CONTRIBUTING to the genetics community has always been one of my primary scientific goals. While my lab has focused on the molecular mechanisms of synaptic transmission, neural development, Notch signaling, and most recently neurodegeneration, many of our efforts relate to developing technologies, generating useful Drosophila stocks, and disseminating genome-wide libraries for a wide range of in vivo analyses. I truly enjoy creating tools and reagents that impact research in many fields and promote the use of our favorite model organism. And so I am very honored to receive this award because it is intended to recognize individuals “who have made outstanding contributions to the community of genetics researchers.”

It is fair to state that, currently, no other multicellular organism allows more sophisticated and elegant manipulations in vivo than the fruit fly, thanks to the efforts of many geneticists and molecular biologists over the past century. Indeed, almost half of the recipients of the Beadle award since its initiation in 1999 are Drosophila geneticists, including Michael Ashburner, Allan Spradling, Gerry Rubin, Norbert Perrimon, Thomas Kaufman, William Gelbart, and Scott Hawley. These individuals and many others in the fly community have developed new methods or tools and helped propagate their use. This spirit of sharing tools and reagents has driven many discoveries in Drosophila and will continue to advance our research.

Continued tool and reagent development is critical for the survival, expansion, and evolution of the Drosophila field.

—H.J.B.
et al. 2010), which allows the mapping and analysis of X-linked mutations. Most recently, we developed a new transposable element named MiMIC that facilitates genomic tagging of proteins (Venken et al. 2011a). We are using MiMICs to tag thousands of genes that allow elegant and specific genetic manipulations in cell culture (Neumüller et al. 2012) and in vivo (S. Nagarkar-Jaiswal and P.-T. Lee, personal communication).

Many adaptations of these methods/tools have been implemented in other model organisms and hence impact other fields. Obviously, this cross-fertilization works both ways. We regularly borrow from other geneticists: P-element enhancer detection was inspired by Bacillus subtilis experiments (O’Kane et al. 1986; O’Kane and Gehring 1987), the GAL4/UAS system was based on elegant experiments developed in yeast (Fischer et al. 1988; Brand and Perrimon 1994), and P[acman] recombineering was based on research on phages and bacteria (Yu et al. 2000; Venken et al. 2006). Numerous other examples of borrowing across species exist (Venken et al. 2011b), and this underscores the need for continued support for genetically tractable organisms such as yeast, bacteria, and viruses.

Hugo has been one of the most selfless contributors to the general good of the Drosophila community over the past two decades. I doubt there is anyone in this field that has not benefited directly from his generosity.

—Ethan Bier, University of California, San Diego

Continued tool and reagent development is critical for the survival, expansion, and evolution of the Drosophila field. In a sense, it is a process of Darwinian selection in the struggle for survival of the fittest organism to perform biological experiments. As long as Drosophila is fit, the field will continue to attract some of the brightest and best biologists. These tools also allow us to assess the function of many genes in vivo, which is needed now more than ever as human geneticists discover disease-causing genes at an unprecedented pace, while <30% of the fly’s genes are functionally annotated in vivo (St Pierre et al. 2014). Because the fly homologs of thousands of human genes are still poorly annotated, detailed functional studies of these genes will contribute to the annotation of vertebrate genome, improve our understanding of evolutionarily conserved pathways/processes, and reveal the underlying mechanisms of many diseases. While the past two decades have found detailed descriptive information about sequences, types of transcripts, regulatory elements, tissue expression, and protein–protein interactions (Boley et al. 2014), functional information on genes/proteins is necessary if we are to translate this valuable information into biological and pathological insight. Drosophila is perfectly situated for the pursuit of these avenues of research and will continue to provide important biological insights at the cellular and organismal level. Continued technological developments and genome-wide reagents will drive the success of Drosophila, and sharing will dramatically accelerate the process. I see many more Beadle Awards for Drosophila geneticists in the future.

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