

Preface

Pat Tranel and I (and others—many of whom are authors of chapters) have been discussing the genomics of weedy plants for quite a few years now. The Plant and Animal Genome (PAG) conference of 2009 was the fourth instance we've held the annual workshop on weedy and invasive plant genomics. The first weedy genomics workshop was held at the 2005 Weed Science Society of America Conference, which was in Hawaii that year. I vividly recall enticing two postdocs in my laboratory with warm beaches on a cold winter's day. If they could successfully write and publish a review paper on the genomics of weedy plants, I promised to pay for their travel to present a paper at the conference in Hawaii that February. They did (*Trends in Plant Science* (2004) 9:391–398) and we all had an aloha good time.

While I and many others have been interested in genes and proteins that confer interesting traits to weeds and invasive plants, there has been surprisingly little research at the genome or proteome levels. Molecular biology of weeds has progressed very slowly, which I think is mainly due to three interrelated factors. First, the weed science research community and culture is vastly different from that of plant genomics and evolutionary biology. Simply, most weed scientists don't know about molecular genetics and most genomicists have yet to discover the world of fast-evolving weeds. I recall a conversation with a weed scientist who asked whether it was offensive to be referred to as a "gene jockey." I reciprocated by asking him whether "nozzlehead" is a derogatory term. We each had a laugh over this exchange, realizing that the two research worlds are indeed polar opposites.

Second, the sources of research funding are also quite different in each of these two areas. Much of the weed science research (done in the United States, anyway) is corporate sponsored and focused on proprietary herbicides. Plant genomicists are typically funded by the National Science Foundation (NSF) or U.S. Department of Agriculture (in the U.S.). No entity has seemed to be very interested in funding weed genomics.

Third, and related to the second point, there is little information on the genomes of any weedy and invasive plant species. Being neither models nor crops, their genomes have fallen through the funding cracks. With little basal genomic information, meager funding, and a lack of collaboration between weed scientists and genomicists, the field has not yet blossomed.

The situation is about to change as these two cultures have been slowly converging on the field of weed genomics, with the promise of more research to come in the near future. Funding agencies are slowly catching on to the synergies of using genomic tools to address fundamental and practical issues of weediness and invasiveness. At the same time, genomics tools, such as next generation sequencing platforms, are becoming increasingly more accessible and reasonably priced. We are now moving from talking about weed genomics to actually doing weed genomics. This new year finds me with a dataset of more than 400,000 horseweed transcriptome sequences to mine, and, indeed, a few other researchers also have recently obtained transcriptomic sequences from their own favorite weeds. It is truly an exciting time in science, and I think this book captures the scintillation of this emerging area.

My motivation for editing this book is that young scientists will discover the fun of combining weeds and genomics. Having never been burdened with either the label of "weed scientist" or "genomicist," emerging young scientists interested in weedy plant genomics will be free to define their own field of study. After a sizable amount of genomic information is made available, which should begin to happen in exponential fashion very soon, many important biological questions will become increasingly accessible and fruitful ground for many scientific careers. I firmly believe that as the science matures, increasing funding opportunities that are needed to accelerate knowledge acquisition will emerge, which will in turn be translated to applications for the more effective control of weedy and invasive plants.

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