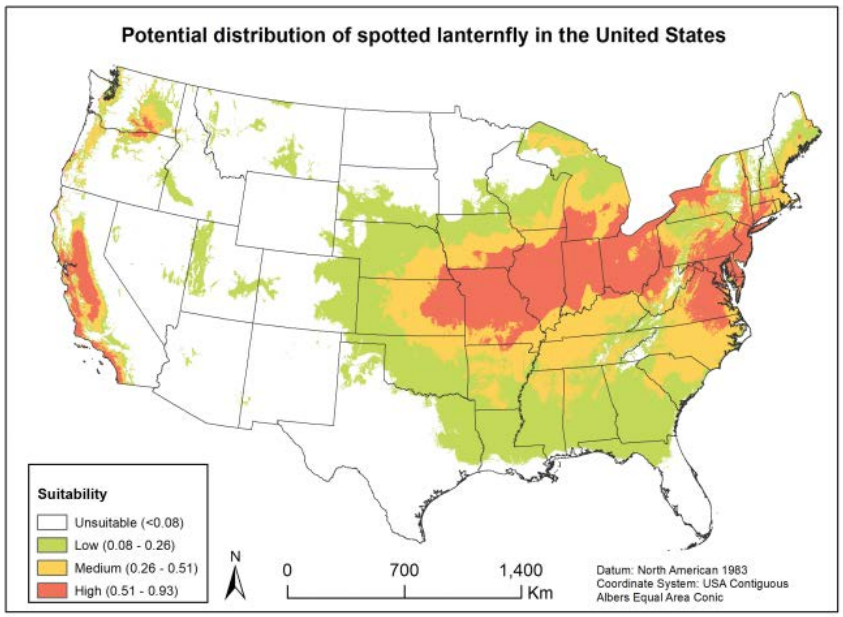
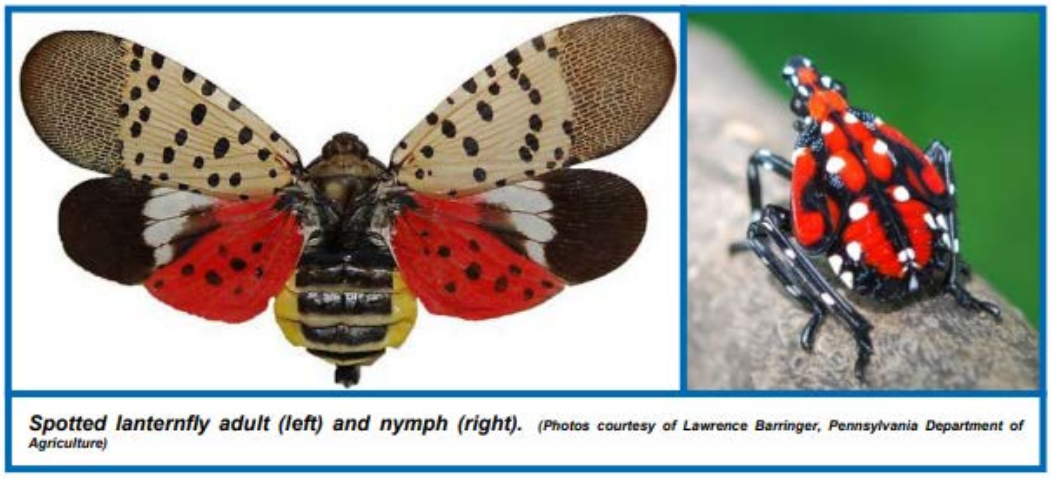


Fig. 3. Potential distribution of *L. delicatula* in the United States. Areas shaded in red, yellow, and green indicate high, medium, and low suitability, respectively. Unshaded/blank areas indicate areas that are unsuitable for *L. delicatula* establishment. Color figures area available in the online version only.

Potential distribution of L. delicatula in the United States. Areas shaded in red, yellow, and green indicate high, medium, and low suitability, respectively. Unshaded/blank areas indicate areas that are unsuitable for L. delicatula establishment. Color figures area available in the online version only. Wakie, 2000.

Appearance:



Spotted lanternfly adult (left) and nymph (right). (Photos courtesy of Lawrence Barringer, Pennsylvania Department of Agriculture)

Adult SLFs are approximately 1 inch long and ½ inch wide when resting. The insects' forewings are light brown to grey with black spots at the base and have a grey net-like pattern at the tips. The hindwings are red with black spots at the base, have white bands near the center, and have a black net-like pattern at the tips. The heads and legs of SLF adults are black, while their abdomens are yellow with broad black bands. When resting, adults fold their wings over their bodies and appear light brown to grey with black spots. Adult female SLFs have a red spot at the tip of their abdomens. SLF egg masses are 1 to 1½ inches long and ½ to ¾ inches wide, greyish-brown, covered with a grey, waxy coating, and contain 30 to 50 eggs. First stage immature SLFs (i.e., nymphs) are wingless and black with white spots. As nymphs mature, they eventually develop red patches, but retain their white spots.

Host Range:

SLF has a wide host range and nymphs appear to feed on leaves and branches of virtually any plant they encounter, often gathering in large numbers. In the fall, adult SLFs gather in large numbers on tree of heaven/paradise tree, willow, maple, birch, poplar, tulip poplar, ash, oak, grape, apple and stone fruit trees (e.g., cherries and plums). Tree of heaven/paradise tree (Ailanthus altissima) is a preferred fall feeding host for SLF adults, as well as a preferred mating and egg laying site. This plant is an invasive species native to China that grows in disturbed sites and along roadsides. SLF damage on grape, apple and stone fruit trees is of particular concern because these plants are important agricultural crops.

Symptoms and Effects:

SLF adults and nymphs feed on a plant's phloem (i.e., food conducting tissue), sucking the sap from young stems and leaves, and reducing the plant's ability to photosynthesize. Affected plants often have weeping/oozing wounds on their trunks that eventually result in greyish-black discolorations. Damage can lead to weakened, withered plants, and potentially even plant death. In addition, SLFs excrete large amounts of honeydew (i.e., sugar-rich feces) which can cover stems and leaves and build up on the ground at the base of plants. Honeydew can become colonized by sooty mold fungi (see University of WisconsinExtension bulletin A2637, "Sooty Mold", available at http://learningstore.uwex.edu) giving leaves and branches a blackish coating that can further reduce photosynthesis and contribute to plant decline and death. Oozing sap and honeydew also attract other insects such as wasps, hornets, bees, and ants.

Life Cycle:

SLF has only one generation per year and overwinters as eggs in egg masses. In the spring and early summer, eggs hatch and SLFs go through four nymphal stages (called instars). Adults begin to appear in July and August. Males and females mate multiple times and females can produce one or two egg

masses University of Wisconsin Pest Alert XHT1236 Provided to you by: Revised Oct. 20, 2016 between September through November (or until they die from the onset of winter). Female SLFs lay egg masses on smooth-barked trunks, branches, and limb bases of medium to large-sized trees, as well as on smooth stone and other natural surfaces, and on man-made items such as yard furniture, cars, trucks, and farm equipment.

Scouting Suggestions:

SLF adults are poor fliers, but strong jumpers, and prefer to walk. Nymphs and adults gather in large numbers on host plants and are easy to find at dusk or at night when they migrate up and down tree trunks. SLFs are harder to find during the day as they tend to stay near the base of the host plants. Beginning in late April to mid-May, watch for nymphs on smaller plants and vines, and on any new growth on trees and shrubs. Watch for adult SLFs in late August through September, when they can be found in large numbers. Sticky tree bands can be helpful for monitoring for young SLFs, but less useful in detecting later stage immature and adult SLFs. From October through spring, watch for SLF egg masses (which can be very inconspicuous), particularly on tree of heaven.

Sources:

Spotted Lanternfly: XHT1236. Christelle Guédot, UW-Madison Entomology
Worldwide Feeding Host Plants of Spotted Lanternfly, With Significant Additions From North America Lawrence Barringer1,3 and Claire M. Ciafré
Tewodros T Wakie, Lisa G Neven, Wee L Yee, Zhaozhi Lu, The Establishment Risk of Lycorma delicatula (Hemiptera: Fulgoridae) in the United States and Globally, Journal of Economic Entomology, Volume 113, Issue 1, February 2020, Pages 306–314, https://doi.org/10.1093/jee/toz259
https://insectlab.russell.wisc.edu/2021/08/31/spotted-lanternfly-wisconsin/

Is Metabolic Herbicide Resistance the Straw That Will Break Weed Management's Back?

By Jed Colquhoun

In a long-term tillage research project in Kansas, a Palmer amaranth population was identified that was resistant to six herbicide sites of action in individual plants. While that's challenging enough, here's the scariest part: in some cases the plants had evolved resistance to herbicides that had never been sprayed in the field (Shyam et al. 2021).

Similarly, in Illinois a waterhemp population was recently identified that's resistant to dicamba, yet the field had never been treated with dicamba or 2,4-D. The population was also resistant to five other herbicide sites of action, which may have been the source of resistance to the sixth herbicide site of action that includes dicamba (see https://aces.illinois.edu/news/first-dicamba-resistant-waterhemp-reported-illinois for an informative summary of this work).

Weeds that have become resistant to herbicides they've never been sprayed with may sound like something out of a CSI type show. The phenomenon is not new but is becoming more common. In fact, one of the potential causes – metabolic resistance – isn't even limited to plants. So how could this happen?

In a broad sense, herbicide resistant weeds can be divided in two groups: those with target site

resistance, and those with non-target site resistance. In target site resistant weeds, the specific enzyme that the herbicide targets is either mutated so that the herbicide can't bind to it (think of pieces of a puzzle not fitting together) or the target enzyme is overproduced to the point that the herbicide can't effectively bind to all the sites.

Non-target site resistance can happen in a few ways: in resistant weeds the herbicide may not be absorbed or translocated (moved within the plant) as well, the herbicide may get sequestered in plant parts away from the target site, or the herbicide may get metabolized by the plant. The remainder of this article will focus on metabolic herbicide resistance because it likely has the greatest implications for production agriculture.

Herbicide metabolism involves the breakdown of the active ingredient into metabolites that are less mobile and less toxic to the plant, and then the "dumping" of the metabolites into plant parts where they are sequestered and not active. Enzymes cause the breakdown, and two of the most involved include cytochrome P450 monooxygenase (P450) and glutathione S-transferase (GST). P450s are among the most common enzymes in living organisms and have the ability to metabolize 11 of the 26 herbicide modes of action. GSTs are also common in living organisms and are responsible for some grass tolerance to herbicides and some observed cases of insecticide resistance (Rigon et al. 2020). Crop safety with many herbicides is based on metabolism by these broad enzymatic families.

Herbicide metabolism has been researched and observed over the past few decades with challenging grass weeds such as rigid ryegrass in Australian wheat production (Yu and Powles 2014). More recently, however, metabolic resistance has been reported among broadleaf weeds and close to home. For example, metabolic resistance to the herbicide S-metolachlor was reported in two waterhemp populations in Illinois (Strom et al. 2020). In this case the resistant waterhemp metabolized 90% of the S-metolachlor in less than 3.2 hours.

Metabolic resistance has sometimes been referred to as "creeping resistance" because of the way that it evolves in populations, where plants that can survive low herbicide doses by metabolizing some of the active ingredient produce seed, and subsequent generations are selected that can metabolize more and more herbicide until they are no longer useful for control. For example, waterhemp control with dicamba in the Illinois population noted above decreased from 80% to 65% over just a few years, and dicamba wasn't even sprayed during that time.

So why is metabolic resistance so concerning compared to target site resistance that's been addressed for years? Target site resistance is very specific to an herbicide active ingredient, the individual target site that it binds to, and a mutation that changes those puzzle pieces. In contrast, in metabolic resistance the enzymatic activity that breaks down the herbicides and other toxins is not specific. Once high metabolic activity is selected for, the plant can breakdown a broad range of herbicides across modes of action, potentially including active ingredients that have never been sprayed on that population before, and even herbicides that have yet to be discovered. For example, in the Kansas study mentioned above, the authors concluded that "these results suggest predominance of metabolic resistance possibly mediated by cytochrome P450 and GST enzyme activity that may have predisposed the KCTR Palmer amaranth population to evolve resistance to multiple herbicides" (Shyam et al. 2021). In practical terms, metabolic resistance adds tremendous unpredictability to weed management decision making and outcomes.

These metabolic enzymatic activities are also not specific to plants and herbicides, which makes for complex resistance scenarios. For example, Clements et al. (2018) reported that some of the fungicides commonly used for potato disease control can upregulate GST enzyme production in Colorado potato beetles, and that increase in enzymatic activity can negatively affect insecticide performance.

Additionally, not only is metabolic resistance more challenging to research than target site resistance, it's also harder to observe in the field. For years growers and scouts have been told to keep an eye out for living target plants that normally would have been killed and that are among other dead weeds, and that stark contrast of living versus dead was often the smoking gun of resistance. In metabolic resistance, the selection pressure creeps along where target weeds may be injured but eventually recover enough to produce a few viable seeds, and the high metabolism selection cycle continues on until multiple herbicides are ineffective.

The increase in likely cases of metabolic resistance observations in recent years speaks to the dire need to develop practical and economical alternatives to herbicides – it's simply not just about rotating herbicides anymore. In the short term, much effort is currently being directed to intervening in the seed production and dispersal step of the resistance selection cycle with mechanical tools like combine weed seed cleaners and collectors. Research is also underway to gain a better understanding of the complex metabolic interactions among pesticides and pests, and how that affects practical management decisions. In the longer term, alternative technologies like weed sensors and highly efficient robotic weeders need to be developed and available for adoption in reasonable and affordable ways.

For the details:

Clements J, Schoville S, Clements A, Armezian D, Davis T, Sanchez-Sedillo B, Bradfield C, Groves RL (2018) Agricultural fungicides inadvertently influence the fitness of Colorado potato beetles, Leptinotarsa decemlineata, and their susceptibility to insecticides. Nature 8:13282 (doi: 10.1038/s41598-018-31663-4)

Rigon CAG, Gaines TA, Kupper A, Dayan FE (2020) Metabolism-based herbicide resistance, the major threat among the non-target site resistance mechanisms. Outlooks on Pest Mgt. 31:164-168 (doi: 10.1564/v31_aug_04)

Strom SA, Hager AG, Seiter NJ, Davis AS, Riechers DE (2020) Metabolic resistance to S-metolachlor in two waterhemp (Amaranthus tuberculatus) populations from Illinois, USA. Pest Mgt. Sci. 76:3139-3148 (doi: 10.1002/ps.5868)

Shyam C, Borgato E, Peterson D, Dille JA, Jugulam M (2021) Predominance of metabolic resistance in a six-way-resistant Palmer Amaranth (Amaranthus palmeri) population. Frontiers in Plant Sci. 11:614618 (doi: 10.3389/fpls.2020.614618)

Yu Q, Powles S (2014) Metabolism-based herbicide resistance and cross-resistance in crop weeds: A threat to herbicide sustainability and global crop production. Plant Phys. 166:1106-1118

The Development and Evolution of Cranberry Genetic Profiles: Perry Red, or Crowley, That Is the Question.

By Allison Jonjak and Juan Zalapa

The USDA Cranberry Genetics and Genomics Lab (CGGL) at the University of Wisconsin-Madison group began compiling genetic fingerprinting data in 2011. Since then, they have identified the consensus genetic profiles and the parentages of many cranberry cultivars. Based on this research, they provided the first free and reliable cranberry DNA fingerprinting method available to Wisconsin

growers (Fajardo et al. 2013).

This work was particularly important and difficult because of the practice of sharing or selling cranberry propagule among growers and the long-lived perennial nature of cranberries, both of which lend themselves for producing genetic contamination overtime. A survey was conducted in 2011 where Wisconsin cranberry growers sent their samples with their cultivar labels. The CGGL then compiled all the samples with different cultivars names and started sorting the different genetic profiles and cultivar names, and hybrid parentages. Since then, thousands and thousands of samples have been submitted from Wisconsin growers. Additionally, data from growers from other states and internationally has been gathered. More recently, the three major cranberry diversity collections have been analyzed such as the USDA National Clonal Repository cranberry collection (2018), the Rutgers University cranberry collection (2020), and the Dubay Wisconsin cranberry collection (2022).

The CGGL has used all the data compiled over time to study cranberry cultivated diversity; data is continually being gathered from growers., and there is still much to learn in the realm of cranberry genetic fingerprinting. The information has been used to create a database of cranberry genetic profiles that includes the true-to-type genotype for most major named cultivars. The database is always evolving and changing as new information becomes available. Additionally, the database is being used to store every incidence of a unique genetic profile produced in growers' fields, and some of these genetic profiles do not match any known cultivar or parentage. These unknown genotypes probably arose from chance seedlings from natural crosses or self-pollination of cultivated cranberries or even from wild cranberries.1 When growers submit their samples, they provide trait information, for example the barren-berry trait, and the database stores trait information for future assessment of troublesome genetic invasions being reported by growers through their submission of sample for genetic analysis.

This progressive approach of refining the data has resulted in some changes in the genetic profiles labels overtime. For example, one the most prevalent barren-berry genetic profiles identified in Wisconsin in the early years of the research was originally labeled as Crowely. This label originated in grower submissions and remained in place based on consensus analysis; in other words, many of the samples submitted by growers of this genetic profile had the name Crowley. Additionally, there was one sample in the national cranberry collection with the label Crowley which had the same genetic profile. Therefore, the name Crowley was adopted and reported back to growers for this barren-berry cultivar. However, recent data from the three cranberry collections analyzed has shed new light on the parentage and true identity of this barren-berry genotype. Based on newly available parentage data, this genetic profile could not be Crowley (McFarlin x Prolific) based on the newly acquired McFarlin genetic profile. Although the genetic profile of Prolific has not been identified, the McFarlin genetic profile clearly shows that this genetic profile is indeed not Crowley. Therefore, a new search of all databases was conducted and based on another genetic hit with the national cranberry collection, the possible name ("Perry Red") was identified for this barren-berry genotype. At this time, the Perry Red name has been identified for this genotype, and there is no indication that this will change in the future since all the major cranberry collections have been analyzed. This genotype has been found to be a prevalent barren-berry invader genotype in both Wisconsin and Massachusetts.

But where did barren-berry Perry Red come from?

All the historic information that we have is that Perry Red was a wild selection from Massachusetts, and it was selected in 1888 (Dana, 1983). According to Dana, "Perry Red was named by J. Perry and planted in Marion, Mass. The medium-sized fruit (80-100 cup) ripens and colors well in storage. The berry is round with a flat calyx end and is covered with heavy bloom. Coarse vines support tall

up-rights with large dark green leaves that are capable of producing good crops." Based on this information it is likely that this wild selection was once grown commercially and was a productive genotype that became contaminated and was lost to the current barren-berry genetic profile we see today. Then, it was passed along among growers and eventually was dropped from cultivation due to its unproductivity. We can conclude that the barren-berry cultivar we have been referring to as Perry Red is likely different from the originally named Perry Red, but the originally named Perry Red has been lost to time and will not reappear, so though the name "Perry Red" was originally used to describe a different cultivar, both cultivars do not 'exist' at the same time today, so it was decided to adopt the name Perry Red to describe this barren-berry cultivar.

Now, what do we know about Crowley? Quoting Vorsa and Zalapa, 2019 on the development of Crowley:

The first breeding and selection cycle was initiated in 1929 by the United States Department of Agriculture (USDA) and the New Jersey and Massachusetts Agricultural Experiment Stations in response to a devastating disease, "false-blossom," caused by a phytoplasma […] the first populations were field planted in 1.5 × 1.5 m plots in 1934 at Whitesbog, […]. Breeding populations from additional crosses were planted in 1937 and 1943. […] From 30 crosses made between 18 native selections a total of 8,692 seedlings were evaluated […] The majority of the parents were [native selections from Massachusetts, Michigan, and Wisconsin]. Selection of progeny from the 1934 planting was initiated in 1938 and carried out over three years through 1940. Of the over 8,000 seedling plots, 1,800 plots that produced at least a pint for two to three consecutive years were further evaluated. The berries were hand-harvested and placed into storage for 2–3 months. The selection criteria included average yield, percent sound berries post-storage and "general appearance." Since only the seedlings producing a minimum quantity of fruit were evaluated, it is likely that indirect selection for establishment (stolon) vigor, precocious fruiting, upright production, fruit set, and fruit size took place. From the Whitesbog planting, 40 selections were initially selected for further testing. In 1945 an additional 182 seedlings were selected for further testing. The selections were further evaluated in a "second test" in New Jersey, Massachusetts, and Wisconsin. From this first breeding and selection cycle, six named varieties were released. The cultivars that were initially released in 1950 from the 40 "numbered" selections in 1940 were 'Stevens', 'Beckwith', and 'Wilcox'. Subsequently 'Pilgrim', 'Bergman', and 'Franklin' were released in 1961 (Dana 1983). A second round of selections were made, […] which were not officially named except for [Willapa Red] and 'Crowley'.

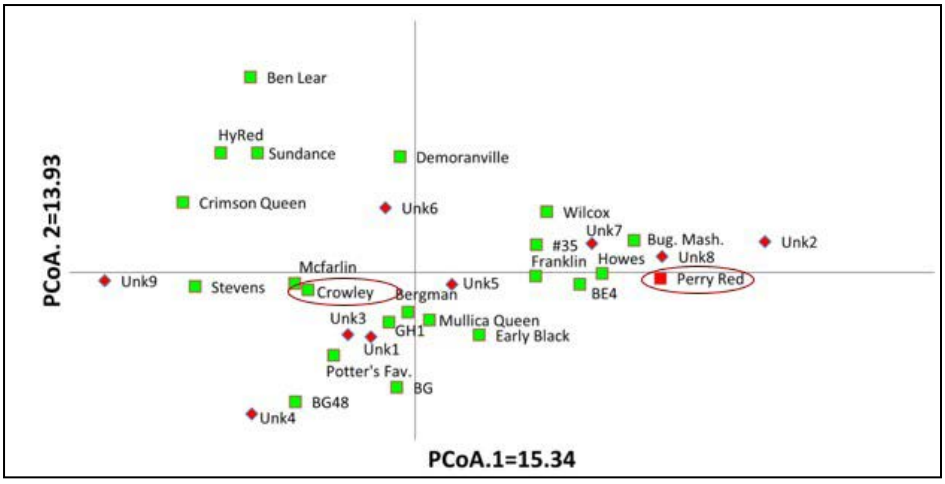


Figure 1: Principal Coordinate Analysis of cranberry varieties courtesy J. Zalapa. Two cultivars-of-interest are circled (Matusinec et al. 2022).

Figure 1 shows a Principal Coordinate Analysis (PCoA), which is a method commonly used to simplify large amounts of cranberry genetic data into visually informative charts. Looking at the chart, the genetic profiles of differences and similarities are seen in a spatial arrangement. Genetic profiles that are more distant from each other are more genetically dissimilar and ones that are closer are more genetically similar (clones match exact positions in the chart). An example of a parentage analysis is illustrated with Crimson Queen, HyRed, and Sundance (all progeny of a Ben Lear x Stevens cross), and they expectedly

cluster in a spatially similar locations between their parents Ben Lear and Stevens. Again, this type of clustering or grouping analysis is a simplification, but it allows the visualization of large data sets, which is useful for growers and geneticists while examining variety purity data and genetic relationships.

When Dr. Zalapa's group began this fingerprinting research, they found that a cultivar name might appear at several different points on the chart. Crowley was one example—appeared in two places on Figure 1–with one genetic fingerprint landing close to the parental McFarlin. The most likely reason for this observation is that some samples had been mis-identified and mis-labeled. The "Crowley" near McFarlin is a fruiting cultivar. The "Crowley" (now labeled Perry Red) near Bugle Mashpee in Figure 1. is non-fruiting. If Crowley was selected from one of 1,800 hybrids that produced at least 1 pint of fruit in a 5'x5' plot two years in a row—and we have two "spots" on in Figure 1. named Crowley—it is more likely that the fruiting cultivar (left dot) is the "true" Crowley; and the non-fruiting cultivar is likely to be a contaminant which was incorrectly labeled, now labeled Perry Red (Figure 1). Additionally, new data provided in Figure 2. shows the genetic profiles of the of the true-to-type Crowley, McFarlin, and the barren-berry Perry Red. It is clear from the genetic profiles that the barren berry Perry Red cultivar is not related to McFarlin or Crowley because it does not share at least half of the genetic profiles, one number in each marker.

Name	Origin	Marker1		Marker2		Marker3		Marker4		Marker5		Marker6		Marker7		Marker8		Marker9	
Crowley	McFarlin x Prolific	151	155	268	289	218	242	268	290	185	201	196	200	122	178	269	271	227	227
McFarlin	Wild Selection, MA	151	157	246	289	216	218	268	290	195	201	200	202	122	171	269	279	223	227
Perry Red	Wild Selection	173	179	271	271	216	252	257	257	187	195	214	214	171	178	291	304	227	227

Figure 2: Genetic Profiles of the of the true-to-type Crowley, McFarlin, and Perry Red.

Since the barren-berry Perry Red cultivar shows up commonly in growers' plantings in both WI and MA, it is likely that this contamination occurred early in the east and was spread through propagation in more recently planted beds in Wisconsin. A current study of Massachusetts contaminated beds labeled as Stevens and Crowley supports this conclusion as the same barren-berry genotype has been identified. This would explain the mislabeling associated with the name Crowley and prevalence of this contaminant in Stevens beds in both states. Dr. Zalapa noted that, since the unfruiting "Crowley" contaminant was already known to many growers, "it would be annoying to withdraw the cultivar's name and replace it with just "unknown 12""—so his team identified the most likely named cultivar first associated in history with this genetic fingerprint. This is Perry Red (1888) based on an accession with that name stored at the USDA National Clonal Repository cranberry collection.

In conclusion, there used to be a cultivar named Perry Red which has been lost to time. Now we are using the name "Perry Red" for this barren-berry cultivar, based on the traits that growers have submitted. In the future, other prevalent barren-berry cultivars may be identified, and if they are prevalent enough to warrant a name, to avoid the question Crowley or Perry Red?, they will be labeled, barren-berry 1, 2, 3, etc.

As we continue the process of fingerprinting cultivars—those produced, those newly bred, and those contaminating our production beds—we are likely to find more information that will highlight areas where we had had misunderstandings in the past. How exciting it is to gain new understanding!

References:

Dana, M.N. 1983. Cranberry cultivar list. Fruit Var. J 37:88–95.

Fajardo, D., J. Morales, H. Zhu, S. Steffan, R. Harbut, N. Bassil, K. Hummer, J. Polashock, N. Vorsa, and J. Zalapa. 2013. Discrimination of American cranberry cultivars and assessment of clonal heterogeneity using microsatellite markers. Plant Molecular Biology Reporter 31(2):264–271. doi:

10.1007/s11105-012-0497-4.

Matusinec D., A. Maule, E. Wiesman, A. Atucha, M. Jyostna Devi, and J. Zalapa (2022) The New Cranberry Wisconsin Research Station: Renovation Priorities of a 'Stevens' Cranberry Marsh Based on Visual Mapping, Genetic Testing, and Yield Data, International Journal of Fruit Science, 22:1, 121-132, DOI: 10.1080/15538362.2021.2014016 https://www.tandfonline.com/doi/full/10.1080/15538362.2021.2014016

Vorsa, N., and J. Zalapa. 2019. Domestication, genetics, and genomics of the American Cranberry. Plant Breeding Reviews 43:279–310.

Update from the Wisconsin Cranberry Research Station

By Wade Brockman

Fruit is starting to turn red with some cooler nights and days. We are ready for harvest as it's fast approaching. Hope everyone has a safe and great harvest.

Grower Updates

Flying Dollar Cranberry

By Seth Rice

Hello everybody! We are finally at our time to see the fruits of our labor. The nights are getting colder and the leaves are changing colors. This is the calm before the storm. Our early variety's are ready but the Steven's are behind as usual. Need colder nights to get some color. Getting harvest equipment is what can be seen on every marsh right about now. Physical and mental preparation is a must for this line of work. Tissue samples were sent in last week during our good weather pattern. I hope everybody is safe and has a amazing harvest! Everybody try to enjoy this time of year as best as you can.

Vilas 51

By Jeremiah Mabie

Everyone's favorite time of the year is finally here! We are all patiently waiting for better color as we have not had the cold nights we usually do. On the plus side we have gained some nice size in the past couple weeks! Everyone is preparing equipment and the final touches around the marsh. Hope everyone has a great harvest with high yields and big smiles!