Hyma K.E., Acharya C, Sun Q, Mitchell SE. *Genotyping by Sequencing Applications: Outcrossing Species and Diversity Studies*. Allele Mining Workshop, International Plant and Animal Genome XXI.  San Diego, CA, January 12-16, 2013.

Genome complexity reduction techniques are gaining popularity as the cost of generating short read sequence data decreases. This type of approach can reduce problems associated with ascertainment bias typically encountered with other genotyping platforms. Genotyping-by-sequencing (GBS), is a high-throughput and low-cost genotyping platform originally developed for highly inbred maize and sorghum populations (<http://www.igd.cornell.edu/index.cfm/page/projects/GBS.htm>). Although this technology was developed for inbred plant materials, we have shown that it can be effectively used for many types of species and populations, both with and without a reference genome. We will present an overview of the technology and current progress in adapting GBS for various applications.