

Commentary on “Complex Variability within the THCA and CBDA Synthase Genes in Cannabis Species”

Article Commentary

We read with great interest the 2016 publication by Allen et al. on variation in *THCA* and *CBDA synthase* DNA sequences from seized marijuana samples [1]. We wish to comment on the question of designing a molecular assay to accurately predict THCA content in *Cannabis* plants. This is an especially important issue in light of current regulatory policy and the expanding *Cannabis* economy.

In concluding that there is “no strong correlation between genotype and chemotype for THCA”, the authors appear to have overlooked the possibility that *CBDA synthase* rather than *THCA synthase* is responsible for the major chemotypic difference between drug-type and non-drug-type *Cannabis*. All five drug-type samples for which *CBDA synthase* sequences are shown in Figure 4 share a four-base (nonsense-inducing) deletion at position 153 compared to sequences encoding a functional enzyme. This finding is consistent with the main conclusion of Weiblen et al., namely in that plants lacking functional *CBDA synthase* produce primarily THCA [2]. We based our conclusion on the fact that THCA synthase and CBDA synthase compete for a common substrate, CBGA. Drug-type, intermediate and non-drug-type plants are widely recognized in the literature according to the ratio of THCA:CBDA [3].

Weiblen et al. showed that the presence or absence of alleles bearing the *CBDA synthase* sequence deletion is perfectly correlated

with the three major classes of *Cannabis* chemotypes. We find it misleading to cast doubt on a diagnostic assay for major differences in THCA content when genotypes may be scored by Sanger sequencing of PCR amplicons spanning the *CBDA synthase* deletion.

References

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