Keywords: Phytocannabinoid; Food security; Molecular farming; Biofuel; Edible vaccine

Introduction

e 'plant of the thousand and one molecules' is what has been said of Cannabis sativa (o en known as marijuana). Together with terpenes and avonoids, phytocannabinoids are the most prevalent compounds discovered in cannabis [1]. Of the more than one hundred phytocannabinoids that have been described so far, tetrahydrocannabinol (THC) and cannabidiol (CBD) are just two [2].

e term "phytocannabinoid" is used to characterise cannabinoids that

e development of novel phytocannabinoids and the history of phytocannabinoid synthases

For thorough structure-function research and for advancing our understanding of phytocannabinoid production, an understanding of evolutionary links can be essential. erefore, it is particularly intriguing to think about how phytocannabinoid synthases came to be. Since Cannabis lupulus, the closest relative of this plant, does not synthesise phytocannabinoids, the enzymatic machinery most likely developed a er the two species split some 25 million years ago. Since THCA, CBDA, and CBCA synthases are all quite similar to one another, they probably come from the same ancestor [8]. According to phylogenetic reconstructions, CBCA synthase and THCA are more closely linked to one another than they are to CBDA synthase. erefore, the current theory for the development of phytocannabinoid synthases maintains that one ancestral gene duplicated and diversi ed to produce the ancestors of THCA/CBCA and CBDA synthase.

A broad family of berberine bridge enzyme-like genes (BBE-like genes) that are present in bacteria, fungi, and plants includes phytocannabinoid synthases. Alkaloid biosynthesis, alcohol oxidation, and phytocannabinoid synthesis are among the diverse processes that are catalysed by BBE-like enzymes using FAD as a cofactor. It is unclear precisely how an enzyme that may catalyse the synthesis of phytocannabinoids originated from a precursor enzyme. e uncharacterized action of several BBE-like enzymes, including many of those closely linked to the phytocannabinoid synthases, further complicates analyses in this area [9].

In conclusion, by screening plants for novel secondary chemicals, there is great potential to discover novel pharmacologically intriguing phytocannabinoids. Sequence data alone may also be used to estimate a putative phytocannabinoid synthesis activity once structure-function correlations of BBE-like enzymes are better understood. is would signi cantly speed up the search for new phytocannabinoids given the abundance of genomic data now accessible. Additionally, employing directed evolution and/or rational design to manipulate the genetic makeup of other BBE-like genes or even existing phytocannabinoid synthase genes may result in the creation of novel phytocannabinoids with medicinal potential [10]. e THCA synthase's crystal structure has been determined, which might help e orts in this regard even more.

Understanding cannabis development for optimised plant breeding and cultivation

Cannabis is no di erent from other crops in that development biology is essential to crop improvement. e basis for novel adaptations and yield boosts will be a thorough understanding of the genetics and physiology of cannabis plant architecture, in orescence, and ower development.

Cannabis plants were chosen for indoor culo ovement. e43 Tw ,1(p)12(m)4(en)19(t)]TJ0.069 Tw -1.57(a)9(n)4(55[(b)12(io)7(log)-23.9.9(a)8.9n

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Con ict of Interest

None

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