DECODING CANNABIS

Having successfully mapped the cannabis genome, Sunrise Genetics
CEO C.J. Schwartz is one step closer to unlocking the plant's limitless potential

By GARRETT RUDOLPH

Talk to any cannabis cultivator for more than a couple minutes and the conversation will ultimately drift toward genetics. While some growers and breeders have a deep understanding of their cultivars' phenotypes, the vast majority of the information about different strains is nothing more than cannabis industry folklore.

Yet, as the business matures, research into the plant has been shifting from secretive, underground operations to universities and well-equipped laboratories overseen by scientists like C.J. Schwartz, who has a Ph.D. in biochemistry and nearly two decades of experience in plant molecular genetics.

More than just a buzzword, genetics are truly the key to unlocking the full potential of cannabis and creating standardized varietals, products designed for a specific purpose, and fine-tuning the cultivation requirements of a crop.

Schwartz is the CEO of Sunrise Genetics, which announced in January that it had mapped the cannabis genome, following a two-year research project in conjunction with the University of Minnesota and CBDRx. Marijuana Venture spoke with Schwartz about what exactly that means for both the short- and long-term future of this fledgling industry.

FIGURE 1

Ancestry-painted Chromosomes
Cultivar: CBDRx

HEMPGENE
CANNABIS | GENOMICS

★ THCA Synthase
- - Centromeric axis

Ancestry

Europe
■ Denmark (marijuana-like)
■ Slavic Lands (hemp-like)

Eurasian Steppe
■ China
■ Uzbekistan
■ Kazakstan

South Asia
■ Nepal
■ North India
■ North Pakistan
■ South Pakistan

Southeast Asia
■ Vietnam
■ Cambodia
■ Malaysia
■ Melanesia

Africa
■ Morocco
■ Lake Malawi
■ West Africa
■ Central Africa
■ Ethiopia

Chris Grassa - Sunrise Genetics

A two-year research project at Sunrise Genetics has resulted in the mapping of the cannabis genome. This genomic map is often illustrated by the "painted chromosome" pictured above, providing a greater level of understanding how strains are related.

MARIJUANA VENTURE: It's been reported that Sunrise Genetics has "mapped the cannabis genome." Can you explain what that means?

C.J. SCHWARTZ: You are correct. In conjunction with both public and private groups, we have determined the order of the approximately 25,000 genes in cannabis' 10 chromosomes for three different types: hemp, a high-CBDA strain and a high-THCA strain. With the genomic map, we can now more precisely identify the genetic differences among these three types to breed tailored cannabis strains.

The reason we call it a genomic map is because it truly is a map. Just as a road map shows where cities are located, a genomic map shows where genes are located. Chromosomes (group of genes) are like states (group of cities). Often to achieve maximum yield of a product, multiple genes are important, and it is actually the specific combinations of those genes that lead to greater productivity. To gener-
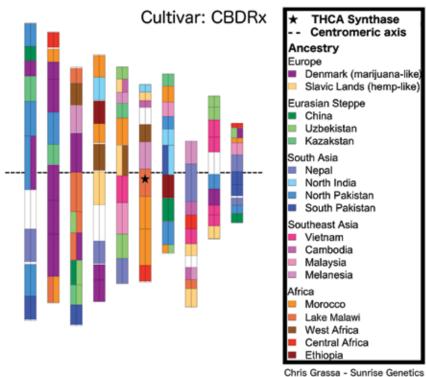
ate strains with multiple combinations of genes, we need to know their locations in the genome. Thus, Sunrise Genetics saw the need for a genomic map, which will vastly accelerate the rate of cannabis research and breeding.

MV: How would this matter for cannabis cultivators?

CJS: The genomic map gives us tenfold greater resolution in determining relatedness among strains, illustrated by what is commonly called a painted chromosome (Figure 1). Determining the genetics of a strain is paramount for accuracy, consistency and transparency. This is exceptionally important for telling strains apart for consumers and validating claims of the uniqueness of a strain, as well as documenting the development of a strain using irrefutable DNA evidence. Finally, having DNA evidence can also be used to protect cultivators and their favorite strain so that no one else can patent the strain and prevent/sue somebody for growing it.

MV: What are some things you learned about the cannabis plant during this process? Did it dispel or support any commonly accepted beliefs about cannabis?

CJS: We are still in the process of evaluating the data, but of great interest is how the cannabinoid and terpene genes are organized in the genome, and how this relates to potency, efficacy and the entourage effect. Many of the terpene genes work together, suggesting that the concentra-

tion of individual compounds may be linked together, making certain combinations generally non-existent. This would explain why we have "classes" of smells in marijuana strains.

With the ability to use genomic map data, which is already available for nearly every other crop, we can find those rare combinations that will unlink those terpenes, creating new combinations that may generate the desired characteristics of new medical strains.

MV: Will this have any immediate impact on the cannabis industry or will it take several years to bring about any changes?

CJS: We expect to publish a peer-reviewed scientific publication at the end of 2018, and the map will then become public information. This will allow all cannabis researchers worldwide to coordinate their data for finding important genes for numerous traits. The impact on the community and the sophistication of cannabis research and development will be substantially changed, bringing cannabis to the same level as other economically lucrative crops.

One immediate major change is how much more rapidly cannabis breeding can move forward. Using DNA information, we can track a specific gene, such as THCAS and choose which version of that gene is best for stability and consistency. By tracking certain genes and eliminating a lot of variation, we can focus more clearly on those genes that have the biggest effects.

Finally, gene discovery. To determine which genes are important, we need to do experiments and/or acquire data for comparing the genes (genotype) to the trait (phenotype). When we see a correlation between a specific gene and a phenotype, we have discovered the likely function of that gene. This process is called QTL (quantitative trait loci) mapping and required a genomic map. QTL mapping is the prima-

ry method of discovering the functions of genes and also assessing the role of each gene in the process.

MV: What does this mean for the future of cannabis cultivation? Could this be a starting point for growing cannabis plants specifically tailored to treat certain medical ailments or for a certain recreational effect?

CJS: That is exactly our goal. Once we have identified a gene that influences a trait, we record the DNA sequence. Then, throughout a breeding program, we can track that gene, as we make new/old combinations for specific chemical profiles tailored for maximum efficacy for specific ailments. This is commonly called marker-assisted selection (MAS), which helps the breeder choose only plants stable for a certain trait.

Multiple traits can be tracked simultaneously to retain stability for some traits (such as percentage of CBDA), while breeding for other traits (such as flowering time). With our technology, you can precisely create the plant you need for both your environment and maximum product.

MV: Most people believe we've only scratched the surface of scientific research into cannabis. Do you agree with this?

CJS: One hundred percent. Because cannabis is such a diverse "chemical cocktail," understanding how these chemicals affect the brain and their interactions with each other is key to making tailored cannabis strains. Using a DNA sequence, we can

trace the development of a strain and make educated decisions as to which plants to pursue to generate novel combinations of cannabinoids and terpenes.

MV: Can you talk a little bit about the roles played by CBDRx and the University of Minnesota in this process?

CJS: Both groups were instrumental in providing the germplasm to complete the project. CBDRx/Functional Remedies had an inbred strain that they have been using for CBD production, while the University of Minnesota had highly inbred hemp and marijuana varieties. For creating the genomic map, inbred strains work best. George Weiblen's group at the University of Minnesota had also crossed the hemp and marijuana varieties, providing a perfect population to delineate the different cannabis chromosomes.

MV: This has been a multi-year process for your company. How does it feel to complete this portion of your mission and what lies ahead for Sunrise Genetics?

CJS: We really felt that the genomic map was necessary to advance cannabis science. More science equals more facts, which equals legitimacy and transparency for an industry that needs both. With the genomic map, we can tell you exactly what you're getting.

Sunrise Genetics also feels privileged to have the opportunity to create a resource that will advance cannabis research, forever changing the cannabis industry.

MV: You've mentioned hosting the first cannabis-specific meeting at the Plant and Animal Genome conference as a highlight of your scientific career. Can you talk a little bit about why this was such a momentous occasion?

CJS: Even being asked to speak at PAG is an honor, since genomics is where modern biological science is at, and genomic data and

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technology are increasing exponentially, just like computer technology has experienced.

As far as understanding and "modifying" living organisms, we are experiencing a new technological revolution. To be given the role of selecting appropriate speakers and organizing the inaugural cannabis genomics session, as well as providing a highly scientific audience with general education about cannabis, is 100% aligned with my goals as an educator, scientist, businessperson and human being.

MV: Is there anything else worth noting about Sunrise Genetics or your research at this time?

CJS: The genomic map allows us to simultaneously map multiple genes for a given trait, since we can now "find" the address of the gene and look in other strains for a new version of that gene that performs better. Using the assembly data, we have already created new markers (DNA changes) linked to production of specific terpenes, cannabinoids, overall cannabinoid quantity, overall terpene quantity and flowering time. Without the complete genome assembly, we were blind as to how to make gene combinations to achieve certain goals, such as maximum yield, but now we can locate the genes and make different combinations that result in

a unique and stable strain.

We are currently working with multiple universities and companies to evaluate their germplasm collections, followed by suggestions on which strains to cross for maximum or minimum diversity. We have a comprehensive set of markers which allow breeders to focus immediately on strains containing a certain combination of genes that lead to the production of a high yielding strain, with highly specific and stable chemical (or other) phenotypes.

This interview has been edited for clarity and length.