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Abstract. This study clarified the variation and role of physical and chemical characteristics of the *H. brasiliensis* projected acetyl-CoA carboxylase genes. The detectable similarity and joining projected acetyl-CoA carboxylase genes of *H. brasiliensis* in the dendrogram may be the outcome of tropical environmental. Six projected acetyl-CoA carboxylase genes from H. Brasiliensis collected from NCBI. The NCBI locus number of the protein sequence utilized in this study was determined. The physical and chemical properties of acetyl-CoA carboxylase from H.brasiliensis. The factors were calculated the designate number of protein, number of amino acids, molecular weight, theoretical isoelectric point values, the total number of atoms, extinction coefficients, estimated half-life, instability index, aliphatic index and grand average of hydropathicity.

1. Introduction

The role of acetyl-CoA (acetyl coenzyme A) in biochemical reactions is vital in the metabolism of proteins, carbohydrates, and lipids. Acetyl types were sent to the citric acid cycle (the Krebs cycle) to be oxidized for energy production is how it works. The relationship between amide and 3-phosphorylated ADP connects the β-mercaptoethylamine group with pantothenic vitamin acid as a constituent of Coenzyme A (CoASH or CoA). The critical role is played by acetyl-CoA in metabolism because of the many crossing pathways of metabolism and transformation. The level of acetyl koa is monitored by cells through modification of different protein acetylation depending on the metabolite, a significant indication of its metabolic state is revealed from the available evidence [1].

Fatty acids, glucose metabolism, and amino acid catabolism are sources of acetyl-CoA. The process of breaking down glucose occurred in the process of glycolysis, into two carbon molecules, three pyruvates. Decarboxylation of pyruvate oxidation is catalyzed by the mitochondrial pyruvate dehydrogenase complex to make acetyl-CoA, a two-carbon acetyl unit linked to an acyl group carrier, CoA [2].

2. Materials and Method

2.1. Materials

Six designed acetyl-CoA carboxylase genes from *H. brasiliensis* collected from NCBI. The NCBI locus number of the protein sequence sequenses utilised in this study with accession and definition below: XP_021686493 (acetyl-CoA carboxylase 1-like [*H. brasiliensis*]), XP_021655145 (acetyl-CoA carboxylase 1-like isoform X1 [*H. brasiliensis*]), XP_021655146 (acetyl-CoA carboxylase 1-like isoform X2 [*H. brasiliensis*]), XP_021655147 (acetyl-CoA carboxylase 1-like isoform X3 [*H. brasiliensis*]), XP_021655148 (acetyl-CoA carboxylase 1-like isoform X4 [*H. brasiliensis*]), XP_021655149 (acetyl-CoA carboxylase 1-like isoform X5 [*H. brasiliensis*]).

2.2. Physicochemical properties of the acetyl-CoA carboxylase

We firstly used EMBOSS Backtranseq (https://www.ebi.ac.uk/Tools/st/emboss_backtranseq/) to the changed protein sequence of the acetyl-CoA carboxylase into a nucleic acid sequence. Than used protparam online analysis (https://web.expasy.org/protparam/) to determine the physical and chemical properties of acetyl-CoA carboxylase from *H. brasiliensis*. The determinants were calculated the designate number of protein, number of amino acids, theoretical isoelectric point values, molecular weight, the total number of atoms, estimated half-life, instability index, aliphatic index, extinction coefficients, and grand average of hydropathicity [3]**.**

2.3. Potential transit of peptide of the acetyl-CoA carboxylase

The targetP 1.1 server online **(**http://www.cbs.dtu.dk/services/TargetP/) applied to estimate transit peptide. The site assignment is according to the estimated presence of any of the N-terminal pre-sequences chloroplast transit peptide (cTP), mitochondrial targeting peptide (mTP), and secretory pathway signal peptide (SP) [4].

2.4. Phylogenetic analysis of the acetyl-CoA carboxylase

The NCBI locus numbers of the sequence of acetyl-CoA carboxylase from six variants of *H.brasiliensis* used this investigation in this manner. CLUSTAL W ver. 1.83 was used to analyze the phylogenetic alignment of amino acids inferred from the monocot acetyl-CoA carboxylase gene carried out with [5] the Japanese DNA Data Bank (Mishima, Shizuoka, Japan) and described with TreeView, ver. 1.6.6 [6], with a neighbor-joining method to measure the knot expertise in a tree, uses bootstrap analysis with 1000 duplications [7].

3. Results and Discussion

Table 1 showed a number of line parameters of physicochemical acetyl-CoA carboxylase in *Hevea brasiliensis*. The acetyl-CoA carboxylase consists of six variants:1-like, X1, X2, X3, X4and X5. The length of protein sequences has differed with the genes defined. Encoded amino acids were from 6693 to 6882. It is noteworthy that theoretical isoelectric point values is the same value 4.59 and the estimated half-life is the same value 4.4h. Moreover, all of the parameters depict that three variants X1, X2, and X3 are similar in the number of analyzed genes. Variant X4 is the most different from the various values in the existing criteria. the diversity of these values is presumably due to the fact that the source of the plant which was the object of research came from a variety of hevea clones. Other research needs to be done by involving more sources of rubber plant clone entres which are also widely planted in various plantations.The balance between carbohydrate and fat metabolism is another advantage of acetyl-CoA. Different genes encode the polypeptides that set up the multi-subunit acetyl-CoA of prokaryotes and plants.

Management of insect pest control must be carried out continuously with due regard to environmental conditions. Insect life cycle is expected to be broken through the application of appropriate control techniques. Other studies related to acetyl-CoA carboxylase focused on the effects of fungicide antibiotics to control insects, especially plant hopper. On the other hand, this pesticide is mostly applied in Asian rice agroecosystems. To damage the reproductive patterns of insects in the

leafhopper union, the brown planthopper (BPH) Nilaparvata lugens and the white leafhopper supported by white leafhopper (WBPH) *Sogatella furcifera*, are both severe revival rice pests. The silencing of RNAi from Acetyl Co-A carboxylase (ACC), significantly involved in BPH processed with JGM, reduced ACC expression (by> 60%) and with JGM induction in BPH the increase in fecundity can be eliminated. These results have a good impact on increasing rice production in the managed planting area [8].

Table 1. Physicochemical characteristics of acetyl-CoA carboxylase from *Hevea brasiliensis*

H. brasiliensis variant	1-like	X1	X2	X3	X4	X5
Length of protein sequences	2268	2294	2294	2294	2269	2231
Number of amino acids	6804	6882	6882	6882	6807	6693
Molecular weight	545240.32	551849.85	551849.85	551849.85	545305.22	536284.61
Theoretical isoelectric point values	4.59	4.59	4.59	4.59	4.59	4.59
Total number of atoms	66609	67422	67422	67422	66620	65558
Extinction coefficients	133750	135250	135250	135250	133500	130625
Estimated half-life	4.4 h	4.4 h	4.4 h	4.4 h	4.4 h	4.4 h
Instability index	48.28	49.36	49.36	49.36	49.12	49.33
Aliphatic index	21.65	21.53	21.53	21.53	21.58	21.62
Grand average of hydropathicity	0.951	0.948	0.948	0.948	0.947	0.943

Table 2 display the similarity of the potential transfer peptide to the likelihood of prospect transfer peptide in *H. brasiliensis* acetyl co carboxylase genes. Four consistencies were observed: chloroplast transit peptide, mitochondrial target peptide, the signal peptide of the secretory pathway, and the reliability foresight. Variant 1-like showed differences from others.

Table 2. The Expectation of the potency transit peptide of Acetyl-CoA carboxylase in *H. Brasiliensis*

H. brasiliensis variant	Reliability			
	Chloroplast transit peptide	Mitochondrial target peptide	The signal peptide of the secretory pathway	Reliability prediction
1-like	0.053	0.662	0.026	5
X1	0.074	0.403	0.038	4
X2	0.074	0.403	0.038	4
X3	0.074	0.403	0.038	4
X4	0.074	0.403	0.038	4
X5	0.074	0.403	0.038	4

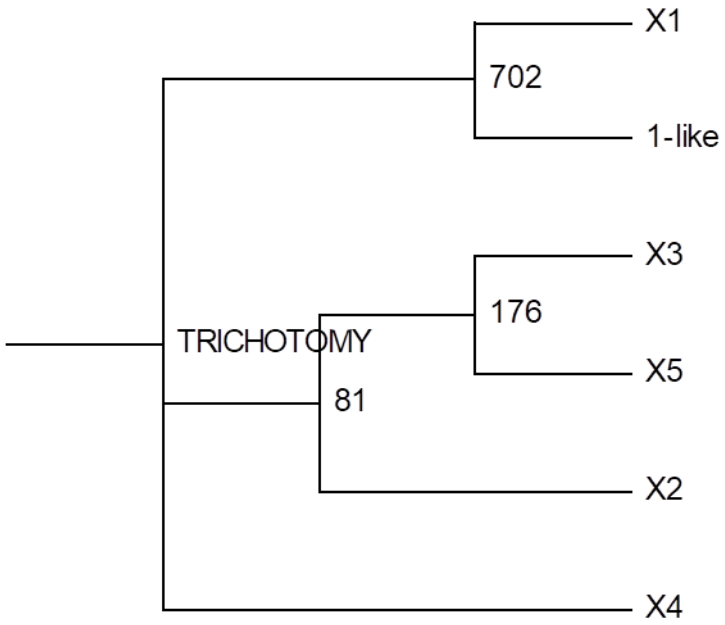

Figure 1. Clustering tree of plant projected acetyl-CoA carboxylase genes from *Hevea brasiliensis* together with six projected acetyl-CoA carboxylase. The directed scale epitomizes 0.1 amino acid replacements in each site. Numerals are depicted bootstrap evaluation from 1000 replications. The materials and methods section is explained the NCBI locus numbers of the amino acid sequence of analyses

The Acetyl CoA Carboxylase (ACC) gene in lipid biosynthesis to produce malonyl-CoA is a biotin-dependent manner, covalently enclosed to the multifunctional fatty acid synthase (FAS) to synthesize palmitic, saturated fatty acids C16. The activity of ACC increases with increasing age or fruit development for each variety. Differences occur in each variety with the same fruit development phase. Oleifera hybrid varieties that have the lowest oil content show the lowest ACC activity. And that ACC has a key role in regulating the accumulation of triaciglycerol or oil in the oil palm mesocarp. Many aspects of physiology are influenced by ACC because it acts at the top of the central metabolic pathway, through its effect on fatty acid synthesis. Silencing essential genes in fatty acid synthesis provides a wide and inclusive effect on genes in several unlinked pathways. More importantly, fatty acids are crucial biomolecules for ovarian physiology, incorporating growth, maturation, compact energy storage, and embryonic development. [9] The consequence of a suppressed ACC causes a reduction in lipid biosynthesis, and in mosquitoes that are silenced with ACC and FAS1 produce fewer eggs. from controlling mosquitoes in the 1st and 2nd gonotrophic cycles [10].

Another study was to examine the activity of mesocarp ACCase in several stages of palm fruit development and to clone cDNA fragments of conservative regions of the heteromeric ACCase encoding gene of the biotin carboxylase (BC-htACCase) of palm fruit mesocarp. ACCase activity was analyzed by HPLC. CDNA amplification was carried out by RT-PCR technique using heterologous degeneration primers at various attachment temperatures and MgCl2 concentrations. The results of BlastX analysis of the DNA sequences of cloned fragments showed that the sequences had high homology, among others, with the encoding gene BC-htACCase [11]. Some research has revealed that ethylene in Hevea skin tissue regulates two main pathways for increasing latex production in which acetyl co a plays a role: a) increasing rubber synthesis, and b) prolonging latex flow. In the early stages ethylene induces changes in pH in the cytosol to become more alkaline. This pH change triggers the activity of several enzymes that play a role in the mevalonate pathway, and increases the availability of adenylate and sucrose compounds in latex, as an important factor in rubber

biosynthesis. Exogenous ethylene induces the expression of the aquaporin gene in the skin tissue so that the water supply around the tapping field increases, and ethylene can also maintain latex stability during latex flow. Factors of water availability in tissues and high latex stability have a positive effect on latex flow of rubber plants [12].

Exogenous ethylene application increases endogenous ethylene in latex vessel cells. This endogenous ethylene induction is associated with an increase in ethylene biosynthesis. The ethylene precursor is S-AdoMet which is synthesized from the amino acid methionine with the help of S-adoMet synthetase (ADS), (EC 2.5.1.6). Adomet is converted by breaking down one ATP into 1-aminopropane-1-carboxylic acid (ACC) by the enzyme ACC synthase (ACS). The ACC is then oxidised to ethylene by ACC oxidase with a by-product in the form of CO and becoming cyanide. 2 ACC can be malonylated to malonyl-ACC (MAAC), a pathway to reduce ACC concentration and reduce ethylene production [13].

4. Conclusions

The variability and function of physical and chemical traits of the *H. brasiliensis* gene that is projected by acetyl-CoA carboxylase are clarified through this study.

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