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Editorial Open Access

A New Technology Enabling New Advances in Strawberry Genetics

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Editorial

Genetics and genomics tools have undergone a revolution in the last decade whether for humans, animals or plants. Although most current tools support organisms with simple genomic architecture (haploids or diploids), plants have diverse ploidy levels and genomic arrangements. For example, rosaceous crops like apple, peach and sweet cherry are diploid; sour cherry is a tetraploid; and cultivated strawberry is an octoploid. The genetic concepts and theories developed in animal or human sciences are transferrable to plants most of the time. However, crops like octoploid strawberry require special tools suited to its genetics.

Breeding can be simply explained as a process of making informed crosses, generating variable progeny, and selecting varieties based on a combination of traits. If diploid species are crossed, there are usually four possible outcomes at a given locus. For example in a diploid crop, parent 1 (AB) is crossed with parent 2 (CD) to generate four possible allelic combinations: AC, AD, BC, and BD. For a tetraploid species, there may be sixteen possible combinations. It is astonishing to think about what possible combinations an octoploid strawberry cross might produce. Cultivated strawberry is an allo-octoploid (2n = 8x = 56), where each linkage group is amalgamation of four subgenomes, and where meiotic pairing occurs within subgenomes. Thus, the allo-octoploid strawberry genome mimics diploid chromosomal segregation.

The whole genome sequence of the diploid ancestor woodland strawberry (*Fragaria vesca*) was made available in 2010, and the international strawberry community was brought together by RosBREED, a NIFA SCRI project, to develop the IStraw90 Axiom® array in collaboration with Affymetrix, Inc. This array was designed to generate sub-genome specific SNPs that could be scored as diploid. Most markers in the array indeed segregated only in subgenomes, being either non-detected or homozygous for other subgenomes for the same marker. This array technology has allowed genetic screening of thousands of individuals at high density for many genetic applications. We have observed excellent accuracy, with 99% marker call identity between duplicate samples, those 1% differences typically being due to missing information. The array is thus helping researchers to identify loci influencing important traits and enabling marker-assisted breeding at a much higher level.

A good quality genetic map is a foundation for understanding the genome architecture of any species. The IStraw90 Axiom® array has provided a plethora of markers for mapping in allo-octoploid strawberry. A few genetic maps are already published using these markers. Transferability of genetic maps is still to be tested, and integrated mapping collaborations are underway. Regardless, for accurate genetic studies, it is recommended to create breeding program-specific genetic maps. Genomic rearrangements are possible, and strawberry germplasm groups are known to possess regions of homozygosity.

The IStraw90 Axiom® array was designed using the diploid woodland strawberry as the reference genome. The two octoploid species that gave birth to *Fragaria* × *ananassa* (cultivated strawberry) are *F. chiloensis* and *F. virginiana* and were part of the panel used for SNP detection. Quality octoploid whole-genome sequences are currently not available, but efforts are underway to assemble all four subgenomes. Furthermore, another putative diploid ancestor, *F. iinumae* has now also been sequenced, lending further ammunition to an improved second-generation array within the next few years. Once complete information on all four subgenomes are available, scientists can precisely locate and develop markers associated with traits/genes.

In addition to high-density mapping, array technology for strawberry also will enable a breeding approach that is common in animals and certain agronomic crops called "genomic selection" (GS). This approach utilizes dense markers and phenotypic data to make statistical predictions of performance for non-phenotyped individuals using markers only. For this approach there is no need for a well-curated genetic map. Accuracy of GS depends on the quality of the marker and input phenotypic data as well as genetic factors such as heritability and genotype by environment interaction. Currently, we hope that GS can effectively deal with ploidy issues and help make early predictions of parental performance in a strawberry breeding program.

While a second generation SNP array for strawberry is still a couple of years away at best, efforts are underway to reduce the cost of the current array, as the IStraw90 is certainly expensive. To this end, mapped SNP probes from multiple groups around the world were collected and are being utilized to develop a smaller but cheaper version called "IStraw35" which contains just over 34K markers. This new tool should enable higher-throughput screening of larger numbers of samples.

Overall, technology is developing at a rapid pace for octoploid strawberry genetics and genomics, providing advances that would have seemed unrealistic a decade ago. In the next couple of years, an explosion of sequence information should facilitate another leap forward in genotyping tools that are useful for breeding applications.