第 41 回

インターゲノミクスセミナー

神戸大学大学院・農学研究科
インターゲノミクス研究会 主催
（若手研究者育成支援経費）

日時：6 月 20 日（火曜）16 時 00 分より　場所：農学部 B101

16 : 00　The Genetics and Consequences of Maize Domestication and Breeding

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Phenotypic variation has been manipulated by humans during crop domestication, which began between 3,000 and 10,000 years ago in the various centers of origin around the world. The process of domestication has profound consequences on crops, where the domesticate has moderately reduced genetic diversity relative to the wild ancestor across the genome, and severely reduced diversity for genes targeted by domestication. The question that remains is whether this reduction in genetic diversity has impacted crop production today. The complementary combination of genome-wide association mapping (GWAS) approaches, large HapMap datasets, and germplasm resources are leading to important discoveries of the relationship between genetic diversity and phenotypic variation, and the impact of domestication on trait variation.

There are a nearly infinite number of rare maize alleles that may play a significant role in important quantitative traits in maize (*Zea mays* ssp. *mays*). Many strongly deleterious alleles have been purged during the inbreeding of maize over the last century, while teosinte (*Zea mays* ssp. *parviglumis*), the non-inbred wild ancestor of maize, contains more deleterious alleles of larger effects that are masked by heterozygosity. Beneficial mutations, however, can be fixed in a population due to their positive fitness effects. It is the goal of plant breeding to increase frequency of beneficial alleles and decrease the frequency of deleterious alleles. Reintroducing variation from teosinte and maize landraces will require an understanding of the relative proportion of and the allelic effects of deleterious and beneficial rare alleles.

We created a randomly intermated population called the “Zea Synthetic,” comprised of 88% inbred line germplasm (the 27 NAM inbred line founders) representing world-wide diversity and 12% teosinte (11 outbred parviglumis accessions). This population combines alleles with differing inbreeding histories (inbred vs outbred) , and has been random mated 10 generations to date in order to break down linkage disequilibrium. We are using the Zea Synthetic to study inbreeding depression (ID): “Mild ID” after one generation of inbreeding and “Severe ID” after doubled haploid(DH) production.

From the Zea Synthetic, we created 2000 DH lines and 924 pairs of selfed-and-outcrossed (S0-S1) families. The S0-S1 and DH lines were phenotyped in three locations in 2014 and 2015 for both agronomic (maturity, plant/ear height, number of ears, kernel weight) and fitness (total kernel number) traits. The S0-S1 and DH lines have been genotyped with high density genetic markers, and the combined trait and marker datasets will be used to identify chromosomal regions of the genome that harbor deleterious and beneficial variation. We are also identifying chromosomal regions with that are underrepresented in teosinte and unadapted inbred parents, indicative of selection against these alleles during inbreeding. This unique germplasm will be released to the public, and will be a useful to maize geneticists and breeders interested in working with teosinte alleles.

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