Beyond the name *sativa*, *indica* and *ruderalis*

How genetics distinguishes industrial hemp cultivars

INTRODUCTION

In the cannabis market, the terms “sativa”, “indica” and “ruderalis” are widely used to describe a plant’s origin and, often, to predict its composition or effects. These terms have deep roots in botany, but genetic and genomic research over the past two decades shows that they do not accurately reflect the actual divisions within the genus Cannabis.

For industrial hemp, this issue has practical importance: cultivars (selected and registered varieties of the plant) must be clearly identified, officially registered and monitored for their THC content. This article examines the origins of traditional names, what contemporary genomics reveals, and which genetic traits are now used to distinguish industrial hemp cultivars.

This article is based on a narrative review of the scientific literature. Sources were identified through searches of Europe PMC, PubMed and Crossref up to November 2026, as well as official EU documents and Albanian legislation.

WHERE DO THE NAMES SATIVA, INDICA AND RUDERALIS COME FROM?

Carl Linnaeus described Cannabis sativa in 1753. In 1785, Jean-Baptiste Lamarck described a second type from India, Cannabis indica, while in 1924 Dmitri Janischewsky added Cannabis ruderalis [1,2]. These descriptions were based on morphological, chemical and geographical traits, long before DNA analyses were available.

Since then, debate has continued over whether the genus comprises one or several species [3]. Small and Cronquist (1976) proposed a single species, C. sativa, with two subspecies, and used the practical threshold of 0.3% THC to distinguish fibre plants from psychoactive ones [4]. Hillig (2005), based on an analysis of enzymes in 157 samples, proposed three separate species [5].

The terms “Sativa” and “Indica” used in today’s market differ fundamentally from their botanical meanings. According to McPartland (2018), the popular “Sativa/Indica” classification does not correspond to the C. sativa and C. indica described by botanists, while extensive cross-breeding has made the distinctions between them “almost meaningless” [6].

WHAT DOES GENOMICS SHOW?

By analysing 14,031 single-nucleotide polymorphisms (SNPs; a change in a single DNA base at a specific position in the genome) in 81 samples of psychoactive cannabis and 43 samples of industrial hemp, Sawler et al. (2015) showed that the two groups differ at the whole-genome level (the plant’s entire genetic material), not only in genes associated with THC. The same study found that commercial strain names for psychoactive cannabis often do not reflect a meaningful genetic identity [7].

Whole-genome sequencing of 110 samples from around the world showed that C. sativa was first domesticated in East Asia during the Early Neolithic, and that all present-day cultivars, both industrial and psychoactive, derive from a common genetic pool [8]. In 2025, a pangenome (a shared genetic

map of the species) constructed from 193 genomes confirmed “surprisingly high” genetic and structural diversity “for a single species” [9].

On the basis of these data, the most recent reviews conclude that the genus Cannabis most likely consists of a single, highly diverse species, although the debate over classification is not considered fully settled [1,6].

WHY IS THE PLANT’S APPEARANCE NOT ENOUGH FOR ITS IDENTIFICATION?

Traditionally, plants with long, narrow leaves have been called “sativa”, while those with broader leaves have been called “indica”. However, a plant’s external appearance (phenotype) is shaped by the interaction between its genotype (genetic makeup) and the environment. In cannabis, light, temperature and growing conditions significantly affect flowering time, sexual expression and plant characteristics [10].

Several studies have directly tested the relationship between these labels and genetics. In an analysis of more than 100 samples, in which over 100,000 SNPs were studied, samples labelled “Sativa” and “Indica” were found to be genetically indistinguishable at the whole-genome level; the label was associated only with differences in some of the plant’s aromatic compounds [11]. There are also cases in which samples with the same commercial name, obtained from different suppliers, showed genetic inconsistencies [12]. A 2026 systematic review that included 28 studies likewise concluded that these labels are not reliable predictors of either product composition or effects [13].

CHEMOTYPE: THE DISTINCTION THAT MATTERS

For industrial hemp, the distinction with the greatest practical importance is chemotype, meaning the profile of the main cannabinoids produced by the plant. THCA and CBDA, the acidic forms from which THC and CBD are derived, are formed from the same precursor, cannabigerolic acid (CBGA), through the action of two enzymes: THCA synthase (THCAS) and CBDA synthase (CBDAS) [14,15].

Classical crossing studies showed that the THC/CBD ratio is inherited according to a simple model: a single gene position on a chromosome (the B locus) with two codominant alleles (different forms of the same gene), BT and BD, meaning that both are expressed simultaneously. BT/BT plants have a THC-dominant chemotype, BD/BD plants have a CBD-dominant chemotype, while heterozygous plants (carrying one allele of each type), BT/BD, have a mixed chemotype [14]. Later studies also described plants with CBG dominance, due to an almost non-functional allele (B0) at the same locus [16], as well as cannabinoid-free plants, caused by a recessive allele (expressed only when inherited from both parents) at another locus (O), which blocks cannabinoid production in the plant [17] (Table 1).

Table 1. Main cannabis chemotypes and their genetic basis (simplified)

Chemotype	Chemical profile	Genotype	Practical significance
I	THC-dominant	BT/BT	Typical of psychoactive cannabis
II	Mixed THC/CBD	BT/BD	Risk of exceeding the THC threshold
III	CBD-dominant	BD/BD	Typical of most industrial cultivars
IV	CBG-dominant	B0/B0	Specialised cultivars
V	Virtually cannabinoid-free	o/o (O locus)	Primarily research material

Genomics has expanded this model. The THCAS and CBDAS genes are located in large regions rich in DNA segments that are copied and relocated within the genome, and which differ substantially between industrial and psychoactive cannabis [15]. Psychoactive cannabis differs from industrial hemp through a non-functional CBDAS gene [18], while in a high-CBD cultivar, the complete copy of the THCAS gene was found to be missing [19].

> Chemotype primarily determines the ratio between THC and CBD, not their total quantity. Cannabinoid levels are also associated with genes on other chromosomes [18,19]; therefore, two plants with the same chemotype may have different THC contents. The cultivar's genetics do not replace laboratory analysis of THC.

This distinction has direct implications for control. A study of industrial hemp cultivars approved in Europe found that some individuals carried the BT allele, which is associated with THC production [20]. Another study identified plants in the "Finola" cultivar with functional THCA synthase and total THC content above the legal threshold, demonstrating genetic variation within the same seed lot [21]. DNA tests (molecular markers) can detect this risk at an early stage and help verify cultivar identity, complementing chemical analysis [14,21,22].

WHAT DOES THIS MEAN FOR ALBANIA?

Law No. 61/2023 defines the cannabis plant for industrial purposes as a plant "of the cannabis sativa and cannabis ruderalis types, of varieties containing no more than 0.8% THC" (Article 3) [23]. As in many other legal acts, the definition uses traditional botanical names. In implementation, however, the limits are established through measurable criteria: only registered seeds and seedlings may be planted (Article 26); imports are monitored for varieties included in the European Common Catalogue (Article 12); and THC content must not exceed 0.8% (compared with 0.3% in the EU) [24].

In a sector being built from the ground up, these criteria are directly supported by the genetic knowledge presented above:

- selection of registered cultivars with a stable chemotype, CBD dominance or very low cannabinoid content;
- use of certified seed to limit genetic variability within seed lots;
- laboratory testing of THC, because cultivar genetics indicate a tendency, but not the exact value;
- molecular markers as a complementary tool for verifying the cultivar and its chemotype.

In practice, therefore, the registered variety and the measured THC content matter more than the botanical name of the plant.

LIMITATIONS

Most genomic studies have been conducted using a relatively limited number of samples and have focused more on psychoactive cannabis than on industrial cultivars. The species' genetic pool remains only partially studied [9]. The relationship between molecular markers and actual THC content under field conditions requires further research, particularly for registered European cultivars.

CONCLUSION

The names sativa, indica and ruderalis are part of the history of botany, but they are not a reliable tool for distinguishing cultivars today. Genetics provides more accurate criteria: chemotype, sex-determination system, flowering behaviour and the molecular identity of the cultivar. For industrial hemp, where compliance with the THC threshold is essential, these criteria must always be accompanied by variety registration and laboratory testing.

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