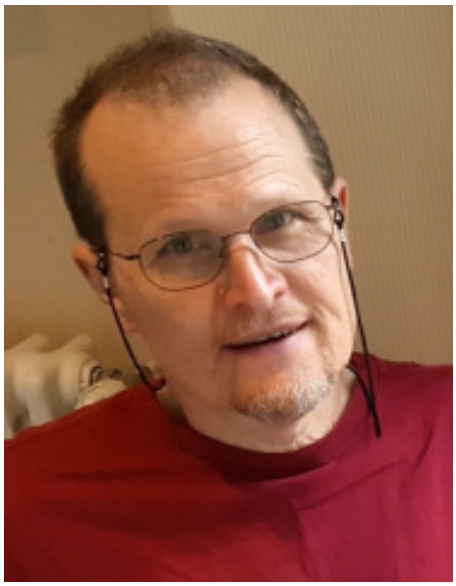
Donald R. McCarty



How did you spend your career?

After completing my PhD in biochemistry and agronomy in 1985 at the University of Wisconsin–Madison, I moved to the University of Florida Vegetable Crops Department (now part of the Horticultural Sciences Department) for postdoctoral research in maize genetics with Curt Hannah. The following year I became a faculty member in that department and began to work on viviparous mutants of maize.

This was an exciting time for a reformed protein biochemist to enter the field of maize genetics, because the emerging transposon tagging techniques gave sudden access to a fascinating collection of classical mutations. Understanding the molecular basis for these mutants proved very fruitful to understanding embryo development (Vp1, Vp8) and synthesis of apocarotenoid hormones, including abscisic acid (ABA) and strigolactones (Vp14). VP1 and VP14, in particular, were pioneer discoveries that led to identification of families of related proteins (B3 transcription factors and carotenoid cleaving dioxygenases, respectively) that have central roles in plant development.

Because these foundational mutants were identified by transposon-tagged alleles, in the mid-1990s I initiated a decades-long genetic program to enable systematic molecular analysis of transposon-induced mutations in maize. By 2001, we had laid the genetic foundation for construction of the UniformMu resource for maize functional genomics. Emergence of next-gen sequencing technologies in 2004 was key to fully realizing the potential of the underlying genetic resource. With support from NSF, we were able continue to build and maintain this popular public resource through the present. As was first envisioned in 1995, UniformMu has proved to be a fruitful engine of gene discovery, especially for genes underlying seed development.

What do you consider to be your most important contributions to plant science?

There are five areas in which I have had significant impact. The first is discovery of the plant-specific B3 domain transcription factor family and functional analysis in maize of its founding member, VIVIPAROUS1 (VP1). This work includes the first demonstration that B3 domains have sequence-specific DNA binding activity, showing that VP1 controls the anthocyanin pathway via regulation of the *C1* MYB transcription factor, and delineation of distinct activator, coactivator, and repressor functions of VP1. We further showed that closely related VAL type B3 proteins are required for repression of the B3 network prior to germination. Other B3 domain transcription factors function in ABA regulation and auxin and ethylene signaling.

A second area is discovery of the carotenoid cleaving oxygenase enzymes that catalyze oxidative cleavage of the carotenoid backbone to form apocarotenoid derivatives. Enzymes in this family synthesize Vitamin A and retinoids in animals and the precursors of ABA and strigolactone hormones in plants. In collaboration with Jan Zeevaart (Michigan State), we demonstrated the predicted biochemical activity of the founding member of this class of enzymes, maize VIVIPAROUS-14 (VP14). In 2010, we determined the structure of VP14, the first plant enzyme in this family to be described. The discovery of VP14 was key to identifying the family of enzymes controlling ABA and strigolactone biosynthesis in Arabidopsis, tomato, maize, and many other species.

The third area of impact was revealing the structure and origin of the maize *White Cap* locus, a dominant inhibitor of carotenoid accumulation in the endosperm that contains a large tandem cluster of CCD1 carotenoid dioxygenase genes. The *White Cap* locus was created shortly after maize domestication by a transposon-mediated macrotransposition, followed by tandem gene duplica-

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tion. Copy-number variation (0 to 22 copies) among alleles generated by unequal crossover events results in a striking proportional quantitative variation in CCD1 expression in endosperm and other organs. This is a striking example of the role played by transposons in generating novelty and genetic variation.

A fourth area was construction of the UniformMu national genetic resource for maize functional genomics. This national resource, constructed in collaboration with Karen Koch (University of Florida), is based on the inbred UniformMu transposon population and includes 72,000 independent germinal Mu transposon insertions mapped in 14,024 genetic stocks. The seed stocks are accessed online at MaizeGDB and distributed by the Maize Coop Stock Center at no cost to the user. To date, more than 27,000 seed packets have been distributed to laboratories worldwide. To facilitate analysis of insertions in the W22 inbred background, we formed a consortium to sequence the W22 genome and developed Mu-seq for high-throughput genotyping of transposon insertions.

Finally, dissection of regulatory networks for embryo development, embryo–endosperm interactions, and vitamin-dependent metabolism in maize has been an important contribution. Key gene discoveries include SWEET4C, CRINKLY4, VAL1/2/3, VIVIPAROUS8, Shohai (small embryo), and BigE1.

When did you become a member of ASPP/ASPB?

I became a member of ASPP in 1979. I attended my first annual meeting in 1980 at Washington State University in Pullman, where I gave a talk on amino acid transport in soybean. I attended with my Agronomy Department (at that time) adviser, Larry Schrader, and a postdoc, Karen Koch, who has since become a lifelong collaborator. Larry introduced us to many leading figures in the transport field, including Robert Giaquinta, and probably a comparatively young Bill Lucas, though that might have occurred the following year at the 1981 ASPP meeting at the University of Illinois at Urbana–Champaign.

How did the Society impact your career, and what motivated you to become a Founding Member of the Legacy Society?

ASPB has impacted my career mainly through its high-quality accessible journals, which provided a channel for broad dissemination of my research. The annual meeting has been an important venue for interacting socially and intellectually with diverse colleagues. Becoming a member of the Legacy Society was one small way to give something back to the community that sustains this vital scientific society.

What important advice would you give to individuals at the start of their career in plant science?

Develop a diverse tool kit, including the computing skills needed to handle large data sets. Biology is becoming ever more data intensive. Follow the problem, not the paradigm or, worse, a pet hypothesis (you know, the one that just has to be right!). In other words, trust your data. If the data don't fit the expected pattern, you might be on to something.

Listen carefully to colleagues, but keep your own counsel and draw your own conclusions. At several points in my career, there have been wise elders who advised that I would not be able to compete with large or prominent labs working on the same problem, and yet I prevailed. In reality, if you're competing with a large lab, you are likely competing with one or two other people (a student or a postdoc) in that lab. Contact them if you can; ASPB meetings are good for that. Chances are your approaches are complementary and there will be opportunities for fruitful collaboration.

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