

Joe Clarke (JC): Evidence suggested there are multiple protections against drought that operate together so we started with a hypothesis-driven candidate gene approach. Early in the process we looked through our genetic library and initially nominated several candidate genes that we believed would affect different plant structures or processes positively to allow the plant to respond to water stress better. From the larger pool, we were able to focus on a set of core genes that met our criteria. Our process also enabled us to identify specifically the right version (allele) of these genes and where on the genome they resided. We then used highly managed field trials to measure and validate the allelic effects.

Q: How did you select the candidate genes?

JC: The candidate genes were selected through a hypothesis-driven approach represented by the integration of microarray-based expression profiling across several crop and model species, relevant genetic information, public literature, and functional annotations. Comparative genomics and extensive sequencing was used to define the "target" candidate gene in corn. The target corn sequence was then converted into a series of genotypic assays intended to distinguish the allele/haplotype for each candidate gene across a diverse population. The genotypic information was used to assess the effect of each allele towards phenotypic diversity with regard to performance under drought. Our success was well above the 5–10% success rate often attributed to the non-hypothesis driven approaches of the time.

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Q: How did you validate the performance of the candidate genes in the field?

DM: We used managed stress environments where we essentially take corn with these genetic backgrounds and grow them in areas that receive no rainfall during growing season. The only water the plant receives is through a sophisticated irrigation system where we closely control and track the water supplied through moisture sensors. We take these plants with the genes in question to the edge of death due to lack of water. Then we recharge the soil profile, allow the plant to recover, and measure yield and final effect on the plants.

Q: What were the results?

DM: We were able to validate performance in the field and determine roughly what each gene candidate contributed to the water-stress response. We were able to move a variable number of these genes into the right genetic backgrounds and produce the Artesian corn hybrids that we ultimately sell to growers. With the ability to identify multiple genes that make up the Artesian trait, we don't have just one or two good ways to protect the corn plant against drought, we have multiple modes of action against drought that help to protect the plant all season long. The performance of Artesian is roughly 2x what we see from other technology in the field, because we've identified functions, processes, and structures that affect the plant's ability to deal with water stress. Under water stress, the plants yield up to about 15% more than a corn hybrid without the Artesian trait. Under extreme water stress, such as a prolonged, significant drought, we've increased corn yield as much as 40% with the Artesian trait versus a hybrid without the trait.

Q: How do you connect the trait to the mode of action?

JC: One of the distinguishing features in our development of Artesian is that it was based on a hypothesis-driven approach. Understanding the modes of action helps understand what is changing inside the plant at the genomic level to make it drought tolerant.

DM: A key loss in corn due to drought is what's called a barren ear, an ear of corn that sets few to no kernels. One of the modes of action that we've identified is a gene that appears to make kernel sets much more consistent in these Artesian hybrids, even under water stress, than in other hybrids. It's that specificity that allowed us to define the genes we're after, describe in general what we think they do, and move them into a testing system. We concluded that under extreme drought conditions this gene performed the way we thought it would. It became one of several core genes that we would locate in our breeding program and use for Artesian hybrids.

JC: Illumina is enabling us to build on the Artesian success by contributing towards the next generation of Artesian alleles at higher resolutions of trait impact and potential modes of action. We are also using Illumina platforms in the expression profile space to help better understand and leverage the modes of action assigned to the current Artesian product release. Our newer Illumina-based expression data sets on the HiSeq System offer several advantages over the existing hybridization-based expression data with regard to resolving potential modes of action.

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Q: What do your customers think of the Artesian hybrids?

DM: Artesian is a fun project to work on because it's a very visual technology. When growers plant these hybrids and see them under water stress, next to another corn hybrid, they see a dramatic difference between the corn plants. Under very hot drought stress conditions, an Artesian hybrid will generally be tall and dark green with its leaves fully unfolded. It looks like it's growing more comfortably than other hybrids, which are likely to be shorter, have poor color, and have the leaves rolled up to conserve water. Growers loathe seeing that response in their fields.

In 2012, I talked to a grower in Colorado, which is a very dry area to grow corn. It was so dry that he lost his entire crop, even his Artesian hybrids. But he called us to say that his Artesian hybrids lasted weeks longer than any other hybrid that he had. He was so enthused that he could go out there and see this visual difference in his field. He said he would likely not see that level of drought again for 20 years, but it proved to him that Artesian corn hybrids were different than the ones he was growing previously.

Q: What impact has genomic technology had on the project?

JC: Artesian was launched in 2012, but the project started in the early 2000s. The plant genomic world changed radically around 2007, facilitated by Illumina. We migrated to Illumina GoldenGate® arrays when they became available to help with the marker introgression aspects after the Artesian alleles were defined. We used GoldenGate arrays to help with the genotyping, characterize the populations, and to help with the molecular breeding and stacking of the alleles.

In 2008, we dove into large-scale Illumina-based sequencing projects in corn to increase our marker platform by an order of magnitude or two. The information was so much better. It was a clear decision to move from the candidate gene/Sanger sequencing approaches that defined the original Artesian to Illumina-based genome-wide association studies (GWAS) to define the next product releases under the Artesian brand. At the time, the cost of analyzing data on a gene-by-gene basis almost equaled the cost of taking an Illumina-based approach over the whole genome.

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Q: How has the success of the Artesian project impacted your approach to hybrid development?

DM: We've seen such success with our project in corn that we're anxious to try a similar approach in other crops. Water is such a limiting resource in so many areas and so many crop production systems. We could use a similar approach, in wheat, which is grown predominantly in the western states under extremely variable precipitation and in many cases under very dry conditions. If we could introduce wheat varieties that might yield 15% better under water stress, it would be a significant addition to agriculture as well as to our business.

JC: Because the hypothesis-driven, knowledge-driven approach worked it means we can continue taking time to understanding the biology behind what the GWAS results are telling us. In addition to using Illumina technology to discover SNP markers that identify GWAS alleles for us to breed with, we can use it to understand the biology behind why these alleles are doing what they're doing. There's some biology driving the decision making and the HiSeq 2500 System is helping us resolve that biology.

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