International Journal of
Plant Biology

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Review

The Role of Jasmonates in Modulating Growth, Trichome Density, and Cannabinoid Accumulation in *Cannabis sativa* L.

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Abstract: Jasmonates have emerged as a prominent elicitor for enhancing trichome development and cannabinoid production in *Cannabis sativa* L. (cannabis). These glandular trichomes synthesize and store important cannabinoids, including tetrahydrocannabinol (THC) and cannabidiol (CBD), which determine the yield, potency, and quality of cannabis flowers. Methyl jasmonate (MeJA) acts through the COI1–JAZ–MYC signaling pathway to upregulate genes associated with trichome initiation and cannabinoid precursor formation. Evidence suggests that moderate MeJA concentrations (typically 50–100 µM) can effectively boost trichome density, elevate hexanoyl-CoA availability, and modestly enhance key biosynthetic enzyme activities, ultimately increasing THC and CBD content. However, higher methyl jasmonate doses can amplify these benefits, yet pose a risk of excessive vegetative stunting, highlighting the crucial trade-off between enhancing cannabinoid potency and maintaining overall biomass yield. Interaction with hormones like gibberellins, salicylic acid, and ethylene further shapes the plant's stress responses and secondary metabolism. Application in controlled environments, such as greenhouses or vertical farms, shows promise for enhancing resin production while minimizing biomass loss. In outdoor conditions, the application may offer additional defense benefits against pests and pathogens. These responses can vary depending on the cultivar, underscoring the importance of cultivar-specific optimization. As demand for high-cannabinoid cannabis products continues to grow and agrochemical options remain limited, leveraging MeJA treatments offers a practical, non-genetically modified approach to optimize yield, quality, and resilience in cannabis cultivation.

Keywords: plant hormones; secondary metabolite; hemp; specialty crops; medicinal plant; methyl jasmonate; jasmonic acid

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Academic Editor: Adriano Sofo

Received: 17 May 2025
Revised: 9 June 2025
Accepted: 13 June 2025
Published: 17 June 2025

Citation: Da Cunha Leme Filho, J.F.; Schuchman, S.; De Sarandy Raposo, R.; Diatta, A.A.; Didaran, F.; Sharma, S.; Walters, A.; Gage, K.L. The Role of Jasmonates in Modulating Growth, Trichome Density, and Cannabinoid Accumulation in *Cannabis sativa* L. *Int. J. Plant Biol.* **2025**, *16*, 68. https://doi.org/10.3390/ijpb16020068

1. Introduction

1.1. Origin and Classification of *Cannabis sativa* L.

Cannabis sativa L. is widely recognized as an annual, typically dioecious herbaceous plant, believed to have originated in Central Asia [1–3]. Archeological and ethnobotanical evidence suggests that humans have interacted with cannabis for at least 12,000 years [4].

However, some scholars argue that its domestication may be even older, due to the plant's strong association with early agricultural settlements [3]. One prevailing hypothesis for its widespread dissemination is the "camp follower" concept [3]. Where prehistoric humans used or discarded plant material around campsites, the disturbed soils in these areas provided fertile ground for cannabis seeds to germinate and proliferate. Over time, this weedy, adaptable plant would have been taken along migration routes, facilitating its global spread and eventual cultivation for various purposes. Throughout history, cannabis has fulfilled a multitude of roles. Early societies cultivated the plant for its bast fibers, which are strong and durable, and thus ideal for rope, textiles, and paper [5]. The seeds, rich in oil and protein, provided a valuable food source and an ingredient for cooking oils. Additionally, the plant's psychoactive properties, attributable to tetrahydrocannabinol (THC), have been found to have ceremonial or medicinal uses in a range of cultural contexts, spanning from ancient Central Asian societies to modern-day therapeutic applications [2,6]. Some historical records indicate that cannabis was employed as an analgesic, sedative, or religious sacrament in regions as varied as the Middle East, China, and India [7]. Consequently, cannabis became intertwined with human culture, mythology, and healthcare, reinforcing its status as one of the oldest known domesticated plants. As human trade networks developed, the geographical range of cannabis expanded, extending to Europe, Africa, and eventually the Americas. Adaptable to a wide range of climates—from temperate to subtropical—cannabis established itself in diverse environments, further broadening its genetic variation. This global presence gave rise to various "landrace" populations, which exhibit traits shaped by local selective pressures such as climate, soil type, and cultural usage [3]. Modern breeding programs continue to leverage these landraces for desired characteristics, including fiber strength, seed yield, or specific cannabinoid profiles.

Although *C. sativa* is the most widely accepted scientific name, its taxonomy remains a subject of contention. Based on taxonomic classification, cannabis is described as a single species, *C. sativa*, with three varieties or sub-species, including *C. sativa* var. sativa, *C. sativa* var. Indica, and *C. sativa* var. ruderalis [3]. When the THCA/CBDA ratio is taken into account, several chemotypes have been individuated: chemotype I (plants with a THCA/CBDA ratio > 1.0); chemotype II (intermediate THCA/CBDA ratio); chemotype III (THCA/CBDA < 1.0 or fiber plants); chemotype IV, where plants have a very high content of cannabigerolic acid (CBGA); and chemotype V, plants with no cannabinoid [8]. Beyond the scientific debates, vernacular terms such as "hemp" and "marijuana" have likewise contributed to public misconceptions. Legally, "hemp" generally refers to cannabis with a THC concentration below a certain threshold (commonly 0.3% in the United States), whereas "marijuana" denotes higher-THC cultivars typically used for medicinal or recreational purposes [9]. From a botanical standpoint, however, both classifications refer to the same species—their main differences lie in the plants' THC content, morphology, and intended use.

In recent decades, the relaxation of prohibition in several regions, marked notably by the 2018 Farm Bill in the United States, has reignited scientific and commercial interest in cannabis [10]. Research has expanded from crop breeding for fiber and grain quality to sophisticated analyses of cannabinoid and terpene profiles for medical applications. This renaissance has been driven in part by emerging data on the pharmacological potential of diverse cannabinoids (CBD, THC, CBG, etc.) for treating conditions ranging from chronic pain to epilepsy [1,2]. As a result, there is an increasing need for evidence-based agronomic practices and clear mechanistic insights into how jasmonates, more specifically methyl jasmonate (MeJA), affect plant physiology, secondary metabolism, yield, and quality. Cannabis produces a wide range of phytocannabinoids. Among these, THC and CBD are the most prominent and well-studied [11,12]. These molecules interact with the human endocannabinoid system by binding to CB1 and CB2 receptors. These receptors regulate diverse processes, including pain sensation, appetite, mood, and immune function [1,2]. Beyond THC and CBD, other minor cannabinoids, such as cannabigerol (CBG), cannabinol (CBN), and tetrahydrocannabivarin (THCV), also contribute to the plant's therapeutic and modulatory potential. Their cumulative pharmacological effect, often referred to as the "entourage effect," has spurred scientific efforts to enhance the total cannabinoid content in commercial cultivars [7].

1.2. Role of Trichomes in Cannabinoid Synthesis and Economic Relevance

Cannabis is a dioecious plant [11] that produces both glandular and non-glandular trichomes on the surface of leaves and other parts of the plant body [12]. However, it is the capitate-stalked glandular trichomes on modified leaves (perigonal bracts) surrounding female flowers that are the primary site of phytocannabinoid production [13]. On the other hand, the male plants produce lower amounts of cannabinoids compared to female plants [14]. These trichomes not only facilitate the production of valuable secondary metabolites, but also defend the plant from environmental stressors. The resinous secretions that are rich in cannabinoids, terpenes, and other compounds can deter herbivory by conferring a bitter taste or sticky texture, while also protecting against UV radiation and certain pathogens [15]. Consequently, trichome density (Figure 1) may be correlated with total cannabinoid yield [16], making it an important breeding and cultivation target not only for cannabinoid levels, but also for flower esthetics and quality.

Figure 1. Trichome density counting on a cannabis bract using a digital microscope. The top panel displays a microscopic image of the cannabis bract, featuring glandular trichomes (clear, globular structures). The bottom panel illustrates the image after processing in ImageJ software 1.54p (ImageJ, U.S. National Institutes of Health, Bethesda, MD, USA, https://imagej.net/ij/), accessed on 14 November 2023.

Given their myriad therapeutic possibilities, from pain management to seizure control, high-cannabinoid varieties of cannabis have become increasingly valuable in medical markets [1]. These varieties often require optimized growing conditions—an optimal light spectrum, optimal nutrition, and targeted hormone applications, especially when supported by a standardized propagation method [17]—to boost glandular trichome development. For producers, maximizing trichome density could translate to higher potency and improved profit margins. As the global demand for high-cannabinoid cultivars increases and regulatory landscapes evolve, there is a critical need for evidence-based agronomic practices that optimize cannabinoid yield and quality. For researchers, understanding the physiological triggers that upregulate trichome biosynthesis helps to unravel the complexities of plant defense and specialized metabolism. Amid conventional breeding and modern genetic techniques, phytohormones—particularly jasmonates (JAs)—have emerged as potent tools to elevate secondary metabolite content. The production of secondary metabolites in cannabis is linked with the accumulation of cannabinoids, which can affect the yield of THC or CBD, depending on the final goal of growers [18]. Jasmonates are central to plant defense signaling, activating pathways that synthesize protective compounds and physical structures, such as trichomes [19]. MeJA has been particularly noted for enhancing glandular trichome formation and promoting the accumulation of specialized metabolites, including cannabinoids [20]. One promising avenue of research explores how jasmonates, plant hormones recognized for their influence on trichome development and secondary metabolism, shape these traits in cannabis. However, the current literature remains scattered across studies on different hormonal interactions, trichome biology, and cannabinoid pathways, making it challenging for researchers and cultivators to apply these findings holistically. This review aims to bridge this gap by synthesizing existing knowledge on jasmonate's mechanistic role and its integration with broader hormonal networks in cannabis. By examining these factors, we aim to provide a clearer understanding of how jasmonate and related hormonal pathways can be strategically leveraged to improve cannabinoid production.

2. Methodology

This review synthesizes existing research on jasmonates and their impact on cannabis growth, yield, trichome development, and cannabinoid biosynthesis. We conducted a narrative search using keyword combinations such as "Jamonates signaling in Cannabis sativa", "MeJA and cannabinoid biosynthesis", "MeJA in controlled environment agriculture", "MeJA hormone signaling", and related terms. Sources were selected from academic databases and platforms, including Google Scholar and ResearchGate, focusing on publications between 1973 and 2025. Priority was given to peer-reviewed articles, reviews, and book chapters addressing the molecular mechanisms, physiological effects, and practical applications of MeJA treatments in cannabis and related plant systems.

3. Trichome Biology in *Cannabis sativa* L.

Trichomes are hair-like epidermal appendages that occur on various aerial surfaces of plants [15,21]. In *C. sativa*, two broad categories exist: non-glandular (cystolithic) and glandular. While non-glandular trichomes often serve mechanical or thermoregulatory functions, the glandular trichomes in cannabis are of primary economic and medicinal importance due to their capacity for cannabinoid secretion. Within each glandular head, specialized secretory disk cells synthesize and secrete cannabinoids, terpenes, and other compounds into a subcuticular storage cavity [22,23]. This compartmentalization enables the plant to safely accumulate high levels of bioactive chemicals without disrupting normal physiological processes. There are three main morphotypes of glandular trichomes on female flowers:

A. Bulbous Trichomes:
    - The smallest glandular form, often difficult to visualize without magnification.
    - Less studied, but still capable of secreting small amounts of resinous metabolites [24].

B. Capitate-Sessile Trichomes:
    - Characterized by a sesquiterpene and cannabinoid-rich head directly attached to the epidermal surface.
    - Typically contain eight secretory disk cells [25].
    - Commonly found on bracts and sugar leaves, but less productive than capitate-stalked types.

C. Capitate-Stalked Trichomes:
    - The largest and most abundant trichomes on mature female inflorescences, often featuring 12–16 secretory cells [24,26].
    - Responsible for the vast majority of cannabinoid production.
    - Highly visible due to their elongated stalk and large, bulbous gland head, making them a key target for horticulture/agronomic manipulation and breeding.

High trichome density in cannabis provides multiple defensive advantages. Dense coverage can help to trap or deter insect pests, reduce water loss under arid conditions, and mitigate harm from intense sunlight or UV radiation [27]. Thus, trichomes are integral to both chemical and physical aspects of the plant's defense strategy [28]. In the context of cannabinoid production, trichome abundance may be correlated with cannabinoid yield [16]. Cultivators seeking maximum potency or medicinal efficacy often prioritize methods that increase glandular trichome development. These can include manipulating light intensity, nutrient availability, or hormonal signals to encourage the plant to produce more resin. Furthermore, a higher trichome density is a desirable trait often associated with quality and potency by consumers.

One of the most compelling strategies to enhance trichome density involves the use of jasmonates, especially MeJA [19,20,29]. By activating jasmonate signaling pathways, MeJA can stimulate glandular trichome initiation, lengthen trichome stalks, and potentially upregulate key enzymes in cannabinoid biosynthesis [30]. For *C. sativa*, this represents an exciting avenue to selectively boost desirable phytochemicals while harnessing the plant's innate defense mechanisms.

4. Jasmonates: Biosynthesis, Signaling, and Functions

Jasmonic acid (JA) and its related derivatives—collectively known as jasmonates (including MeJA, JA–amino acid conjugates such as JA-isoleucine, and various oxylipin intermediates)—play fundamental roles in regulating plant growth, defense, and stress responses [31]. Their biosynthesis largely follows the octadecanoid pathway, unfolding in the chloroplasts and peroxisomes through a series of well-orchestrated steps. Initially, wounding, insect feeding, or other stress triggers the release of α-linolenic acid (18:3) from membrane lipids via phospholipases, such as phospholipase A (PLA). The liberated α-linolenic acid is then transformed into 13(S)-hydroperoxyl linolenic acid (13-HPOT) by lipoxygenase (LOX), a process whose specificity can vary according to different LOX isoforms and their tissue-specific expression. Subsequent reactions in the chloroplast involve allene oxide synthase (AOS) converting 13-HPOT to an unstable epoxide (13-HPDE), and allene oxide cyclase (AOC) catalyzing intramolecular cyclization to produce 12-oxo-phytodienoic acid (OPDA). OPDA is transported to the peroxisome, where it is reduced by OPDA reductase and subjected to three rounds of β-oxidation, ultimately yielding (+)-7-iso-JA. From there, JA can be conjugated to various amino acids, such as isoleucine (JA–Ile), by the JAR1 enzyme, forming bioactive molecules that are critical for receptor binding [32]. Another important derivative is MeJA, produced when JA is methylated by JA carboxyl methyltransferase (JMT). As MeJA is volatile, it can diffuse or be transported systemically, extending its signaling influence across tissues or even neighboring plants [31].

The enzymes involved in these steps, including LOX, AOS, AOC, and OPDA reductase, are tightly regulated at both the transcriptional and post-translational levels in response to environmental inputs, such as pathogen attack, mechanical injury, UV irradiation, or temperature stress [33]. Specialized transporters also facilitate the flux of OPDA and other oxylipins between subcellular compartments, coordinating the production of jasmonates. The reversible conversion of JA to MeJA enhances the complexity of this hormonal network by allowing for the rapid transmission of signals that trigger defense in distant tissues or adjacent plants [34]. Beyond their contributions to plant immunity, jasmonates oversee a wide range of developmental processes, including anther dehiscence, pollen maturation, tuber formation, and leaf senescence [35]. They also interact with additional phytohormones, such as salicylic acid, gibberellins, and ethylene, to navigate the crucial balance between plant growth and defense.

4.1. *MeJA as an Elicitor of Secondary Metabolism*

Among the various jasmonate derivatives, MeJA stands out for its remarkable ability to induce secondary metabolism [36]. When applied to either foliage or roots, MeJA simulates the biochemical signals associated with wounding or herbivore attack, priming the plant to redirect resources away from primary growth and toward the production of protective or specialized metabolites [37] (Figure 2).

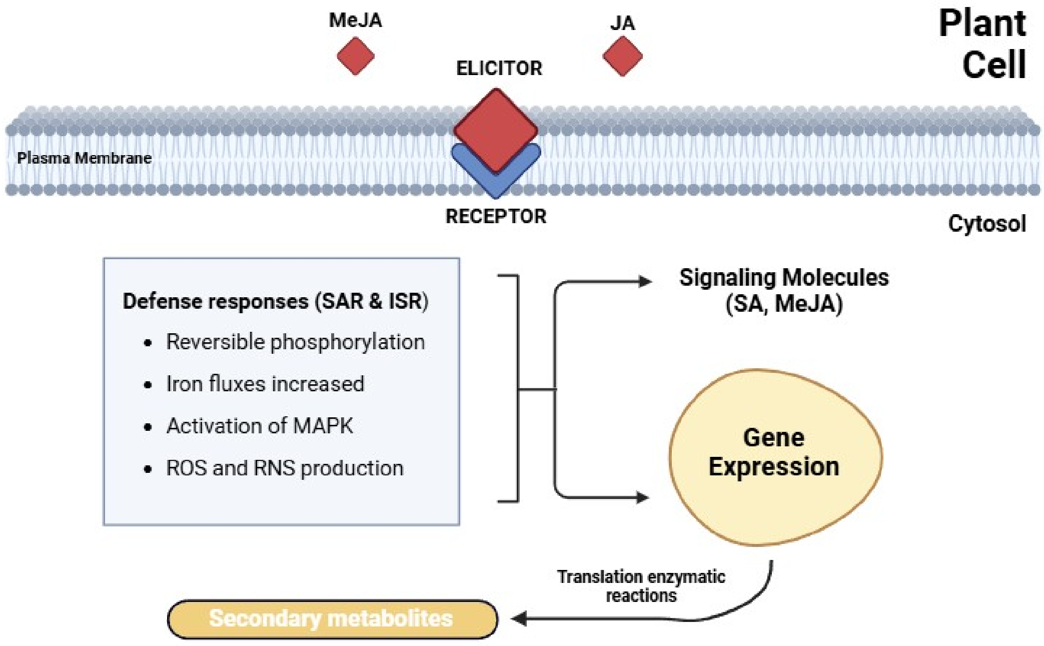

Figure 2. Methyl jasmonate (MeJA) and Jasmonic acid (JA) as elicitors of secondary metabolism: activation of defense responses and gene expression, leading to enhanced secondary metabolite production. Figure created using Biorender.com.

Well-documented examples include increases in nicotine content in *Nicotiana tabacum* L., where MeJA causes transcriptional activation of core nicotine biosynthetic genes (e.g., PMT and QPT), effectively doubling alkaloid levels [38]. Another noteworthy illustration is the several-fold rise in paclitaxel (Taxol) production in Taxus cell suspension cultures exposed to MeJA [39]. Salvia species respond to MeJA by enhancing key enzymes in the phenylpropanoid pathway, resulting in higher levels of rosmarinic acid and related antioxidant compounds [36].

In the context of cannabis, recent studies indicate that concentrations of MeJA ranging from 1 mM to 15 mM can notably elevate THC and CBD in floral tissues [40]. This upregulation aligns with the broader pattern of jasmonate-driven enhancement of specialized metabolites, and appears to be attributable to several factors. First, MeJA prompts the initiation of additional glandular trichomes, effectively increasing the number of sites capable of synthesizing cannabinoids and terpenes [19]. By generating extra "biochemical factories," cannabis plants may produce more secondary metabolites without necessarily overexpressing the final enzymes, such as THCA synthase or CBDA synthase. Second, MeJA upregulates upstream components of the cannabinoid pathway, notably genes involved in fatty acid metabolism or polyketide synthesis, which leads to olivetolic acid production [24,41]. In particular, an increase in hexanoyl-CoA availability is crucial for supporting higher rates of CBGA biosynthesis, which subsequently contributes to the formation of THC and CBD. Third, MeJA often redirects carbon skeletons away from vegetative growth and towards defense-oriented metabolism, a phenomenon that clarifies why plants occasionally exhibit stunted growth, yet display more abundant resin production [31,42]. Similarly, MeJA application was found to increase artemisinin and related secondary metabolites in *Artemisia annua* L., highlighting its broad influence in triggering the plant's secondary metabolism [43]. In controlled-environment agriculture facilities, where potency is occasionally favored over biomass, this trade-off may be advantageous for producers.

Interactions between MeJA and other hormones such as ethylene, salicylic acid, or gibberellins can produce synergistic or antagonistic effects on plant physiology. MeJA often collaborates with ethylene to bolster defenses against necrotrophic pathogens [44], yet it can clash with salicylic acid, which governs many responses to biotrophic pathogens [45]. Jasmonate signaling also commonly inhibits gibberellin-related growth processes, thereby shifting resource allocation toward defense and secondary metabolism [46]. Taken as a whole, these interactions mold the final phenotype of MeJA-treated cannabis, reconciling height reduction with improved cannabinoid yield [40]. From a cultivation standpoint, exogenous MeJA application may be a reliable method to boost trichome density and enhance the phytochemical profile of cannabis, particularly under controlled conditions such as greenhouses or vertical farms [20]. Applicators must, however, calibrate dosing and treatment schedules carefully to avoid excessive biomass loss. Light manipulation, tailored nutrition, or additional elicitors can be combined with MeJA to refine the biochemical attributes of cannabis even further, all without relying on genetic modification.

4.2. Deeper Mechanistic Insights: How MeJA Modulates Trichome Development and Cannabinoid Biosynthesis

4.2.1. MeJA Signaling Pathway and Gene Regulation in *C. sativa*

MeJA exerts its regulatory effects primarily via the COI1–JAZ–MYC signaling pathway, which is widely conserved across angiosperms [47]. In this canonical model, exogenous MeJA enters plant cells and is frequently demethylated to JA. The free JA is then conjugated to isoleucine (Ile) by the JAR1 enzyme, producing JA-Ile, the bioactive form that binds to the SCFCOI1–JAZ receptor complex [32]. When JA-Ile attaches to this complex, it triggers the ubiquitin-mediated degradation of JAZ repressor proteins, which normally sequester MYC-type transcription factors (TFs). Freed from JAZ inhibition, MYC TFs can then activate downstream jasmonate-responsive genes. Among the best-characterized bHLH TFs in this pathway are MYC2, MYC3, and MYC4, which bind to G-box motifs in JA-responsive promoters and initiate the expression of defense- and secondary-metabolism-related genes. This activation encompasses genes associated with glandular trichome development, directly linking MeJA signaling to the production of protective and specialized metabolites [48] (Figure 3).

4.2.2. Specific Regulators in Cannabis

Recent investigations in cannabis highlight CsMYC4, a bHLH transcription factor that responds to exogenous MeJA, as a major regulator of glandular trichome density and cannabinoid accumulation [49]. Overexpression studies suggest that CsMYC4 can drive the initiation and expansion of capitate-stalked trichomes, which are the primary sites of cannabinoid production [41]. By relieving JAZ repression, MeJA permits CsMYC4 and other transcription factors, such as MYB or HD-ZIP proteins, to trigger genes involved in trichome cell division, cell expansion, and resin secretion [50]. This includes genes encoding cuticle biosynthetic enzymes, cell-wall modifiers, and transporters for secreted metabolites, all of which may be upregulated in tandem to enhance trichome functionality. Although short-term MeJA treatments do not always cause dramatic increases in the final cannabinoid synthases (e.g., THCA or CBDA synthase), there is consistent enhancement of upstream enzymes and trichome regulatory genes [51]. As these regulatory factors expand trichome capacity, any baseline expression of THCA synthase or CBDA synthase can process a larger flux of precursors, ultimately raising the total cannabinoid output.

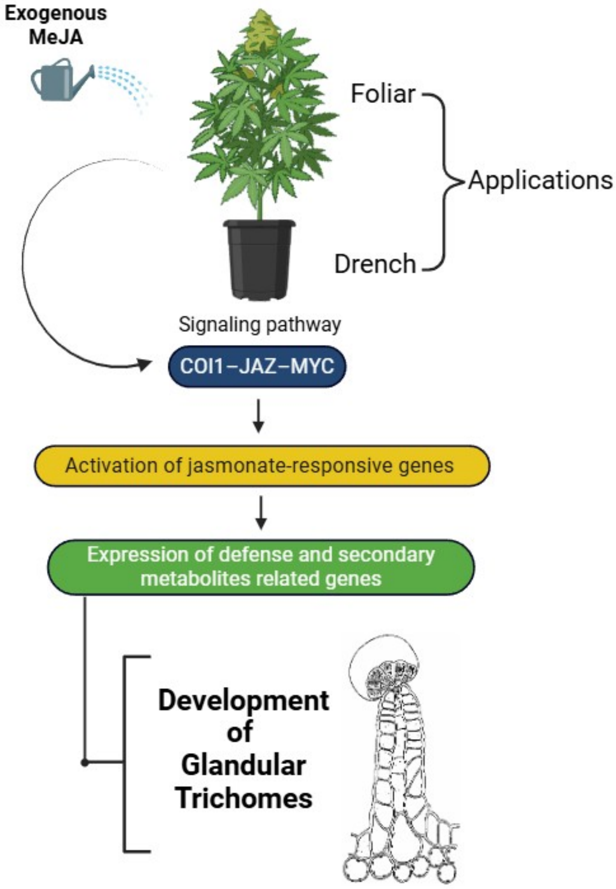

Figure 3. Exogenous methyl jasmonate (MeJA) induces the COI1–JAZ–MYC signaling pathway, leading to the activation of jasmonate-responsive genes, the expression of defense and secondary metabolism pathways, and the development of glandular trichomes in *Cannabis sativa* L. Figure created using Biorender.com.

4.2.3. Role of Epigenetics and Post-Translational Modifications

Emerging evidence from other plant systems indicates that JA-related transcription factors may recruit or be influenced by histone modifiers, such as H3K9 acetylation or methylation, thereby leaving a transcriptional "memory" of MeJA treatment [52]. In *Arabidopsis thaliana*, MeJA treatment has been shown to induce genome-wide changes in histone acetylation and methylation, particularly H4Ac and H3K27me3, leading to a transcriptional memory that primes plants for enhanced stress responses [53]. Similarly, in *Nicotiana benthamiana*, MAPK-mediated phosphorylation of WRKY transcription factors increases their DNA-binding affinity, activating defense-related genes that are critical for the plant's immune response [54]. If a similar mechanism applies to cannabis, certain genes could remain primed for rapid activation during subsequent stress or hormone exposure, although data for cannabis remains scarce. Additionally, phosphorylation of MYC factors by MAP kinases could alter their stability or DNA-binding affinity, adding yet another layer of regulation to the MeJA–trichome developmental cascade [55]. These epigenetic and post-translational controls underscore the complexity of hormonal crosstalk and illustrate why different cannabis cultivars may exhibit varying responses to MeJA.

4.2.4. Metabolite Fluxes and Enzymatic Activity

Cannabinoid biosynthesis depends on two essential precursor molecules: hexanoyl-CoA, which comes from fatty acid metabolism, and geranyl diphosphate (GPP), produced through the isoprenoid pathway [11]. Proteomic analysis shows that ACC1, STADs, and GPPS.lsu reach peak abundance during the secretory phase, highlighting their crucial roles in driving the production of CBGA, the central intermediate in cannabinoid synthesis [54].

Under MeJA-induced stress, plants typically upregulate enzymes such as LOX (lipoxygenase), AOC (allene oxide cyclase), and HPL (hydroperoxide lyase), which drive the production of short-chain fatty acid derivatives like hexanal [49]. Further enzymatic steps channel these carbon compounds into hexanoyl-CoA, thereby increasing the carbon pool available for CBGA synthesis [41]. MeJA can also alter the supply of GPP by upregulating genes involved in the isoprenoid pathway, ultimately boosting CBGA formation [56]. Some cultivars exhibit a metabolic shift that favors different cannabinoids, such as THCV, rather than pentyl cannabinoids like THC, suggesting that MeJA influences precursor flow or enzyme specificity.

Although the most conspicuous MeJA-mediated effects often appear as changes in trichome density or precursor availability, certain biosynthetic enzymes may also experience moderate or transient induction. The prenyltransferase CsPT4, responsible for linking GPP and olivetolic acid to form CBGA, can show subtle increases in both transcription and enzyme stability under MeJA [56]. Meanwhile, genes tied to fatty acid desaturation, β-oxidation, and coenzyme A activation may also be upregulated, thereby maintaining a robust supply of hexanoyl-CoA [24]. In parallel, MeJA can induce ABC or MATE transporters, promoting the relocation of intermediates or final products into the subcuticular cavity of glandular trichomes, thus preventing feedback inhibition [41]. The expansion of trichome structures themselves increases storage capacity, helping cannabinoids to accumulate at higher levels without harming the secretory cells. Multi-omics studies, incorporating transcriptomics, metabolomics, and proteomics, confirm that MeJA-treated cannabis exhibits a distinct metabolic signature characterized by enrichment in cannabinoids and terpenoids [49]. By correlating specific gene expression modules—for instance, those containing LOX, AOC, or PT4—with changes in metabolite profiles, researchers can identify master regulators of the MeJA response. Such high-level findings open avenues for breeding or genome-editing strategies that aim to optimize trichome development and cannabinoid biosynthesis with greater precision.

4.2.5. Crosstalk with Other Hormones at the Molecular Level

Gibberellins (GA) typically promote growth and biomass accumulation, whereas jasmonates, such as MeJA, shift resource allocation toward defense and secondary metabolism. In cannabis, MeJA drives the expression of GA2-oxidases, which degrade active GA, causing DELLA proteins to accumulate and hinder GA-responsive genes [46,57]. This process results in shorter internodes and reduced overall biomass, but it promotes enhanced trichome formation and the accumulation of secondary metabolites. For indoor or vertical cultivation, reduced plant stature may be advantageous when paired with elevated cannabinoid production, illustrating how GA–JA antagonism can be harnessed to optimize yield and space management.

Salicylic acid (SA) is generally associated with defense against biotrophic pathogens, whereas jasmonic acid (JA) and MeJA are more effective against herbivores and necrotrophic pathogens [45]. Although both SA and MeJA can independently raise cannabinoid levels in cannabis, the combination or sequential application of these hormones remains insufficiently explored [51]. High levels of SA often downregulate certain JA-responsive genes through WRKY transcription factors or NPR1-mediated pathways, potentially constraining MeJA-induced increases in trichome density [58,59]. Conversely, heightened JA/MeJA signaling can suppress some SA-linked defenses, which might influence susceptibility to biotrophic pathogens. These dynamics highlight the importance of carefully managing timing and dosages if SA and MeJA are to be used together in integrated pest management strategies for cannabis.

Ethylene (ET) can strengthen JA responses, especially in defending against necrotrophic pathogens. In cannabis, ET is best known for its role in sex expression, particularly in encouraging female flower development. Nevertheless, there is a theoretical possibility that ET and MeJA co-activation could heighten the expression of certain defense genes, such as PDF1.2, and accelerate shifts toward trichome-based defenses [60]. Although direct evidence on cannabis remains sparse, co-applying MeJA with an ethylene precursor (for instance, ACC) may intensify certain stress-induced phenotypes and further increase resin production. Such synergy could become a valuable horticultural tool, though excessive hormone exposure must be avoided to prevent yield penalties or unintentional stress responses. By integrating these perspectives on JA–GA antagonism, JA–SA trade-offs, and JA–ET synergy, it becomes clear that MeJA is only one component within a complex hormonal network that regulates plant growth and defense. In cannabis, the net effects of MeJA on trichome formation and cannabinoid production depend substantially on interactions with other signaling molecules. This understanding supports the idea that, with careful timing and precise application, MeJA can be strategically employed to bolster trichome-based chemical defenses and elevate the overall yield of medically and commercially valuable cannabinoids.

5. Practical Applications in Cannabis Cultivation

5.1. Controlled Environment Agriculture

Studies have shown that the exogenous application of MeJA at concentrations ranging from 0.1 mM to 15 mM can significantly enhance cannabinoid levels, often by 15–100% compared to untreated controls. Although this range underscores MeJA's potency as an elicitor, it is essential to note that the optimal dose varies depending on the cultivar, the plant's developmental phase, and the specific growing conditions [20]. Generally, moderate doses of MeJA, in the range of 0.05–0.1 mM, tend to maximize trichome density and boost cannabinoid yield without significantly restricting vegetative growth. This moderate approach is often accomplished through foliar sprays administered one or two times at key moments in flower development—usually early-to-mid-flowering—so that the plant dedicates ample resources to resin production. Some growers have also experimented with atomizing or vaporizing MeJA in indoor growing chambers to achieve uniform distribution; however, the efficiency of this method depends on various factors, including airflow, temperature, plant morphology, and growing practices. At higher concentrations, around 15 mM or more, MeJA can produce more pronounced increases in total cannabinoid accumulation, sometimes approaching two-fold gains. However, these stronger treatments often induce substantial dwarfing, reduced biomass, and occasional leaf stress symptoms [40]. While reduced vegetative growth can be advantageous in vertical or space-limited indoor farms, the potential drawbacks include lower overall yields of harvestable material if the primary goal is biomass production [61]. In some cases, increased biomass may lead to cannabinoid dilution, as the concentration of secondary metabolites becomes lower relative to the overall dry weight compared to more compact, denser plants [62].

Consequently, cultivators who prefer to grow shorter plants for space optimization may find that MeJA-induced dwarfing in conjunction with increased trichome formation strikes a desirable compromise. When applying MeJA in controlled environments, timing also plays a key role.

Many growers opt to introduce MeJA applications during the early-to-mid-stages of flowering, once or twice, so that plants have time to form additional glandular trichomes before harvest (Table 1). Repeated treatments require careful scheduling to prevent overwhelming the plants with phytohormones, an approach that can sometimes lead to leaf chlorosis or developmental abnormalities. Some growers have even explored pairing MeJA treatment with specific nutrient regimens or specialized lighting conditions, such as enriched blue or UV wavelengths, to create synergistic effects that further stimulate secondary metabolism. Although MeJA costs more than conventional fertilizers, its ability to considerably raise cannabinoid potency can offer a strong return on investment for producers catering to the medical and high-end markets.

Table 1. Practical and empirical summary of MeJA treatments in cannabis: application timing, trichome and cannabinoid responses, and risks.

MeJA Concentration	Timing of Application	Observed Effects on Trichomes	Impact on Cannabinoid Yield	Associated Risks
0.05–0.1 mM	Early-to-mid-flowering; 1–2 foliar sprays	Moderate increase in trichome density	15–30% increase in THC/CBD content	Minimal vegetative impact; safe for most cultivars
0.5–1 mM	Early flowering; may require repeated applications	Substantial increase in trichome initiation and stalk elongation	30–60% increase, depending on cultivar	Mild stunting, potential for leaf chlorosis
5–15 mM	Early flowering or late vegetative stage; single dose	Maximal trichome formation; high resin output	Up to 100% increase, but variable	Severe dwarfing, biomass reduction, and potential stress symptoms

5.2. Field Production and Stress Resistance

Beyond the confines of carefully controlled indoor facilities, MeJA application in open-field or less protective greenhouse environments presents additional opportunities and challenges for growers. In these less controlled settings, plants are exposed to a range of environmental stressors, including temperature fluctuations, variable humidity levels, and naturally occurring pressures from pests or pathogens. By mimicking a wound or attack response, MeJA primes cannabis to mount stronger defenses, which include higher levels of cannabinoid and terpene compounds [42]. These compounds, secreted in resin glands, can deter herbivory and inhibit certain fungal pathogens. Particularly in regions where cannabis flowers are susceptible to diseases such as *Botrytis cinerea* ("bud rot"), hormonal crosstalk with the ethylene pathway may further enhance the plant's necrotrophy resistance, but research detailing this effect in cannabis specifically is still limited [59]. The feasibility of applying broad-spectrum MeJA in field conditions depends on the local climate, cost considerations, and potential side effects, such as unintentional stunting or slowed growth, which may reduce the overall biomass. Lower-to-moderate MeJA doses can sometimes avert extreme growth inhibition while still conferring partial disease protection and heightened resin production. Larger-scale trials remain necessary, however, to confirm whether these improved defense traits translate into a reduction in loss caused by insects and pathogens, and whether the monetary gains from higher cannabinoid yields outweigh the cost of repeated elicitor applications.

5.3. Integration with Other Elicitors or Stressors

The idea of combining MeJA with other plant elicitors or mild environmental stresses represents a promising frontier in cannabis cultivation. Research has demonstrated that chitosan, for instance, can enhance specific defense pathways in a manner complementary to MeJA, thereby potentially amplifying secondary metabolite production [51]. Such combinations are also used in other medicinal plants, where pairing distinct elicitors leads to synergistic gains in valuable phytochemicals. In the case of cannabis, growers may experiment with combining moderate MeJA treatments alongside moderate water-deficit stress or low-intensity UV-B exposure to encourage increased trichome development without excessively harming yield [63]. This approach does, however, require precise monitoring, since even mild water-deficit stress or excessive UV could stress cannabis to the point of diminishing returns, even considering that cannabis presents evident plasticity traits. As a result, small-scale pilot studies are recommended to fine-tune methods before applying them across larger commercial plots.

Despite the potential benefits of multifactorial elicitation, growers should remain cautious about unintended interactions. For example, SA may antagonize certain JA- or MeJA-driven pathways. Simultaneously elevating SA and JA responses can disrupt metabolic allocation, reducing efficiency for the desired type of defense or secondary metabolite accumulation. While future research may clarify how best to stagger SA and MeJA treatments, blindly co-applying multiple elicitors can inadvertently undermine gains in cannabinoid yield or cause physiological imbalances. Another concern is cost-effectiveness; if products like chitosan or certain micronutrient formulations are expensive, measuring their impact on the final cannabinoid output is crucial for assessing a favorable cost–benefit ratio. Ultimately, combining MeJA with other elicitors or mild environmental stressors exemplifies the growing complexity of cannabis in agronomy/horticulture systems, underscoring the need for integrative studies that draw on genetics, multi-omics analyses, and field-scale trials.

By employing MeJA strategically—whether in tightly controlled indoor settings or under field conditions—cannabis cultivators can target improved trichome formation, elevated cannabinoid profiles, and potentially stronger defenses against pests and diseases. As research expands, standardized protocols for optimal doses, application timings, and compatible elicitors will likely emerge. This knowledge will enable the cannabis industry to refine cultivation methods that boost product quality while maintaining desirable growth characteristics.

6. Conclusions

Studies across multiple disciplines highlight the central role of glandular trichomes in *Cannabis sativa* L. for synthesizing pharmacologically important cannabinoids. As the demand for high-cannabinoid cultivars increases, new research is focusing on how factors such as genotype, environment, and phytohormones, including jasmonates, regulate trichome development and cannabinoid biosynthesis. MeJA emerges as a promising elicitor by activating the COI1–JAZ–MYC signaling cascade, which enhances precursor availability and modestly upregulates key enzymes, boosting trichome density and cannabinoid accumulation. However, while higher MeJA concentrations can further increase potency, they often stunt vegetative growth, highlighting the trade-off between maximizing cannabinoid yield and preserving biomass. Notably, hormonal crosstalk, especially with gibberellins and salicylic acid, further shapes plant responses, while potential epigenetic and post-translational modifications may leave a transcriptional memory of MeJA exposure. In order to fully harness MeJA's potential, researchers and cultivators must carefully calibrate its dosage and application timing, ideally in conjunction with mild abiotic stress and supported by validation through field trials. Overall, MeJA presents a promising tool for the sustainable enhancement of resin production in cannabis. Future work should integrate "omics" technologies, targeted breeding, and broader field studies to translate these insights into robust, evidence-based agronomic practices.

Author Contributions: The authors confirm their contributions to the paper as follows: study conception, design, revision, and writing: J.F.D.C.L.F.; draft manuscript preparation: S.S. (Spencer Schuchman); study revision, editing, and design: R.D.S.R.; study design: A.A.D.; study conception and writing: F.D.; study revision and editing: S.S. (Shiksha Sharma); study conception and design: A.W.; study conception and design: K.L.G. All authors have read and agreed to the published version of the manuscript.

Funding: This research received no external funding.

Data Availability Statement: The original contributions presented in the study are included in the article; further inquiries can be directed to the corresponding authors.

Conflicts of Interest: The authors declare no conflicts of interest.

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