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Commentary on: Datwyler SL, Weiblen GD. Genetic Variation in Hemp and Marijuana (*Cannabis sativa* L.) According to Amplified Fragment Length Polymorphisms. J Forensic Sci 2006; 51:371–5.

Sir:

The authors are commended for their careful methods, important results, and unique perspectives. I want to extend their results by embedding them in recent *Cannabis* taxonomic research based on cannabinoid variation (1), terpenoid variation (2), genetic variation (3), morphological traits (4), and host–parasite relationships (5). A taxonomic proposal by Hillig and coworkers is presented in Table 1, alongside previous taxonomic concepts cited by Datwyler and Weiblen.

The four *Cannabis* populations studied by Datwyler and Weiblen can be placed in this classification with reasonable certainty, because the works of Datwyler, Weiblen, and Hillig intersect at a character trait: plant production of tetrahydrocannabinol (THC) and cannabidiol (CBD). According to Hillig and de Meijer (6), THC production in *Cannabis* is controlled by two co-dominant alleles at a single locus, termed B_T (encoding THC-synthase) and B_D (encoding CBD-synthase). *Cannabis indica* biotypes are dominated by the B_T allele and plants of this biotype generally produce a high THC: low CBD profile. Datwyler and Weiblen reported that "Skunk #1" produced this profile, consistent with "Skunk #1"s pedigree—a hybrid of *C. indica* narrow-leafed and wide-leafed drug biotypes (7). The *C. sativa* hemp biotype is dominated by the B_D allele and these plants usually produce a high CBD: low THC profile. Datwyler and Weiblen reported that "Carmen" yielded this profile, which agrees with its origin as a European *C. sativa* hemp cultivar (Gordon Scheifele, personal communication, 2006).

The lineages of "Minneapolis" and "Shakopee" are unknown, but their high CBD: low THC profile suggests they are likely feral descendents of European *C. sativa* hemp. In the principal coordinates scatterplot by Datwyler and Weiblen, the three hemp populations and "Skunk #1" are at opposite ends of PC 1. Similarly, *C. sativa* populations and *C. indica* populations cluster at opposite ends of PC 1 in a scatterplot based on allozyme frequencies (8).

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TABLE 1—*Seven putative Cannabis taxa recognized by Hillig (4), compared with taxonomic delimitation of Cannabis by previous researchers.*

Hillig (4)	Vavilov et al. (12)	Schultes et al. (10)	Small & Cronquist (11)	McPartland et al. (9)
C. ruderalis	*C. sativa* var. *spontanea*	*C. ruderalis*	*C. sativa* subsp. *sativa* var. *spontanea*	*C. ruderalis*
C. sativa Hemp biotype	*C. sativa* var. *sativa*	*C. sativa*	*C. sativa* subsp. *sativa* var. *sativa*	*C. sativa*
C. sativa Feral biotype	*C. sativa* var. *spontanea*	*C. sativa*	*C. sativa* subsp. *sativa* var. *spontanea*	*C. sativa*
C. indica Narrow-leaflet rug (NLD) biotype	*C. indica* var. *indica*	*C. sativa*	*C. sativa* subsp. *indica* var. *indica*	*C. indica*
C. indica Wide-leaflet drug (WLD) biotype	Not known	*C. indica*	*C. sativa* subsp. *indica* var. *indica*	*C. afghanica*
C. indica Feral biotype	*C. indica* var. kafiristanica	*C. sativa* (small-seeded)	*C. sativa* subsp. *indica* var. *kafiristanica*	*C. indica*
C. indica Hemp biotype	Not known	*C. sativa*	*C. sativa* subsp. *sativa* var. *sativa*	*C. sativa*