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

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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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