Determining biological roles of four unique Vernicia fordii acyl-CoA Binding Proteins

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Determining biological roles of four unique Vernicia fordii acyl-CoA Binding Proteins

A Thesis

Submitted to the Graduate Faculty of the University of New Orleans in partial fulfillment of the requirements for the degree of

Master of Science in Biological Sciences

by

Steven Pastor

B.S. University of New Orleans, 2008

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Abstract

High-value industrial oils are essential for many processes and have great economic and environmental impacts. The tung tree produces a high-value seed oil. Approximately 80% of tung oil is α-eleostearic acid, which has a high degree of unsaturation thus giving it properties as a drying oil. The identification of the biological components in tung is imperative to further the knowledge of its processes. Four unique tung acyl-CoA binding proteins, VfACBP3a, VfACBP3b, VfACBP4, and VfACBP6 were identified and the genes encoding them were cloned and analyzed to determine their biological roles. The VfACBPs were observed to be similar to other organisms’ ACBPs, especially Arabidopsis thaliana. In addition, each gene was expressed in all tung tissues. They were shown to interact with VfDGAT1 and VfDGAT2, two known components of tung lipid metabolism. Finally, VfACBP3a and VfACBP6 were expressed in the seeds of transgenic plants to study the effects of VfACBP expression on seed lipid fatty acid content.

Keywords: acyl-CoA binding protein, Vernicia fordii, Arabidopsis thaliana, lipid biosynthesis, lipid metabolism, eleostearic acid, tung, Kennedy pathway, biofuel, industrial feedstocks, qPCR, split ubiquitin
Introduction

Alternate energy sources and their economic impacts

Fossil fuels power nearly everything in the modern world. Coal and natural gas power plants generate large amounts of electricity, distributed through countries by massive power grids. Gasoline and diesel are used as the primary energy sources for many vehicles. Ships, planes, rockets, motorcycles, and virtually everything else that moves uses some form of fossil fuel. The supply of fossil fuels on the planet is a finite resource, and is quickly dwindling, causing concerns about controlling steady supplies. At the same time, environmental concerns about fossil fuels are growing steadily. It is estimated that roughly 21.3 billion tons of carbon dioxide are generated by fossil fuels each year, with only about half of that absorbed by natural processes (ISTA Mielke GmbH Hamburg, 2002).

Fuel is necessary for everyday activities and extremely important for specific activities. Alternative fuel sources could alleviate the usage of current fuel sources without interruption of necessary processes. Some of the more popular forms of alternative energy include but are not limited to: solar energy, wind energy, hydroelectric energy, tidal energy and biomass. The positive aspects of alternative energy sources must outweigh the negatives greatly and provide a monetary advantage over current petroleum usage and main sources of energy. Determining whether alternative fuels provide advantages over the fossil fuels they displace requires thorough investigations into the inputs and outputs for their production and use life cycles over short and long periods of time.

In the most general sense, an alternative fuel is any substance that can be utilized in place of conventional fuels (Metzger, et. al., 2006). There has been much concern over creation and implementation of alternative fuels into current applications. Alternative fuels must provide
some specific benefits in order to replace any of the conventional fuels currently in use. In order to be a viable substitute for a fossil fuel, an alternative fuel should not only exceed any potential environmental benefits over the fossil fuel it replaces, but be at least economically competitive with it, and be producible in large quantities to make an impact on the high energy demands of modern societies. In addition, it must provide a net energy gain over the energy sources used to produce it.

There has been a growing interest in biofuels recently, which has largely been driven by rising energy prices, increasing energy imports, concerns about petroleum supply, and an increased recognition of the environmental consequences of fossil fuel uses. The production of biofuels, many of which are derived from biomass, require energy to grow crops and convert them to biofuels. These energy demands can have negative environmental impacts through movement and usage of agricultural chemicals, especially nitrogen, phosphorus, and various pesticides from farms to other regions of the environment (Biermann, et. al., 2000).

The usage of fossil energy may present more issues than simply deciding how cost-effective they are or characterizing their emissions. For example, there are environmental costs which cannot be captured in market prices, meaning a biofuel’s impacts on society depends on not only cost-competitive properties, but also its environmental costs, influences, and benefits. This could mean that subsidizing biofuels that are typically economically uncompetitive can be justified if their environmental impacts are much less than for current alternatives. There was no biofuel that was cost competitive with any of the petroleum-based fuels without subsidy in 2005 (FAOSTAT, 2007). Ethanol’s net production cost in 2005 was $0.46 per energy equivalent liter of gasoline (FAOSTAT, 2007), versus gasoline prices which averaged $0.44 per liter (FAOSTAT, 2007). Similarly, another biofuel, soybean oil, had an estimated production cost of
$0.55 per energy equivalent liter of diesel (FAOSTAT, 2007), compared to diesel prices that averaged $0.46 per liter (FAOSTAT, 2007). Since 2005, petroleum prices have risen (FAOSTAT, 2007), and this seems to have improved the cost competitiveness of biofuels. Again though, if biofuels prove to not be as cost competitive as expected, their production may still be profitable due to large subsidies. For example, the United States government provides subsidies of $0.20 per energy equivalent liter for ethanol and $0.29 for biodiesel (FAOSTAT, 2007). The producers of biodiesel and ethanol can also benefit from subsidies that lower corn and soybean prices.

One of the underlying issues with the utilization of biofuels is the effect it has on food sources. For example, in 2005, 14.3% of the United States’ harvested corn was processed to produce $1.48 \times 10^{10}$ liters of ethanol (FAOSTAT, 2007). This is energetically equivalent to 1.72% of the United States’ usage of gasoline (FAOSTAT, 2007). Likewise, soybean oil, which made up 1.5% of the United States’ soybean harvest in 2005, was used to produce $2.56 \times 10^8$ liters of biodiesel, which was only 0.09% of Unites States’ use of diesel (FAOSTAT, 2007). These results illustrate how little both soybean oil and corn oil contribute to gasoline and diesel usage in America; thus even devoting all sources to biodiesel and ethanol production would not offset production completely. Due to the fossil energy that is needed to produce ethanol and biodiesel, this devotion would allow for a net energy gain equal to only 2.4% and 2.9% of United States gasoline and diesel consumption respectively (FAOSTAT, 2007). Given this information, it is currently unrealistic to ascertain the maximal rates of biofuel supply since crops utilized in the process are integral in human and livestock consumption.

Within the next 50 years, the global demand for food is expected to increase (Gunstone, et. al., 2006), while the global demand for transport fuels is expected to increase even more...
quickly compared to that of food (Metzger, et. al., 2006). Thus, it is imperative to provide any renewable energy supplies that would not cause adverse environmental impacts and, perhaps just as importantly, do not compete with food supply. As previously mentioned, biofuels from food sources can meet only a small portion of transportation energy needs and biofuels that are not food-based may be of greater importance over the long term. For example, there are biofuels such as synfuel hydrocarbons that can be produced with minimal agricultural requirements and lands with minimal pesticides, fertilizers, and fossil energy inputs, or even produced from agricultural residues (Durrett, et. el., 2008). These have the potential to provide fuel supplies with increased environmental benefits relative to petroleum or food-based biofuels.

**The general impacts of oilseed crops**

For thousands of years, oilseed crops, which are grown primarily for the oil contained in the seeds, have been produced to serve as food sources for humans and livestock, and as such, the fatty acid composition of storage oils is tailored towards the necessities of human and animal nutrition (Ohlrogge, Browse, 1995). There are a variety of nontraditional plant species; however, that accumulate large amounts of unusual fatty acids stored in their seed oils that have potential uses in industrial applications (Dyer, et. al., 2002). The identification of genes that are responsible for the synthesis, accumulation, and storage of these exotic fatty acids has made possible the production of oleochemicals in the seed oils of transgenic crops. Unfortunately, expression of certain transgenes has met with very limited success due to the low accumulation of the desired fatty acids (Dyer, et. al., 2002). As it stands, multiple genes will be required in order to efficiently synthesize and accumulate exotic fatty acids in transgenic hosts.
The tung tree

Tung is a subtropical tree with very limited agronomic characteristics, meaning, it has difficulty growing unless there are very specific accommodations made for its growth, and thus there is interest in producing tung-specific drying oils in more conventional, easier to grow, oilseed crops (Duke, 1979). The tung tree (*Vernicia fordii*) accumulates α-eleostearic acid, a trienoic fatty acid with conjugated double bonds (9\(cis\), 11\(trans\), 13\(trans\) octadecatrienoic acid; see Figure 1-1 for nomenclature and structures of fatty acids), utilized for industrial applications (Duke, 1983). As alluded to previously, a fatty acid that is industrially important is highly important in studies for transgenic crops aiming to provide alternatives to the traditional industrial energy sources. Currently, U.S. industries import the majority of tung oil from South America and China, and both the quality and price of the oil can fluctuate appreciably (FAOSTAT, 2007). Methods have to be developed for converting regular vegetable oils into industrial drying oils; such methods would have the potential to create new markets for vegetable oils while defining the minimal sets of genes that are necessary for the efficient accumulation of industrially-important fatty acids in transgenic hosts.

Usages of the tung tree

For the most part, tung has been known to be cultivated primarily for its oil (Duke, 1983). The oil that is pressed from tung seeds makes an exceptionally efficient wood finish. Tung oil dries quickly to form a tough, glossy, waterproof surface on the object it is coating. Tung oil is also used as a drying agent for paints and varnishes; as waterproofing for paper, cloth, and ceramic products; and in the manufacture of linoleum, oilcloth, inks, resins, artificial leather, lubricants, brake linings, and cleaning and polishing compounds. It is also used in coatings for food containers and electronic parts (Brown, Keeler, 2005). Interestingly, during World War II,
the Chinese developed a way to process tung oil to supplement gasoline, as a blended mixture, for motor fuel (Brown, Keeler, 2005). Although it is toxic, tung oil has been used to treat skin conditions and constipation (Brown, Keeler, 2005). In addition, tung extracts have recently shown potential as termite control compounds (Brown, Keeler, 2005).

With regard to this study, the most relevant piece of information is that tung produces a unique fatty acid in large quantity: α-eleostearic acid (Brown, Keeler, 2005). General properties of fatty acids and an exhaustive description of eleostearic acid will be described.

A visual description of the tung tree

*Vernicia fordii*, which is a species of the genus *Vernicia* in the spurge (Euphorbiaceae) family, is a round-crowned deciduous tree that has the potential to grow to roughly 30-40 ft (9.1-12.2 m) in size, but usually stays half that size upon completion of its growth cycle (Brown, Keeler, 2005). The flowers open before the leaves come out in early spring. It has several round-tipped ivory petals on its flowers that are streaked with orange. They are borne in long-stemmed clusters that consist of dozens of flowers (Duke, 1983). On the majority of the trees, all but one in each cluster are staminate male flowers. When the female flowers are pollinated, they develop into 2-3 in (5.1-7.6 cm) hard, round, green or purple-green fruits that can contain upwards of 1-15 seeds, but usually have about five on average. They ripen in the fall as the foliage turns yellow color (Duke, 1983).

Locations of the tung tree’s growth

A large contingency of tung trees come from the subtropical foothills of western China (Duke, 1979). The trees are cultivated in China, Argentina, Paraguay, and, to a lesser extent, Africa and the southeastern region of the United States. There are many naturalized populations in the southeastern U.S. around abandoned commercial tung oil groves in the vicinities of
A general description of Fatty acids

A fatty acid is a multiple-linked hydrocarbon that possesses a carboxyl (-COOH) group at one of its ends. The majority of fatty acids are straight-chain compounds containing an even number of carbon atoms (Rigaudy, Klesney, 1979). Their carbon chain-lengths can range anywhere from 2 to 80 but commonly are found in the 12 to 24 range (Rigaudy, Klesney, 1979). Fatty acids may be divided into four distinct classes, depending upon their chain length. Those which contain chain lengths of 2 to 6 are termed short-chain, 8 to 10 are termed medium-chain, 12 to 18 are termed long-chain, and greater than 20 are termed very long-chain fatty acids (Gunstone, Harwood, 2006). The physical and biological properties of fatty acids are highly dependent upon chain length. In addition, chain length is a crucial parameter in acyl chain contribution to membrane structure and stability (Gunstone, Harwood, 2006). As fatty acyl chain length is increased, melting point is increased while solubility is decreased. This effect results from the weak apolar interactions that determine how the membrane can interact with its surrounding environment. As an example, the restricted solubility of lipids in the surrounding aqueous milieu is dictated by the tendency of acyl chains to remain associated with one another as opposed to associating with the aqueous environment (Gunstone, Harwood, 2006). Similarly, responses to temperature fluctuations are modulated by the extent to which thermal influences allow the acyl chains to dissociate from one another and assume a much more randomized structure (Gunstone, Harwood, 2006).

There are two general types of fatty acids: saturated or unsaturated. Saturated fatty acids do not contain carbon-carbon double bonds, meaning they are saturated with hydrogen, as
opposed to unsaturated fatty acids that typically have anywhere from one to three double bonds (Christie, 1986). Some fatty acids may also contain additional functional groups such as hydroxyl, epoxy, conjugated, acetylenic, and many others that also may play specific roles in their conformations and functions (Christie, W.W., 1993). One of the more prominent abilities of fatty acids in a cell is to maintain the fluidity of a membrane. One of the major strategies that is incorporated by a cell in order to maintain membrane fluidity at physiological temperatures, is to change the composition of membrane phospholipids by adjusting the ratio of saturated to unsaturated fatty acids (Christie, W.W., 1993). Many times, unsaturated fatty acids can have profound effects on the fluidity and function of biological membranes. In a variety of organisms, unsaturated fatty acid homeostasis can be achieved by feedback regulation (Aguilar and de Mendoza, 2006). In the majority of plant tissues, approximately 75% of the fatty acids they contain are unsaturated (Aguilar and de Mendoza, 2006).

Saturated fatty acids are straight chains, with free rotation about the carbon-carbon double bonds. This property allows them to pack closely together and produce a membrane that is virtually solid at low temperatures, adversely impacting membrane fluidity and thus a cell’s survival. When a more loosely packed membrane structure is more advantageous, the rigidity of the lengthy saturated acyl chains can be contravened by acyl chains with double bonds (Gunstone, Harwood, 2006). A carbon-carbon double bond in unsaturated fatty acids is introduced by a desaturase reaction and produces a bend in the carbon chain. Upon the introduction of a double bond of cis (Latin for “on the same side”) geometric configuration, a bend of the chain is introduced that moves the straight chain approximately 30° away from the original linearity of the saturated chain (Gunstone, Harwood, 2006). Also, double bonds are non-rotating and restrict any acyl chain movement (Gunstone, Harwood, 2006). The result is that Van
der Waals forces expand the distance between chains, thereby decreasing the potential for any chain to chain interactions (Gunstone, Harwood, 2006). Furthermore, around the double bond, some charge concentration can increase the polarity of the acyl chain (Gunstone, Harwood, 2006). While double bonds have the potential to cause bends or curved shapes within the biological membrane, the extent to which they do this is poorly understood. Physical and biochemical data, however, have clearly shown that unsaturated acids decrease membrane rigidity and melting point (Gunstone, Harwood, 2006).

The introduction of additional bends in the fatty acid chain can occur due to multiple desaturase reactions. The membrane bilayer or lipid body containing the fatty acid cannot pack into a regular structure due to the bends introduced into the hydrocarbon backbone, which allows the membrane to remain more fluid at low temperatures (Hamilton, 2007). The most prominent strategy that is employed by the cell in order to ensure that membranes remain sufficiently fluid to maintain cellular function at any temperature is to change the ratio of saturated to unsaturated fatty acids (Hamilton, 2007). An increase in temperature is followed by an increase in saturated with a concomitant decrease in unsaturated fatty acids, while decreasing temperatures results in an increase in the amount of unsaturated with a decrease in saturated fatty acids in cell membranes (Gunstone, Harwood, 2006).

The acyl chain length and both the number and positions of double bonds, heavily influence the fluidity, permeability and stability of biological membranes within membrane phospholipids. As such, fatty acids are named using these parameters since the physiological properties of unsaturated fatty acids are heavily dependent upon the length and position of double bonds (IUPAC Compendium of Chemical Terminology, 1997). To name fatty acids, two numbers separated by a colon, for example, 18:1, denotes the number of carbon atoms
number before the colon) followed by the number double bonds (the number after the colon). In addition to the number system other naming conventions are also used, since bond position and orientation are important contributors to the physiological properties of fatty acids. The carbons that are counted from the carboxyl (-COOH) end of the fatty acid are deemed to be in the delta (Δ) position, while those that are counted back from the terminal carbon are deemed to be in the omega (ω) position (IUPAC Compendium of Chemical Terminology, 1997). The delta (Δ) nomenclature is assigned to the position of an individual double bond, or the specificity of an enzyme that is inserting it. The (n-) nomenclature is used to designate a fatty acid within a family of structurally related acids. There is also still a wide use of the (ω-) designation in order to designate the position of a double bond from the methyl end. As an example of this, linoleic acid (18:2 ω-6), is an 18-carbon chain containing 2 double bonds, that has the first double bond in the sixth position from the methyl end. Also, linoleic acid can be designated as 18:2Δ⁹,¹² to indicate that there are 2 double bonds, one at the 9th and one at the 12th carbon position, counting from the carboxyl end of the fatty acid (IUPAC Compendium of Chemical Terminology, 1997). The double bonds are in the cis-configuration in most naturally occurring fatty acids, and thus it is assumed that all double bonds are cis, and separated by a single methylene group, unless noted otherwise (IUPAC Compendium of Chemical Terminology, 1997). Using linoleic acid as an example again, it is described by 18:2cisΔ⁹,¹² to illustrate both the position and orientation of the double bonds. Figure 1-1 illustrates an example of a fatty acid along with some naming conventions.
Figure 1-1. Identification of fatty acids. Part A illustrates the basic structure of a fatty acid through oleic acid, a monounsaturated fatty acid containing a cis double bond at the ninth carbon, as an example. Part B illustrates the amphipathic nature of a fatty acid. Part C lists many of the common fatty acids; the first three being saturated and the last four being unsaturated.

**Tung seed oil**

The tung produces fruit once a year during the summer months, and the large seeds of these fruit contain roughly 50% dry weight oil (Brown, Keeler, 2005). As mentioned earlier, this oil consists of about 80% eleostearic acid (wt/wt total fatty acids) which is a trienoic fatty acid with conjugated double bonds (Duke, 1983). This conjugated bond system can be easily
oxidized, resulting in the polymerization of the oil and also results in the formation of tough resistant films (Brown, Keeler, 2005). Tung oil also contains smaller amounts of oleic, linoleic and palmitic acids (Duke, 1983). Eleostearic acid also occurs as a beta acid (9, 11, 13 all trans), typically due to irradiation of the alpha form of the acid (Cahoon, et. al., 2006).

**Biosynthetic pathways**

Cell membranes are comprised of phospholipids, each of which contains two fatty acids. In addition, fatty acids are also used for protein modifications. Fatty acid metabolism, therefore, consists of catabolic processes which generate energy and primary metabolites from fatty acids, along with anabolic processes that create biologically important molecules from fatty acids and other dietary carbon sources (Browse, Sommerville, 1991).

Plants synthesize a very large variety of fatty acids; however, only a few of these are major and common constituents (Napier, 2007). Generally speaking, long chain fatty acids are synthesised *de novo* from smaller precursors that are ultimately derived from photosynthate (Gurr, et. al., 2002). There are two enzyme systems that are incorporated: acetyl-CoA carboxylase and fatty acid synthase (Gurr, et. al., 2002). This synthesis produces end products that are usually palmitate and stearate with the latter predominating in many plants by as much as 2-3 times that of palmitate (Gurr, et. al., 2002). Most stearate is desaturated by a stromal acyl-acyl carrier protein desaturase to form oleic acid (Whittle, et. al., 2005). The long chain acids can be subjected to elongation, desaturation, and further modifications or processes (Gurr, et. al., 2002). As opposed to acetyl-CoA carboxylase and fatty acid synthase, which are soluble enzymes, the elongases are membrane-bound and are situated in the endoplasmic reticulum (Gunstone, Harwood, 2006). Recently, the details of such reactions have begun to be elucidated.
at the molecular level (Gunstone et. al., 2006). The elongases are coded by FAE genes while the desaturases are coded by FAD genes (Gunstone, Harwood, 2006).

As for the tung tree, some plants can produce unusual fatty acids in their seed oils, many of which having industrial applications. These include hydroxyl fatty acids, cyclopropane fatty acids, epoxy fatty acids and conjugated unsaturated fatty acids, to name a few (Gunstone, Harwood, 2006). It is important to mention that these unusual fatty acids accumulate preferentially in triacylglycerols (TAGs) and are essentially excluded from membrane acyl lipids, presumably because they would disrupt or impair function (Gunstone et. al., 2006).

**Triacylglycerols (TAGs)**

Almost all of the commercially important fats and oils of both animal and plant origin consist almost exclusively of the simple lipid class, triacylglycerols (Baud, Lepiniec, 2010). This is inclusive of all the vegetable oils, like those from corn, olive, palm, and sunflower, and the animal fats, like tallow, lard and butter, as well as many commercial products such as margarines. The more prominent animal triacylglycerols are either fats from adipose tissue or the milk fats, where their main function may be energy storage, but some triacylglycerols may confer more dynamic roles (Baud, Lepiniec, 2010). An example of these triacylglycerols would be those of blood plasma or the liver. Likewise, in plants, seed oils provide an energy source and structural fatty acids for the developing embryo (Biermann, et. al., 2000).

More specifically, triacylglycerols consist of the trihydric alcohol glycerol that is esterified with long-chain fatty acids. Upon the esterification of the three primary hydroxyl groups with different fatty acids, there results a triacylglycerol that can be asymmetric and thus can display optical activity, although this activity is usually far too low to be measured (Li-Beisson, et. al., 2010). Problems arise in the application of the conventional D/L or R/S systems
that designate enantiomers without ambiguity (as with simple molecules), due to the complexity of the mixtures of triacylglycerols that are found throughout nature (Li-Beisson, et. al., 2010). These problems can be circumvented; however, if the stereochemistry of triacylglycerols and that of other glycerolipids is described by the stereospecific numbering system, termed \( sn \), as recommended by the IUPAC-IUB (IUPAC Compendium of Chemical Terminology, 1997).

**Biosynthesis of triacylglycerols**

All eukaryotic organisms, along with some prokaryotes, have the capability to synthesize TAGs and how this synthesis occurs has been studied extensively in plants and animals (Mu and Høy, 2004, Murphy, 2001). There are many different cell types and organs that are able to synthesize TAGs. In animals, the predominant organs that participate in this synthesis with the greatest activity are the liver and intestines; however, most of the body stores TAGs in adipose tissue (Murphy, 2001). Within all types of cells, TAGs are stored as cytoplasmic lipid droplets, also known as fat globules, oil bodies, lipid particles, or adiposomes. These are encased by a monolayer of phospholipids and hydrophobic proteins, including perilipins in adipose tissue or oleosins in seeds. These lipid droplets can be distinguished as distinctive organelles, complete with their own unique metabolic pathways and enzymes. Mycobacteria and yeast have similar lipid inclusions (Kohlwein, 2010). Lipids mainly function as a store of energy and a reserve of essential fatty acids, but they may also exist as a measure of protection to enable the eradication of the excess of biologically active and potentially harmful lipids including free fatty acids, diacylglycerols (DAGs), cholesterol esters and coenzyme A esters (Murphy, 2001).

Two principal biosynthetic pathways for TAG synthesis have been elucidated, the sn-glycerol-3-phosphate pathway, also known as the Kennedy pathway, which predominates in adipose tissue and the liver, and a monoacylglycerol pathway located in the intestines (Coleman
A third pathway has been recognized in a few animal tissues and maturing plant seeds, in which a diacylglycerol transferase (DAG:DAG transacylase) is involved (Coleman and Lee, 2004). Of these three pathways, perhaps the most important is the sn-glycerol-3-phosphate pathway, which was first described by Professor Eugene Kennedy and colleagues in the 1950s (Coleman and Lee, 2004). More than 90% of the liver TAGs are produced by the Kennedy pathway (Schittmayer and Birner-Gruenberger, 2009).

In this pathway, the major source of the glycerol backbone is believed to be sn-glycerol-3-phosphate, which is assembled by the catabolism of glucose via glycolysis, or to a lesser degree by the activity of glycerol kinase on free glycerol (Coleman and Lee, 2004). There is evidence, however, that a portion of the glycerol is produced in a de novo fashion by glyceroneogenesis through pyruvate (Coleman and Lee, 2004).

After these events, all subsequent reactions take place in the endoplasmic reticulum (Coleman and Lee, 2004). Initially, a fatty acid coenzyme A ester esterifies sn-glycerol-3-phosphate in a reaction that is catalyzed by glycerol-3-phosphate acyltransferase (GPAT) at the sn-1 position to form lysophosphatidic acid. Lysophosphatidic acid is then acylated by an acylglycerophosphate acyltransferase in the sn-2 position, leading to the formation of an important intermediate in the biosynthesis of all glycerolipids: phosphatidic acid (Coleman and Lee, 2004).

The removal of the phosphate group is catalyzed by the enzyme phosphatidic acid phosphohydrolase (PAP). The importance of PAP is also illustrated in its ability to produce diacylglycerols as key intermediates in the biosynthetic production of phosphatidylcholine and phosphatidylethanolamine (Murphy, 2001). In direct opposition to the processes involved in and responsible for the biosynthesis of phospholipids in mammals, much of the phosphatase activity
culminating in the biosynthesis of triacylglycerol resides in three inter-related cytoplasmic proteins, termed lipin-1, lipin-2, and lipin-3 (Murphy, 2001). Each of the lipins is specific for certain tissues, and each seems to have distinct expression and functions. Lipin-1 (PAP1), however, is responsible for all the PAP activity in adipose tissue and skeletal muscle. In response to elevated levels of fatty acids within cells, lipin-1 is translocated to the endoplasmic reticulum from the cytoplasmic compartment of cells. Lipin-1 requires Mg\(^{2+}\) ions and is inhibited by N-ethylmaleimide, as opposed to the membrane-bound activity responsible for synthesizing diacylglycerols as a phospholipid intermediate. The latter is independent of Mg\(^{2+}\) ion concentration and is also not sensitive or reactive to the inhibitor (Coleman and Lee, 2004).

Lastly, the resulting 1,2-diacyl-sn-glycerol is acylated by a diacylglycerol acyltransferase (DGAT) to lead to form triacyl-sn-glycerol (Coleman and Lee, 2004). The glycerol-3-phosphate acyltransferase has the lowest specific activity of these enzymes, so this step is potentially rate-limiting (Coleman and Lee, 2004). Moreover, DGAT is the enzyme that is dedicated to the formation of triacylglycerols, making DGAT an attractive anti-obesity target for the pharmaceutical industry (Mu and Høy, 2004).

In the third and less well-known biosynthetic pathway, the synthesis of triacylglycerols is dependent upon an acyl-CoA independent transacylation among two racemic diacylglycerols (Zammit, et. al., 2008). This reaction is catalyzed by a diacylglycerol transacylase, and was first observed in intestinal microvillus cells (Zammit, et. al., 2008). The two diacylglycerol enantiomers engage equally in the reaction for the transfer of a fatty acyl group with the propagation of triacylglycerols along with a 2-monoacyl-sn-glycerol. Seed oils have been observed to contain a similar reaction to these processes (Zammit, et. al., 2008).
**The synthesis of triacylglycerols in plants**

Within plant seeds, fatty acid storage occurs in the embryo or endosperm tissues as triacylglycerols (TAGs) within lipid droplets. These lipid droplets reside in close vicinity with glyoxysomes (peroxisomes) (Dugail and Hajduch, 2007). The vast majority of the enzymes that are necessary to oxidize fatty acids produced from the TAGs via acetyl-CoA to four-carbon compounds comes from glyoxysomes. These organelles also supply structural elements, well before seedlings develop the ability to photosynthesize (Dugail and Hajduch, 2007).

The synthesis of triacylglycerols occurs in developing seeds by way of the Kennedy pathway, as described above. There is an accumulation of oil droplets in the endoplasmic reticulum by mechanisms that are currently not well understood (Coleman and Lee, 2004). These oil droplets are surrounded by a monolayer of proteins and phospholipids, which in *Arabidopsis* include the oleosins, a caleosin, a stereoleosin, an aquaporin, and a glycosylphosphatidylinositol-anchored protein (Voelker and Kinney, 2001). Lipases are activated upon germination, and lipolysis lipid breakdown initiates at the surface of oil bodies. It is at these oil bodies that the oleosins, which are the most prominent structural proteins, assist in the docking of lipases. There have been many lipases that have been cloned from many species of plants (Schittmayer and Birner-Gruenberger, 2009). These lipases are prototypical α/β-hydrolases, containing a conserved catalytic triad of serine, histidine, and aspartic acid or glutamic acid. This class of proteins is capable of hydrolyzing triacylglycerols but not phospholipids or galactolipids. Perhaps the most important lipase is the sugar-dependent lipase 1 (SDP1) (Schittmayer and Birner-Gruenberger, 2009). It is a patatin-like lipase that is very much like the mammalian adipose triacylglycerol lipase, and it is found on the surface of the oil body. SDP1 is mostly active mainly against triacylglycerols for the purpose of generating diacylglycerols, but has been
suggested to work in concordance with mono- and diacylglycerol lipases to propagate glycerol and free fatty acids. It is not known how the products are transported to the peroxisomes for further metabolic processes, and these transport processes are controlled by a specific regulatory network. As an aside, in plants, the oil droplets in the anthers of flowers produce the lipids and oleosins that are capable of coating and stabilizing pollen (Schittmayer and Birner-Gruenberger, 2009).

Lipid droplets’ size and triacylglycerol content in many yeast vary in the different stages of growth and development (Kohlwein, 2010). The majority of the biosynthetic and catabolic enzymes that participate in the metabolism of triacylglycerols are conserved among yeast and mammals, and yeast currently prove to be the most useful model for research involving the homeostasis of triacylglycerols (Kohlwein, 2010).

**Lipid biosynthesis in tung**

This study is focused on the identification and functional analysis of the enzymes and other proteins that are involved in tung oil biosynthesis, specifically acyl-coA binding proteins (ACBPs) as will be discussed. All of the enzymes and cofactors required for the synthesis of polyunsaturated fatty acid components in tung oil, including eleostearic acid, have been identified. This large list of enzymes includes of an oleate desaturase (*FAD2*), a diverged *FAD2* (*FADX*), three isoforms of ω-3 fatty acid desaturase (*FAD3*), four isoforms of cytochrome b₅, and two isoforms of NADH cytochrome b₅ reductase (Shockey, et. al., 2006). In earlier work it was shown that the expression of the tung *FADX* in transgenic *Arabidopsis*, tobacco, or yeast cells only resulted in accumulation of a small percentage of eleostearic acid compared to other fatty acids produced (Shockey, et. al., 2006). Given this low accumulation, it is obvious that additional enzymes will be necessary for the synthesis and high-yield accumulation of eleostearic
acid in seed oils that are transgenically produced. In addition, the full-length or partial gene sequences have been identified for the primary acyltransferases that may channel eleostearic acid into storage oils: \textit{GPAT, LPAAT, DGAT1, DGAT2, and PDAT}. Full-length \textit{Arabidopsis} counterparts for these enzymes have also been obtained. There have also been several isoforms of long chain acyl-CoA synthetases (\textit{LACS}) and acyl-CoA binding proteins (\textit{ACBPs}) that have been cloned as well. The goal of this study is to study the role of ACBPs in developing tung seeds. These tung-derived enzymes may show preferential incorporation of eleostearic acid into storage oils in comparison to orthologous proteins from \textit{Arabidopsis} or yeast cells.

\textbf{Acyl-CoA Binding Proteins (ACBPs)}

It has long been known that lipids are important in many biological processes. In order to deliver their functions, some of them require transport within and between subcellular compartments during lipid metabolism (Faergeman, et. al., 2007). In plant cells, lipid-transfer proteins (LTPs) and acyl-CoA-binding proteins (ACBPs) have been identified as potential candidates for the transfer of lipids within the cell (Burton, et. al., 2005). LTPs are small proteins, roughly 9 kDa, while the various isoforms of ACBPs in plants range from 10 to 73 kDa in size (Burton, et. al., 2005). Many eukaryotes studied were found to contain the 10-kDa small, soluble ACBP (Yurchenko, et. al., 2009, Xiao, et. al., 2009, Mogensen, et. al., 1987, Schjerling, et. al., 1996, Taskinen, et. al., 2007). There is also evidence of several larger ACBPs, many of which have yet to be characterized, while others are better studied (Chye, et. al., 1999, Chye, et. al., 2000, Leung, et. al., 2006). Currently, there is a shortage of information on many of these larger proteins with acyl-CoA-binding domains available from the data mining of sequenced genomes (Burton, et. al., 2005). A total of 30 plant \textit{ACBP} gene sequences have been published (Faergeman, et. al., 2007).
Acyl-Coenzyme A binding protein (ACBP) is named after the protein’s ability to bind specifically to CoA esters of fatty acids (Burton, et. al., 2005). ACBP, is known to be found in some prokaryotes (Alves-Bezerra, et. al., 2010), some species of yeast (Schjerling, et. al., 1996), and in animals (Larsen, et. al., 2006, Mandrup et. al., 1991, Taskinen, et. al., 2007) and plants (Chye, et. al., 1998, Yurchenlo, et. al., 2009, Xiao, et. al., 2009). The biological function of ACBP is not well known; however, analysis of the yeast gene has illustrated that ACBP may participate as a housekeeping gene, thus suggesting that ACBP appears to be important for essential biochemical functions in cells (Schjerling, et. al., 1996). In addition, the nuclear magnetic resonance (NMR) structures of the bovine ACBP have been determined for both the apo-protein and for the ACBP complexed with palmitoyl-CoA (Andersen et. al., 1991).

Long chain acyl-CoA esters function as important intermediates in the synthesis of lipids and the degradation of fatty acids (Faergeman, Knudsen, 2009). Aside from this role as intermediates, long chain acyl-CoA esters have been implicated in both regulation of intermediary metabolism and the regulation of gene expression (Faergeman, Knudsen, 2009). Long chain acyl-CoA esters are amphipathic molecules which partition into phospholipid vesicles (Faergeman, Knudsen, 2009). They are believed to inhibit many cellular functions and a host of enzymes at low concentrations (Faergeman, Knudsen, 2009). Thus, a specific and specialized acyl-CoA pool former and transporter is necessary for the function of long chain acyl-CoAs as intermediates in the metabolism of lipids and as signaling molecules (Faergeman, Knudsen, 2009). ACBP is found to fulfill this role in the cytoplasm of the cell (Post-Beittenmiller, et. al., 1992).

The majority of the eukaryotic ACBPs that have been investigated are low molecular weight, about ~10 kDa, cytosolic proteins that are highly conserved in their amino acid

20
sequences among many species (Burton, et. al., 2005, Xiao and Chye, 2009). There have been several ACBP homologues that were identified in all four eukaryotic kingdoms, Animalia, Plantae, Fungi and Protista, in addition to eleven species of eubacteria (Yurchenko, et. al., 2009, Xiao, et. al., 2009, Mogensen, et. al., 1987, Schjerling, et. al., 1996, Taskinen, et. al., 2007, Burton et. al., 2005). It is important to note that most of the bacteria that contain ACBPs have been shown to be pathogenic to plants or animals, suggesting that their pathogens may have acquired a host ACBP via horizontal gene transfer (Burton, et. al., 2005). ACBPs appeared very early in plant evolution, implying that there is a very important role of ACBPs in acyl-CoA metabolism in plant species (Faergeman, et. al., 2007).

The acyl-CoA-binding domain is well-conserved in each ACBP and allows it to bind acyl-CoA esters (Xiao and Chye, 2009). This has been observed in in vitro binding assays, like the Lipidex assay, where recombinant ACBPs have been observed to bind CoA esters (Leung, et. al., 2006). Recombinant Arabidopsis ACBPs that have been expressed in Escherichia coli, have been utilized to establish the function of the acyl-CoA binding domain through the usage of site-directed mutagenesis followed by in vitro binding assays (Leung, et. al., 2006, Xiao and Chye, 2009). A few of the Arabidopsis ACBPs have also been observed to bind phospholipids in filter binding assays (Chen, et. al., 2008). An example of this is a recombinant ACBP6 that binds phosphatidylcholine (PC) (Chen, et. al., 2008). The recombinant Arabidopsis ACBPs show certain preferences for various acyl-CoA esters and phospholipids in in vitro binding assays (Chen, et. al., 2008, Leung, et. al., 2006, Xiao, Chye, 2009). Because of this, it has been hypothesized that different subclasses of ACBPs in Arabidopsis do not have redundant functions (Leung, et. al., 2006).
Acyl-CoA binding to a single binding site on ACBP has been demonstrated by several in vitro studies (Chen, et. al., 2008, Leung, et. al., 2006, Xiao, Chye, 2009, Andersen, et. al., 1991, Faergeman et. al., 1996). It has been calculated that the stoichiometric values for hexadecanoyl-CoA binding by bovine and rat ACBP were approximately 1 mol/mol (Andersen, et. al., 1991). The ACBP binding site is arranged in such a manner that only acyl-CoA esters and not any other certain types of ligand can bind strongly (Andersen, et. al., 1991). Therefore, both the acyl chain and CoA portions are necessary for the correct orientation and the strong interaction between the ligand and the ACBP (Andersen, et. al., 1991). Consequently, ACBP binds specifically to acyl-CoA esters as opposed to free fatty acids, free CoA, ATP, NADH, NADPH, GABA, palmitoyl carnitine, or cholesterols (Andersen, et. al., 1991, Faergeman et. al., 1996).

ACBPs from different organisms each specifically bind to acyl-CoA esters via a one-to-one binding process (Andersen, et. al., 1991, Faergeman et. al., 1996). ACBPs cannot bind free fatty acids; however, they can bind Coenzyme A alone (Faergeman et. al., 1996). The 3’ phosphate of ribose of the CoA moiety has been observed to contribute up to 40% of the complete binding energy (Andersen, et. al., 1991), thus indicating that the head group of the CoA performs an important role in dictating the specificity for the binding capacity of the acyl-CoA esters (Faergeman et. al., 1996).

Through multiple in vitro experiments, ACBP’s ability to perform as an intracellular acyl-CoA transporter and pool former has been demonstrated (Knudsen, et. al., 2000, Kader, 1996, Xiao and Chye, 2009). It is capable of acting as a powerful protector of acetyl-CoA carboxylase, acyl-CoA synthetase, and adenylate translocase against the inhibition provided by long chain acyl-CoA esters (Knudsen, et. al., 2000). In addition, ACBP may be capable of
mediating intermembrane acyl-CoA transport and has the ability to protect long chain acyl-CoA esters from the hydrolysis of cellular acyl-CoA hydrolases (Knudsen, et. al., 2000).

**Arabidopsis thaliana** acyl-CoA binding proteins

In *Arabidopsis*, six genes encode ACBPs (Xiao and Chye, 2009). They are designated as ACBP1 through ACBP6 (Xiao and Chye, 2009). ACBP1 and ACBP2 are membrane-associated proteins (Chye, et. al., 2000), ACBP3 is extracellularly-targeted (Leung, et. al., 2006), and ACBP4 and ACBP5 are cytosolic proteins containing kelch-motifs (Li, et. al., 2008). Acyl-CoA-binding domains in all 6 ACBPs have been observed to bind long-chain acyl-CoA esters *in vitro*, with varying affinities, perhaps suggestive of their non-overlapping roles in plant lipid metabolism (Xiao and Chye, 2009). These ACBPs are mostly conserved at the acyl-CoA-binding domain and range in size from 10.4 to 73.1 kD (Xiao and Chye, 2009). C-terminal ankyrin repeats in ACBP1 and ACBP2 and kelch motifs in ACBP4 and ACBP5, can potentially mediate protein-protein interactions, while N-terminal transmembrane domains in ACBP1 and ACBP2 target them to the endoplasmic reticulum (ER) and the plasma membrane (PM) (Chye, et. al., 2000).

**Vernicia fordii** acyl-CoA binding proteins

To date, there have been 4 unique acyl-CoA binding proteins identified in *Vernicia fordii*, which have been named based upon the *Arabidopsis thaliana* nomenclature adapted by Chye and her colleagues (Xiao and Chye, 2009). The *Vernicia fordii* ACBPs include VfACBP3a, VfACBP3b, VfACBP4, and VfACBP6. These were named as such due to sequence similarities to the *Arabidopsis* ACBPs. This similarity was found by utilizing the BLAST search engine comparing the sequences obtained for the *V. fordii* ACBPs to the sequences of the *A. thaliana* ACBPs. To date, there have been no known studies or elucidation of the sequences of the tung
ACBPs. The purpose of this study is to elucidate the roles of ACBPs in tung. Figure 1-2 shows both the naming conventions of *Vernicia fordii* ACBPs and *Arabidopsis thaliana* ACBPs as determined by Chye.

<table>
<thead>
<tr>
<th><em>A. thaliana</em></th>
<th>Base Pairs</th>
<th>Localization</th>
<th><em>V. fordii</em></th>
<th>Base Pairs</th>
<th>Localization</th>
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</thead>
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<td>ACBP1</td>
<td>1014</td>
<td>Plasma membrane and ER</td>
</tr>
<tr>
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<td>Plasma membrane and ER</td>
<td>ACBP2</td>
<td>1062</td>
<td>Plasma membrane and ER</td>
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</tr>
<tr>
<td></td>
<td></td>
<td></td>
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<td>1125</td>
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<td>ACBP4</td>
<td>1995</td>
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<td>Cytoplasm</td>
<td>ACBP6</td>
<td>276</td>
<td>Cytoplasm</td>
</tr>
</tbody>
</table>

Table 1-2. *Arabidopsis thaliana* Acyl-CoA Binding Proteins (ACBPs) as compared to *Vernicia fordii* ACBPs.

**Comparison of plant ACBPs**

*Arabidopsis thaliana* ACBPs have various structural features that not only provide a unique way to identify each one but also determine their functions. ACBP1 and ACBP2, of which there are currently no known tung counterparts, contain ankyrin repeats (Chye, et. al., 2000), which are 33-residue motifs in proteins consisting of two alpha helices separated by loops that are amongst the most common protein-protein interaction motifs in nature (Chye et. al., 2000).

Dr. M. L. Chye observed enhanced cold acclimation provided to *Arabidopsis thaliana* via a reduction in ACBP1 but not in ACBP2, 338 amino acids and 334 amino acids with molecular weights of 37.5 and 38.5 kDa respectively, despite the sequence homology (Identities = 258/349 (74%), Positives = 294/349 (85%)) (Chye et. al., 2000). ACBP1 contains an amino-terminal transmembrane domain that targets it to the plasma membrane and the endoplasmic reticulum. The function of ACBP1 was analyzed by overexpression in transgenic *Arabidopsis* plants. Five-week-old wild-type, acbp1 mutant, and ACBP1-complemented plants were grown at 23°C and then subjected to freezing treatment ranging from -4°C to -12°C. The plants were then thawed
overnight at 4°C and recovered in a growth chamber (16-h-light [23°C]/8-h-dark [21°C] photoperiods) for 7 days. AtACBP1 overexpressors showed reduction in several species of diunsaturated phosphatidylcholine (PC), prompting an investigation into whether they were altered in response to freezing stress. AtACBP1 overexpressors demonstrated increased freezing sensitivity accompanied by a decrease in PC and an increase in phosphatidic acid (PA), while acbp1 mutant plants showed enhanced freezing tolerance associated with PC accumulation and PA reduction. It was also shown that the binding of a recombinant eukaryotic AtACBP (ACBP1) to PA, indicating the possibility of enhanced PA interaction in ACBP1 overexpressors.

Since phospholipase Da1 (PLDa1) promotes the hydrolysis of PC to PA, PLDa1 expression was examined and was observed to be higher in AtACBP1 overexpressors than in Atacbp1 mutant plants. In contrast, the expression of PLDδ, which plays a positive role in freezing tolerance, declined in the AtACBP1 overexpressors but increased in acbp1 mutant plants. Since AtACBP1 is localized to the endoplasmic reticulum and plasma membrane, it may regulate the expression of PLDa1 and PLDδ by maintaining a membrane-associated PA pool through its ability to bind PA. Moreover, both genotypes showed no alterations in proline and soluble sugar content or in cold-regulated (COR6.6 and COR47) gene expression, suggesting that the AtACBP1-mediated response is PLD associated and is independent of osmolyte accumulation (Chye et. al., 2008).

Arabidopsis thaliana ACBP2 was observed to interact with farnesylated protein 6 (AtFP6), which has a metal-binding motif (M/LXCXXC). Yeast two-hybrid analysis and in vitro assays showed that an AtACBP2 derivative lacking ankyrin repeats did not interact with AtFP6, indicating that the ankyrin repeats mediate protein–protein interaction. Fluorescent-tagged AtACBP2 and AtFP6 transiently co-expressed in tobacco were both targeted to the plasma
membrane. Reverse transcriptase polymerase chain reaction and northern blot analyses revealed that AtFP6 mRNA was induced by cadmium (Cd(II)) in A. thaliana roots. Assays using metal-chelate affinity chromatography demonstrated that in vitro translated AtACBP2 and AtFP6 bound lead (Pb(II)), Cd(II) and copper (Cu(II)). Consistently, assays using fluorescence analysis confirmed that (His)6-AtFP6 bound Pb(II), as does (His)6-AtACBP2. Arabidopsis thaliana plants overexpressing AtACBP2 or AtFP6 were more tolerant to Cd(II) than wild-type plants. Plasma membrane-localized AtACBP2 and AtFP6 may mediate Pb(II), Cd(II) and Cu(II) transport in A. thaliana roots. In addition, (His)6-AtACBP2 binds [14C]linoleoyl-CoA and [14C]linolenoyl-CoA, the precursors for phospholipid repair following lipid peroxidation under heavy metal stress at the plasma membrane. AtACBP2-overexpressing plants were more tolerant of hydrogen peroxide than wild-type plants, further supporting a role for AtACBP2 in post-stress membrane repair. (Chye, et. al., 2009).

Again, both of these ACBPs were localized to the ER and plasma membrane. Targeting of ACBPs to the ER would potentially be compatible with a role in TAG metabolism in oil bodies of seeds. De novo fatty acid synthesis occurs in the plastid and while subsequent lipid synthesis and storage processes occur in the cytoplasm and ER, it may be reasonable to wonder if a tung ACBP similar to AtACBP1 or AtACBP2 in Arabidopsis could play a role in the processes involved in the channeling and accumulation of eleostearic acid-containing intermediates, especially since ACBPs across many organisms have been shown to bind fatty acyl-CoA esters with great affinity (Larsen, et. al., 2006, Mandrup et. al., 1991, Schjerling, et. al., 2006, Taskinen, et. al., 2007). These fatty acyl-CoA esters play a large role in lipid biosynthesis, elongation, channeling, and accumulation processes. Perhaps comparable ACBPs in tung provide similar measures as listed here for the Arabidopsis ACBP1 and ACBP2 as well.
It would be interesting to analyze, if a tung ACBP1 equivalent were found, if its expression was downregulated in colder weather while upregulated in warm weather in tung, so as to provide similar freezing tolerance benefits and potentially allow for some benefit in the seed development process that occurs in the hot mid-summer months. Tung ACBP2, on the other hand, may prove useful in the tolerance of cadmium, or other metals if it contains an ankyrin repeat like *Arabidopsis* ACBP2 that allows for protein-protein interactions.

*At*ACBP3 is a 362 amino acid and 39.2 kDa protein. To determine the localization of AtACBP3, it was expressed as AtACBP3-red fluorescent protein (DsRed2) from the CaMV 35S promoter. AtACBP3-DsRed was localized extracellularly in transiently expressed tobacco BY-2 cells and onion epidermal cells. In addition, through Lipidex binding assays, it was observed to bind [14C]arachidonyl-CoA with high affinity in comparison to [14C]palmitoyl-CoA and [14C]oleoyl-CoA binds arachidonyl-CoA. Although arachidonyl-CoA is not known to be synthesized by the plant, it nonetheless is commercially available and would represent a polyunsaturated fatty acid for in vitro tests. However, further binding assays did not indicate any occurrence of competitive binding with linolenoyl-CoA, a polyunsaturated fatty acid present in plants. To identify the residues functional in the binding, five mutants with single amino acid substitutions in the acyl-CoA-binding domain of (His)6-AtACBP3 and (His)6-AtACBP1 (which also binds [14C]arachidonyl-CoA) were generated by site-directed mutagenesis (Leung, et. al., 2006). Binding assays with arachidonyl-CoA revealed that replacement of a conserved R residue (R150A in AtACBP1 and R284A in AtACBP3), disrupted binding (Leung, et. al., 2006). In contrast, other substitutions in AtACBP1 (Y126A, K130A, K152A and Y171A) and in AtACBP3 (F260A, K264A, K286A and Y305A) did not affect arachidonyl-CoA binding, unlike their equivalents in (His)6-AtACBP2, (His)6-AtACBP4, and (His)6-AtACBP5, which had altered
binding to palmitoyl-CoA or oleoyl-CoA (Leung, et. al., 2006). Since R and Y residues have
been implicated to be critical in binding carboxylic acid moieties of arachidonic acid in mouse
prostaglandin endoperoxide synthase-2 (Rowlinson et al. 1999), R150 and R284, the only
conserved R residues within the acyl-CoA-binding domains in ACBP1 and ACBP3, respectively,
were subjected to site-directed mutagenesis and were shown to impair arachidonoyl-CoA binding.
Their equivalent in ACBP2 (R160) is also conserved and (His)6-AtACBP2 binds arachidonoyl-
CoA as well as it binds palmitoyl-CoA (Leung et al. 2004). The lack of this R equivalent in
AtACBP4 and AtACBP5 could be the reason for their inability to bind arachidonoyl-CoA. It is
predicted that this R residue, critical in arachidonoyl-CoA binding, likely governs AtACBP1 and
AtACBP3 functions in planta (Leung, et. al., 2006).

Further investigations on AtACBP3 show its upregulation upon dark treatment and in
senescing rosettes. Transgenic Arabidopsis thaliana overexpressing AtACBP3 displayed
accelerated leaf senescence, whereas an Atacbp3 T-DNA insertional mutant and AtACBP3 RNA
interference transgenic Arabidopsis lines were delayed in dark-induced leaf senescence. Acyl-
CoA and lipid profiling revealed that the overexpression of AtACBP3 led to an increase in acyl-
CoA and phosphatidylethanolamine (PE) levels, whereas AtACBP3 downregulation reduced PE
content. Significant losses in phosphatidylcholine (PC) and phosphatidylinositol, and gains in
phosphatidic acid (PA), lysophospholipids, and oxylipin-containing galactolipids (arabidopsides)
were evident in 3-week-old dark-treated and 6-week-old premature senescing Arabidopsis
overexpressing AtACBP3. Such accumulation of PA and arabidopsides resulting from lipid
peroxidation in overexpressing AtACBP3 plants likely promoted leaf senescence. The N-
terminal signal sequence/transmembrane domain in AtACBP3 was shown to be essential in
AtACBP3-green fluorescent protein targeting and in promoting senescence. Observations that
recombinant AtACBP3 binds PC, PE, and unsaturated acyl-CoAs in vitro and that AtACBP3 overexpression enhances degradation of the autophagy (ATG)-related protein ATG8 and disrupts autophagosome formation suggest a role for AtACBP3 as a phospholipid binding protein involved in the regulation of leaf senescence, perhaps by modulating membrane phospholipid metabolism and ATG8 stability in Arabidopsis. Accelerated senescence in plants overexpressing AtACBP3 is dependent on salicylic acid but not jasmonic acid signaling (Chye, et. al., 2010).

The binding of arachidonyl-CoA is very interesting because this molecule is not known to be synthesized by Arabidopsis or by several other plants. A possible explanation for this involves AtACBP3 in lipid-mediated signaling during a fungal infection. The expression of 3-hydroxy-3-methylglutaryl CoA reductase is induced by arachidonic acid in the lipids of plant pathogenic fungi during a fungal invasion in potato (Choi, et al, 1994). Since AtACBP3 is localized at the periphery of tobacco BY-2 cells and onion epidermal cells (extracellular localization), it could be in a prime location to interact in the invasion of fungus and trigger the defense responses against the potential pathogen (Chye, et. al., 2005).

Recently, it was observed that tung trees were stricken with an unknown fungus (Figure 1-3) (Yicun Chen, Institute of Subtropical Forestry, Fuyang, China, personal communication). Since ACBP3 of Arabidopsis was found to be involved in binding arachidonyl-CoA as described above, it is possible that there may be a role for tung ACBP3a and ACBP3b in defense from fungal infections of the tung tree. A good indicator of this would be to compare VfACBP3a and VfACBP3b gene expression levels in healthy and infected tree tissues. Mutational and overexpression experiments determining the threshold defense of tung involving the two known VfACBP3 isoforms could provide insight into the potential defense roles these VfACBPs may play.
In a 2004 study by Walz, et. al., a network of defense proteins in *Cucurbita maxima* was revealed. Many different proteins can be separated from the sap of mature sieve tubes of various plant species. Only a small number of those have been identified. Due to sieve tubes’ inability to perform transcription and translation, the proteins are possibly synthesized in the tightly connected companion cells. They are then transported into sieve elements through plasmodesmata. The protein composition of phloem sap suggests a role of these proteins not only for sieve tube maintenance, but also for plant physiology and development (Walz et. al., 2004).

Over 300 partial sequences generated by hybrid mass spectrometry were used to identify 45 different proteins from the phloem exudates of cucumber (*Cucumis sativus* L. cv. Hoffmanns Giganta) and pumpkin (*Cucurbita maxima* Duch. cv. Gelber Zentner) plants. In addition to previously described phloem proteins, it was possible to localize proteins with high similarity to an acyl-CoA binding protein, a glyoxalase, a malate dehydrogenase, a rhodanese-like protein, a drought-induced protein, and a β-glucosidase. It was found that the majority of the identified proteins are involved in stress and defense reactions (Walz, et. al., 2004).
AtACBP3 preferentially binds to arachidonyl-CoA that may allow for defense against fungal infections.

Figures 1-4, 1-5, and 1-6 show the transmembrane domain analyses of VfACBP3a, VfACBP3b, and AtACBP3 as determined by the TMHMM server that predicts transmembrane helices in proteins (http://www.cbs.dtu.dk/services/TMHMM/). Protein sequences of interest were entered into a text box provided on the website for transmembrane prediction calculations. VfACBP3a has its domain located at residue positions 5-27, VfACBP3b has its domain located at
positions 7-28 while AtACBP3 has its domain located at residue positions 7-26. It is important to note the location of the binding domains is in the N-terminal portion of both of these VfACBPs, which is well before the acyl-CoA binding domain that is located at residues 170-257 in VfACBP3a and residues 187-274 in VfACBP3b. The term transmembrane domain (TMD) may characterize a single transmembrane alpha helix of a transmembrane protein. An alpha-helix in a membrane can be folded independently apart from the rest of the protein, much like the domains of water-soluble proteins. More generally, a TMD represents a three-dimensional protein structure that is thermodynamically stable within a membrane. It would be interesting to analyze the TMDs of VfACBP3a and VfACBP3b to see if there is any targeting of the proteins to extracellular spaces to perform their duties. An N-terminal secretory signaling peptide (amino acids 1-26) was found to overlap the TMD (amino acids 7-26) in AtACBP3 (Chye 2009) and targets AtACBP3 to extracellular spaces. This part of the protein is necessary for targeting GFP fusion protein, and for the overexpressed gene to impart its role in age-dependent leaf senescence mentioned earlier (Chye, et. al., 2010).
Figure 1-4. *Vf*ACBP3a hydropathy plot illustrating the potential transmembrane domain (TMD) location. *Vf*ACBP3a has a TMD located in the N-terminal portion at amino acids 5-27.

Figure 1-5. *Vf*ACBP3b hydropathy plot illustrating the potential transmembrane domain (TMD) location. *Vf*ACBP3a has a TMD located in the N-terminal portion at amino acids 7-28.
AtACBP3 has a TMD located in the N-terminal portion at amino acids 7-26.

AtACBP4 and AtACBP5, comprised of 668 amino acids and 648 amino acids with molecular weights of 73.1 and 71.0 kDa respectively, are localized to the cytoplasm and in the case of AtACBP5, to both the cytosol and the peroxisome. Both proteins were found to bind oleoyl-CoA with great affinity. Analysis of lipid profiles illustrated that an acbp4 knockout mutant contained less membrane lipids, such as digalactosyldiacylglycerol, monogalactosyldiacylglycerol, phosphatidylcholine, phosphatidylethanolamine and phosphatidylinositol, as opposed to acbp4-complemented lines that achieved levels similar to wild type, suggesting that ACBP4 may play a role in membrane lipid biosynthesis (Chye, et. al., 2008). The role of AtACBP5 has yet to be determined.

VfACBP4 has only been worked on for a short time before this publication, therefore, it is still a work in progress. Its full-length ORF has yet to be completely determined. Expression patterns in various tissues of tung will be discussed later, using a partial sequence of VfACBP4. VfACBP5 has not been cloned.
AtACBP6 is a 92 amino acid, 10.4 kDa protein, that is localized to the cytoplasm (Chye, et. al., 2008). It preferentially binds oleoyl-CoA and palmitoyl-CoA. This ACBP is highly conserved throughout eukaryotes, as figure 1-7 depicts. It is essentially a binding domain for fatty acyl-CoA esters with very little extra sequence added onto the N- or C-terminal end. It has no structural additions that are present in several other Arabidopsis ACBPs (Chye, et. al., 2008).

Figure 1-7. A collection of various eukaryotic soluble ACBPs illustrating the high conservation of sequences.

This high conservation in the sequences across organisms hints at the functions it can provide, such as in acyl-CoA pool maintenance and transportation functions in the cytoplasm, that it performs in many organisms (Chye, et. al., 2008). More specifically, overexpression of ACBP6 in Arabidopsis can enhance freeze tolerance (Chye, et. al., 2008). Filter binding assays, performed in vitro, indicated that histidine-tagged AtACBP6 binds phosphatidylcholine, but not phosphatidic acid or lysophosphatidylcholine, implying a role for AtACBP6 in phospholipid metabolism in Arabidopsis, including the possibility of AtACBP6 in the cytosolic trafficking of phosphatidylcholine (Chye, et. al., 2008). In humans, ACBP has shown to perform a variety of functions, including regulation of rate-limiting enzymes in cholesterol and fatty acid metabolism (Vock, 2010). In yeast, there are two homologs of ACBP and they have an influence on intracellular acyl-CoA pool size (Fedderson, et. al., 2007). So, pinpointing the function(s) of tung ACBP6 may be difficult, but as shown later, it exhibits a very general expression in tung tissues and this could be attributed to general role(s). Given the universal nature of ACBP6-like proteins
across nature, and the variety of roles these proteins play, it is likely that tung ACBP6 also fulfills many important roles. These roles may include transporting newly synthesized acyl-CoAs away from plastids (Johnson, et. al., 2000, Johnson, et. al., 2002) and/or facilitating lipid remodeling in phospholipid pathways (Yurchenko, et. al., 2009). This fits in with eleostearic acid biosynthesis, the removal from phospholipids, and the channeling into triacylglycerols. It may have no specific pathway involvement but provide with multiple utility-like duties in the cytoplasm, as seen throughout various eukaryotes.

**Research focus**

As previously mentioned, on a very broad scope, this study attempts to ascertain any functionalities or impacts ACBPs may have on tung. On a more specific scale, ACBPs in other organisms have been shown to provide transportation functions in biosynthetic pathways (Burton, et. al., 2005), potential defense mechanisms (Leung, et. al., 2006), and many other abilities. The results here will further the knowledge base of ACBPs.

**Research objective**

Identification of the sequences of *Vernicia fordii* ACBPs and analysis of expression patterns and protein:protein interactions provide insight to the potential role(s) of ACBPs in tung lipid metabolic pathways.

Obtaining the full-length sequences of VfACBPs allows for phylogenetic comparisons between ACBPs from tung and to other organisms’ ACBPs. Some eukaryotic organisms have had more extensive studies to date on their functions and some of them show sequence similarity to tung ACBPs, thus allowing for potential connections to be made on their functions. Of course, not all proteins act the same in every organism, but a basic foundation for the path of research provides a large advantage. The tung tree produces its oil in the summer. Quantifying the
expression of VfACBP and comparing it to this crucial time frame in biosynthesis is key in attempting to shed light on potential VfACBP function. In addition, many protein-protein interactions occur en route to the production, modification, and storage of fatty acids in triacylglycerols in oil bodies in seeds. Some proteins are directly involved in the tung lipid biosynthetic processes. Thus, it was crucial to observe their potential interactions(s) with VfACBPs.

Protein targeting may also play an important role in regulating lipid biosynthesis and many of the enzymes involved in storage oil biosynthesis in developing seeds are also involved in production of lipids destined for normal cell membranes. Because of this, VfACBPs’ presumed role in binding acyl-CoA and interacting with other proteins via protein-protein interactions, and the observations in other eukaryotic organisms of VfACBPs’ general roles and transportation, results from this study may provide additional insight into the interplay of proteins in the tung biosynthetic system and if VfACBP is involved.

Even if ACBPs do not play a specific role in tung lipid biosynthesis, storage, and/or accumulation processes, VfACBPs may allow for defense mechanisms for tung. Other ACBPs, such as AtACBP6, provide freezing tolerance, which is important for growth in wintry seasons. The goals of the research involved in this study allow for a broad perspective on the prospective roles of ACBPS in tung lipid metabolism, pathogen defense mechanisms, or any other processes in tung trees.
Materials and Methods

Expressed Sequence Tag (EST)

Expressed Sequence Tag services for tung sequences, including VfACBPs, were conducted by the Agricultural Research Service Mid South Area Genomics Facility in Stoneville, MS. Expressed Sequence Tag (EST) sequences were generated from randomly selected cDNA from a developing tung seed cDNA library. This was performed from an arrayed library and annotated by the staff at the Agricultural Research Service Mid South Area Genomics Facility in Stoneville, MS. Homology-based comparisons using the Basic Local Alignment Search Tool (BLAST, http://blast.ncbi.nlm.nih.gov/Blast.cgi), to publicly available databases, namely, GenBank (http://www.ncbi.nlm.nih.gov/genbank/), were used to identify these clones. In this manner, ACBP6 and ACBP3a were identified in the library along with several other clones in the tung biosynthetic pathway.

Pyrosequencing

Pyrosequencing services for tung sequences, including VfACBPs, were performed by the Agricultural Research Service Mid South Area Genomics Facility in Stoneville, MS. In the same manner as EST, homology-based comparisons using the Basic Local Alignment Search Tool (BLAST, http://blast.ncbi.nlm.nih.gov/Blast.cgi), to publicly available databases, namely, GenBank (http://www.ncbi.nlm.nih.gov/genbank/), were used to identify the clones for VfACBPs. Through the efforts of this process, ACBP3b and ACBP4 were determined. Along with EST data, pyrosequencing allowed for the template for genome walking to determine the remainder of the sequences of each VfACBP.
Genome walking

Two gene-specific primers were designed. One was for the primary PCR reaction (GSP1) and one for the secondary PCR reaction (GSP2) for each ACBP. Primers are listed in figure 2-1. In general, the gene-specific primers were derived from sequences as close to the end of the known sequence as possible. For walking upstream from cDNA sequence, the primer was as close to the 5' end as possible. Gene-specific primers were chosen to be 25–28 nucleotides in length with a GC-content of 40–60% to ensure that the primers effectively anneal to the template at the recommended annealing and extension temperature of 67°C. Another constraint was that there be no more than three G’s and C’s in the last six positions at the 3' end of the primer. Five restriction sites were incorporated into the Genome Walker Adaptor, including Sal I (cohesive ends), Mlu I (cohesive ends), and overlapping Srf I (cohesive ends), Sma I (blunt ends), and Xma I (cohesive ends) sites.

The primary PCR master mix was prepared by combining the following reagents in a 0.5 mL tube: 40µL H2O, 5µL 10X PCR Buffer, 1µL dNTP mix, 1µL anchored primer 1 (Invitrogen) (10 µM), 1µL GSP1 (10 µM), and 1µL BD Advantage 2 Polymerase mix (50X) (Invitrogen). These components were vortexed and briefly spun in a microcentrifuge. Forty-nine µL of the primary PCR master mix was added to the appropriately labeled tubes. One µL of each DNA library (EcoR V, DraI, Pvu II, and SspI) was added to the appropriately labeled tubes.

The following two-step cycle parameters were used in PCR: 7 cycles: 94°C for 25 seconds and 72°C for 4 minutes, then 32 cycles: 94°C for 25 seconds, 67°C for 4 minutes, and 67°C for an additional 4 min after the final cycle. Five µL of the primary PCR products were analyzed on a 1.5% agarose/2% EtBr gel, along with DNA size markers (BioRad). PCR products were analyzed by agarose gel electrophoresis and imaged on a GE Healthcare Fujifilm LAS-
3000 image analyzer. One µl of each primary PCR product was diluted into 49 µl of sterile H2O. A secondary PCR master mix was prepared by combining the following reagents in an 0.5-ml tube:

40 µL H2O, 5µL 10X PCR Buffer, 1µL dNTP (10 mM each), 1µL anchored primer 2 (Invitrogen) (10 µM), 1µL GSP2 (10 µM), and 1µL BD Advantage 2 Polymerase Mix (50X). The components were vortexed and briefly spun in a microcentrifuge. Forty-nine µL of the secondary PCR master mix was added to the appropriately labeled tubes. One µL of each diluted primary PCR product was added to the appropriate tube. The following two-step cycle parameters for secondary PCR were used: 5 cycles: 94°C for 25 seconds and 72°C for 4 minutes, then 18–22 cycles: 94°C for 25 seconds, 67°C for 4 minutes, and 67°C for an additional 4 minutes after the final cycle. Five µL of the secondary PCR products was analyzed on a 1.2% agarose/EtBr gel, along with DNA size markers such as a 1 kb DNA ladder. Fragments of interest were cloned and analyzed using the pCR®2.1-TOPO® procedure outlined in the cloning section.

<table>
<thead>
<tr>
<th>VfACBP3b</th>
<th>VfACBP4</th>
</tr>
</thead>
<tbody>
<tr>
<td>5’-CGACGAAATTCATCGACCATTTCGCAAC-3’</td>
<td>5’-GGGGGAGCTGCAAAGTTGCAAGCACTGGC-3’</td>
</tr>
<tr>
<td>5’-GACGCTCTAGAATACCAACCTGGAT-3’</td>
<td>5’-TGATTCATTTCATGTCTACAAACAG-3’</td>
</tr>
</tbody>
</table>

Figure 2-1. Genome walking primers for VfACBP3b and VfACBP4.  

**Rapid Amplification of cDNA Ends (RACE)**

EST and pyrosequencing allow for determination of partial cDNA sequences for some of the *ACBP* genes. Full-length sequences were obtained by Rapid Amplification of cDNA Ends (RACE). The full-length of *VfACBP3a* and *VfACBP6* was obtained from the library annotation EST. Portions of the sequences for *VfACBP3b* and *VfACBP4* were obtained via EST and pyrosequencing thereafter the 5’ ends up until the start codon and the 3’ ends until the stop
codon were determined by 5’ and 3’RACE. These procedures used the Invitrogen (Invitrogen Corporation (Headquarters), 5791 Van Allen Way PO Box 6482 Carlsbad, California 92008) protocols with slight modifications. In order to obtain the first strand of cDNA synthesis in 5’RACE, the Invitrogen method for 3’RACE was used in addition to using the reverse transcriptase III enzyme provided by the 3’RACE kit along with sequencing parameters and other components of the protocol for 3’RACE. Components of the reaction included: 20 mM Tris- HCl (pH 8.4 at 22°C), 50 mM KCl, 2.5 mM MgCl₂, 10 mM DTT, 500 nM anchored primer (Invitrogen), 500 μM each dATP, dCTP, dGTP, dTTP, and 1 μg (≤50 ng/μl) of RNA. One μg of a previously isolated pooled RNA template, representative of all time points in seed development ranging from June 23 until September 1st was used as a template. The reaction was mixed and equilibrated at 42°C for 5 minutes and 1 μL of SuperscriptIII RT was added followed by incubation at 42°C for 50 minutes. The reaction was terminated at 70°C and μL RNase H was added followed by incubation at 37°C for 20 minutes.

Following this, the typical 5’RACE protocol presented by Invitrogen was employed. A column purification procedure was used, involving the addition of 120 μL of 6 M NaI to the cDNA obtained from first strand synthesis followed by centrifugation at 13,000 x g. Preheated distilled water was used to elute the cDNA.

This was followed by a homopolymeric Terminal deoxynucleotidyl transferase (TdT)-tailing reaction of the cDNA. Components of the reaction include: 10 mM Tris-HCl (pH 8.4), 25 mM KCl, 1.5 mM MgCl₂, 200 μM dCTP, and cDNA. This reaction was incubated at 94°C for 2 minutes followed by addition of TdT and an incubation for 10 minutes at 37°C. The TdT was heat inactivated for 10 minutes at 65°C.
Lastly, amplification of the cDNA was performed using gradient PCR parameters. Components of the PCR include: 20 mM Tris-HCl (pH 8.4), 50 mM KCl, 1.5 mM MgCl₂, 400 nM GSP, 400 nM Abridged Anchor Primer (Invitrogen), 200 μM each dATP, dCTP, dGTP, dTTP, tailed cDNA, and 2.5 units Taq DNA polymerase. PCR protocol was as follows: 30 to 35 cycles, 94°C for 1-2 min, 94°C for 0.5-1 min, (gradient): 55°C to 70°C for 0.5-1 min, 72°C for 1-2 min, followed by: 72°C, 5-7 min, and an indefinite hold: 5°C, until the samples were removed.

cDNA was amplified by PCR using gene-specific nested reverse oligonucleotide primers (GSP) listed in Table 2-2, along with the Abridged Anchor Primer (AAP), 5’-GGCCACGCGTCGACTAGTACGGGIIGGGIIGGIIG-3’, provided by Invitrogen. 5-20 μl of 5’ RACE products were analyzed by agarose gel electrophoresis according to standard protocols, using appropriate size standards followed by ultraviolet (UV) visualization of ethidium bromide-stained products. If samples’ bands were not clear enough, an additional gradient PCR reaction was performed using another GSP, listed in table 2-3, along with an Abridged Universal Amplification Primer (AUAP), 5’-GGCCACGCGTCGACTAGTAC-3’, instead of the AAP.

<table>
<thead>
<tr>
<th>VfACBP3b GSP</th>
<th>VfACBP4 GSP</th>
</tr>
</thead>
<tbody>
<tr>
<td>5’-ATACTGCTCCATAGCCACTTGTGATC-3’</td>
<td>5’-GGATCCAGCAAGCCAACCCACACA-3’</td>
</tr>
</tbody>
</table>

Figure 2-2. 5’RACE Gene Specific Primers (GSP) for VfACBP3b and VfACBP4

<table>
<thead>
<tr>
<th>VfACBP3b Nested GSP</th>
<th>VfACBP4 Nested GSP</th>
</tr>
</thead>
<tbody>
<tr>
<td>5’-GTTTCCAAGCCTTTTGCCAAGCATCTGAC-3’</td>
<td>5’-CACCACAGAGCCCTGCTCTGTTTG-3’</td>
</tr>
</tbody>
</table>

Figure 2-3. 5’RACE Nested Gene Specific Primers (GSP) for VfACBP3b and VfACBP4.

Much like the 5’RACE protocol detailed above, the Invitrogen method for 3’RACE was used with the reverse transcriptase III enzyme along with sequencing parameters and other components from the 3’RACE kit. Components of the reaction included: 20 mM Tris-HCl (pH 8.4 at 22°C), 50 mM KCl, 2.5 mM MgCl₂, 10 mM DTT, 500 nM AP, 500 μM each dATP,
dCTP, dGTP, dTTP, and 1 μg (≤50 ng/μl) of RNA. One μg of a previously isolated pooled RNA template, representative of all time points in seed development ranging from June 23 until September 1st was used here. The reaction was mixed and equilibrated at 42°C for 5 minutes and 1 μL of SuperscriptIII RT was added followed by incubation at 42°C for 50 minutes. The reaction was terminated at 70°C and μL RNase H was added followed by incubation at 37°C for 20 minutes.

The components of the reaction employed in amplifying the cDNA were as follows: 20 mM Tris-HCl (pH 8.4), 50 mM KCl, 1.5 mM MgCl₂, 200 nM GSP, 200 nM Abridged Universal Amplification Primer (AUAP) or Universal Amplification Primer (UAP) (Invitrogen), 200 μM each dATP, dCTP, dGTP, dTTP, and 0.1 unit/μL Taq DNA polymerase. Two μL from the cDNA synthesis reaction was added to a PCR tube. The reaction was then centrifuged. The reaction was incubated at 94°C for 3 min. Gradient PCR was performed at 35 cycles. PCR protocol was as follows: 30 to 35 cycles, 94°C for 1-2 min, 94°C for 0.5-1 min, (gradient): 55°C to 70°C for 0.5-1 min, 72°C for 1-2 min, followed by: 72°C, 5-7 min, and an indefinite hold at 5°C, until the samples were removed. Following amplification, 10 to 20 μL of the amplified sample was analyzed using agarose gel electrophoresis and ethidium bromide staining, and the appropriate molecular size standards. The optimal products of the PCR were chosen in a secondary gradient PCR reaction, using another GSP, listed in figure 2-5, along with an Abridged Universal Amplification Primer (AUAP), 5’-GGCCACGCGTGCAGTAGTAC-3’.
**Table:**

<table>
<thead>
<tr>
<th>Primer Name</th>
<th>Sequence</th>
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</thead>
<tbody>
<tr>
<td>VfACBP3b GSP</td>
<td>5’-GGTTTCATCGCGGTTAACCAGTTTCTCAG-3’</td>
</tr>
<tr>
<td>VfACBP4 GSP</td>
<td>5’-GCATCAATTTCATCCCAAGTCTGTTCTCG-3’</td>
</tr>
<tr>
<td>VfACBP3b Nested GSP</td>
<td>5’-CTGGTTCGTCAAGAAATTCATCGACCA-3’</td>
</tr>
<tr>
<td>VfACBP4 Nested GSP</td>
<td>5’-GTGTAACAGATTGACCCCCAGGTGGAGAC-3’</td>
</tr>
<tr>
<td>VfACBP3b Sense Primer</td>
<td>5’-GGATCCATGACGCTTTTCTTGAATTGG-3’</td>
</tr>
<tr>
<td>VfACBP3a Sense Primer</td>
<td>5’-CTATAGGATCAGCTGGCTTCAAGAGCTCTTTGTC-3’</td>
</tr>
<tr>
<td>VfACBP6 Sense Primer</td>
<td>5’-GGATCCATGGTCTGGAAGGGAATTGAGT-3’</td>
</tr>
<tr>
<td>VfACBP3a Antisense Primer</td>
<td>5’-ATGGGTCGACTAGGCGTGCAACTTTCTCACTTGG-3’</td>
</tr>
<tr>
<td>VfACBP3b Antisense Primer</td>
<td>5’-ACTTAGTCGACTCATTCTGTAGCCCTGTTCTCCAA-3’</td>
</tr>
<tr>
<td>VfACBP6 Antisense Primer</td>
<td>5’-ATCAGTCGACCCTAAAGAAGCAGCAGCAGCAGCTTC-3’</td>
</tr>
</tbody>
</table>

**Figure 2-4.** 3’RACE Gene Specific Primers (GSP) for VfACBP3b and VfACBP4

**Figure 2-5.** 3’RACE Nested Gene Specific Primers (GSP) for VfACBP3b and VfACBP4.

The amplification products were cloned into the pCR®2.1-TOPO® vector provided by Invitrogen, as described in the bacterial transformation section. DNA was extracted from two individual transformants and sequenced.

**Polymerase Chain Reaction (PCR) to amplify full-length open reading frames**

The full-length open reading frames of three of the VfACBPs were amplified with the respective primers in figure 2-6.

**Table:**

<table>
<thead>
<tr>
<th>Primer Name</th>
<th>Sequence</th>
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</thead>
<tbody>
<tr>
<td>VfACBP3a Sense Primer</td>
<td>5’-GGATCCATGACGCTTTTCTTGAATTGG-3’</td>
</tr>
<tr>
<td>VfACBP3a Antisense Primer</td>
<td>5’-ATGGGTCGACTAGGCGTGCAACTTTCTCACTTGG-3’</td>
</tr>
<tr>
<td>VfACBP3b Sense Primer</td>
<td>5’-CTATAGGATCAGCTGGCTTCAAGAGCTCTTTGTC-3’</td>
</tr>
<tr>
<td>VfACBP3b Antisense Primer</td>
<td>5’-ACTTAGTCGACTCATTCTGTAGCCCTGTTCTCCAA-3’</td>
</tr>
<tr>
<td>VfACBP6 Sense Primer</td>
<td>5’-GGATCCATGGTCTGGAAGGGAATTGAGT-3’</td>
</tr>
<tr>
<td>VfACBP6 Antisense Primer</td>
<td>5’-ATCAGTCGACCCTAAAGAAGCAGCAGCAGCAGCTTC-3’</td>
</tr>
</tbody>
</table>

**Figure 2-6.** PCR Primers for VfACBP3a, VfACBP3b, and VfACBP6 to amplify the full-length ORFs.

One μg of a pooled cDNA template, representative of all time points in seed development (henceforth termed as weeks after fluorescence, WAF) ranging from June 23 until September 1st was used for amplification of each the ACBPs along with the Platinum® Pfx enzyme and accompanying manufacturer’s protocol (Invitrogen). Components of the reaction include: 10X Pfx Amplification Buffer at 5 μl, 10 mM dNTP mixture at 1.5 μl, 50 mM MgSO₄ at 1 μl, primer mix (10 μM each) at 1.5 μl, template DNA (10 pg - 200 ng) ≥1 μl, Platinum® Pfx DNA polymerase at 0.4-1 μl, autoclaved, distilled water to 50 μl. The PCR cycling parameters used in
the amplifications of the full-length ORFs for VfACBP3a and VfACBP3b were initial
denaturation at 94°C for 30 seconds followed by 30 cycles of 94°C for 1 minute and 60°C for 1
minute, and a final extension at 72°C for 3 minutes. For VfACBP6, the cycling parameters were
the same except the 60°C step was for 20 seconds. PCR products were analyzed by agarose gel
electrophoresis and imaged on a GE Healthcare Fujifilm LAS-3000 image analyzer. Samples
were cleaned and concentrated in Zymo columns (Zymo Research Corporation, 625 W. Katella
Ave., Suite #30, Orange, CA 92867 U.S.A.) and resulting DNA was used to transform bacteria
(see bacterial transformation protocol).

The amplification products were cloned into the pB50 vector, as described in the bacterial
transformation section. DNA was extracted from two individual transformants and sequenced.

**Bacterial transformation**

Four μL of fresh PCR product was added to 1 μL salt solution (TOPO®) and 1 μL
TOPO® vector and incubated at room temperature for 30 minutes. This reaction mix was added
to TOP10 competent cells on ice and incubated for 15 minutes. It was heat-shocked in a 42°C
water bath and chilled on ice for 2 minutes. 250 μL super optimal broth with catabolite
repression (SOC) was added and incubated at 37°C for one hour. 100μL aliquots were plated and
incubated at 37°C overnight on 2XYT with kanamycin antibiotic plates. Bacterial colonies were
subject to PCR screening using the M13 forward and reverse sequencing primers,
GTAAAACGACGGCCAGT and AACAGCTATGACCATG respectively, provided by the
TOPO® kit. Two bacterial colonies were picked with a sterile spreading stick and the stick was
used to inoculate an 8 mL 2XYT plus kanamycin culture (100 micrograms per mL kanamycin).
Cultures were shaken at 250 RPM at 37°C overnight. Cells were centrifuged at 10,000 x g for 10
minutes and DNA was extracted from the pellet using Wizard Plus Mini-preps (Promega
Corporation, 2800 Woods Hollow Road Madison, WI 53711 USA), and eluted with 50 μL Tris-EDTA.

**Sequencing**

All of the DNA constructs generated were sequenced utilizing the DTCS Quickstart kit 1 (Beckman Coulter, Fullerton, CA) and analyzed with a Beckman Coulter 8800 Genetic Analysis System equipped with the CEQ8000 software suite. The sequences were manipulated and analyzed using VectorNTI Advance 10.0 and 11.0 software (InforMax, Invitrogen Life Science, Frederick, MD), and compared to other sequences employing World Wide Web based BLAST algorithm programs. Phylogenetic comparisons were performed by the generation of multiple sequence alignments using the CLUSTALX program, with default settings.

**Reverse transcription polymerase chain reaction (RT-PCR)**

Reverse transcription (RT) reactions were carried out using the BioRad (Life Science Research 2000 Alfred Nobel Drive Hercules, CA 94547 USA) iScript™ cDNA Synthesis Kit as per manufacturer’s protocol. Components of the reaction included: 5x iScript reaction mix 4 at μL, iScript reverse transcriptase at 1 μL, nuclease-free water to 20 μl, and RNA template at 1 μg (total RNA). The reaction protocol of this mixture, in PCR microtubes, was as follows: 5 minutes at 25ºC, 30 minutes at 42ºC, 5 minutes at 85ºC, followed by 4ºC. As mentioned earlier, the templates used in this reaction were the RNAs ranging from (weekly) June 23rd until September 1st (11 individual samples) along with leaf and flower RNA with the exception that these were not pooled. A non-reverse transcriptase template was used as a negative control. Following RT-PCR, the nucleic acid concentration of each sample (13 total) was quantified on a Nanodrop ND-1000 spectrophotometer and diluted to 1 μg/μL.
Quantitative Real-time Polymerase Chain Reaction (qPCR)

Real-time PCR was performed with a BioRad C1000 core unit PCR thermocycler with a BioRad CFX96 head unit for qPCR. The PCR reaction was carried out in a final volume of 25 μL, which included 2 μL cDNA, 10 μL SYBR Green master mix, 2.5 μL of 5 μM sense and antisense primers, and H₂O. The PCR conditions consisted of 40 cycles at 95 °C for 30 s, 60 °C for 30 s, and 72°C for 1 60 s. The reference gene included with each run was tung ubiquitin ligase. Samples were assayed in triplicate. Means and standard deviations were calculated from the data obtained. For each sample, at least three assays were performed. The data was normalized using BioRad software (BioRad CFX Manager version 1.5). Each baseline was adjusted based upon a value that was found from taking the average of all the combined runs per VfACBP. This average baseline value was subsequently applied to each run. In addition, any c(t) value that deviated by more than 0.5 from the average c(t) value of a specific time point in all runs for one VfACBP, was not taken into consideration. The c(t) value, which is the threshold crossing cycle, was calculated as the mean of three different assays.

Split-ubiquitin-based membrane yeast two-hybrid analysis

Protein:protein interactions between different tung ACBP proteins and other proteins expressed in developing seeds were assayed using the Dualsystems Biotech (San Pedro, CA) DUAL-membrane split-ubiquitin system. The yeast strain NMY51, genotype: MATa his3delta200 trp1-901 leu2-3,112 ade2 LYS2::(lexAop)4-HIS3 ura3::(lexAop)8-lacZ (lexAop)8-ADE2 GAL4), was used to perform this procedure. NMY51 has a ura3 genotype. Two different growth markers and a lacZ reporter ensure the highest possible stringency in a library screen, resulting in fewer false positives. This yeast strain was transformed with different combinations of bait and prey plasmids. Yeast containing bait and prey plasmids were cultured overnight in a
medium consisting of 8 mL synthetic dextrose (SD) (2% [w/v] dextrose, 0.67% [w/v] yeast nitrogen base without amino acids, 2 g L\(^{-1}\) synthetic mix of amino acid supplements, minus leucine and tryptophan; SD-LT) (Bufferad, IL) in an orbital incubator at 30ºC and 250 RPM. Then, ~500 µL of cell culture was transferred to 10 mL of fresh SD-LT medium and the cells were cultured again for another 4-6 hours. Cells were pelleted by centrifugation, washed with water, and then resuspended in 1 mL of water. The activation of the histidine and adenine reporter genes was tested by performing a serial dilution assay where the first cell suspension had an OD\(_{600}\) value of 0.5, and 6 subsequent samples were prepared via 1:5 serial dilutions. Cells from each dilution were plated on SD-LT and SD-LTHA plates (SD-LT also lacking histidine and adenine) and were incubated for 3 days at 30ºC. Plates were observed after 24 hours, 42 hours, and 72 hours respectively in order to monitor cell growth on a GE Healthcare Fujifilm LAS-3000 image analyzer using the digital white-light setting.

The lacZ reporter activation was observed by β-galactosidase activity for quantitative analysis using the β-galactosidase assay kit from Pierce Protein Research Products (Thermo Scientific, Rockford, IL). Cultures were grown exactly as described above in SD-LT liquid media. After back-dilution, cultures were spun down for 10 minutes at 3500 rpm. Supernatant was poured off and pellets were resuspended in the remaining volume of SD-LT media and centrifuged at 14,500 RPM for 1 minute. Supernatant was removed and pellet was washed once with water and resuspended in 1 mL water. The OD\(_{600}\) of the culture was measured and the volume of cells needed to make 350 µL of 1 OD concentration was calculated. A working solution (350 µL) contained within the kit was added and the mixture was incubated at 37ºC at 300 RPM until a yellow color change was observed (minutes for strong interactors and up to 24 hours for weak ones). A stop solution (300 µL) provided with the kit was added once yellow
color was observed and the elapsed time was recorded. Cell debris was removed by centrifugation at 14,500 rpm for 30 seconds followed by transferring 900 µL of the supernatant to a fresh tube and stored at 4°C until absorbance measurements were taken. The absorbance was measured in triplicate at 420 nm using a Nanodrop ND-1000 spectrophotometer against a blank containing sterile water with working solution and stop solution. Enzyme activity was calculated in Miller units (Miller 1972), using the equation:

$$\beta\text{-galactosidase activity} = \frac{1000 \cdot A_{420}}{t \cdot V \cdot OD_{600}}$$

where, $t$ = time (minutes) of incubation, $V$ = volume of cells (mL) used in the assay.

![Figure 2-7. Illustration of the split ubiquitin system.](image)

Two proteins of interest, P1 and P2, produce a whole ubiquitin moiety due to the NubI half having a high affinity for the Cub half of the split ubiquitin, despite the proteins not being in close proximity. The LexA reporter gene is cleaved and is later transcribed. Mutated Nub, NubG, will only produce a whole ubiquitin moiety with Cub when the two proteins of interest are in close enough proximity to bring the two halves of ubiquitin together.

Ubiquitin-specific proteases (UBPs) recognize and cleave the fusions of ubiquitin and a target protein immediately after a double glycine motif (Gly-Gly-X) that is located at the C-terminus of ubiquitin (http://www.dualsystems.com/technologies/protein-interaction-
UBPs recognize the folded ubiquitin as opposed to a specific sequence of a polypeptide chain as in other proteases. The expression of ubiquitin in yeast can occur as an N-terminal half (Nub) in addition to a C-terminal half (Cub). The affinity the halves have for each other remains unchanged, and they can spontaneously reassemble to form a split-ubiquitin. Nub and Cub moieties are co-expressed within a single cell, and a reporter protein that is fused to the C-terminus of ubiquitin will be cleaved off upon re-assembly of the Nub and Cub moieties into split-ubiquitin. To facilitate use of split ubiquitin as a sensor of protein:protein interaction strength, a point mutation was introduced into the N-terminal half of ubiquitin to produce NubG. This mutation completely eliminates the affinity of the two halves for one another. Separate NubG and Cub portions are not recognized by UBPs, and thus no cleavage of the reporter gene occurs. In this system, a prey protein is fused to NubG while the bait is fused to Cub followed by a reporter gene. Upon interaction of the bait and prey, NubG and Cub are brought close enough together to reconstitute split-ubiquitin. This results in the release of the reporter protein through the action of the UBPs.

**Binary vector plasmid construction for in planta applications**

Two constructs were created and used for different purposes. The first construct consisted of a plasmid vector used for the expression of V/FADX driven by the β-conglycinin promoter in
conjunction with either VfACBP3a or VfACBP6 to analyze eleostearic acid content in seeds of transformed *Arabidopsis thaliana*. The second construct consisted of VfACBPs (Figures 2-8 through 2-10) placed into a plasmid allowing for the expression of DsRed fluorescence (Figure 2-12) to analyze total fatty acid changes in wild type *Arabidopsis thaliana* upon the introduction of VfACBP3a (Figure 2-9) or VfACBP6 (Figure 2-10). The protocol used to transform the vectors is similar in approach to the TOPO® protocol, with a key exception. Both VfACBPs were placed into the pB50 vectors mentioned earlier, and were cut with the restriction enzyme, AscI. AscI cut out the promoter-gene-terminator cassette, which was ligated into either the AscI site (for pB110 the DsRed vector) or the MluI site of pE29 (which contains VfFADX, see Figure 2-11). Components of the restriction digest included: 5 µL NE buffer (New England Biolabs (NEB) 240 County Road Ipswich, MA 01938-2723 USA), 0.5 µL 100x BSA, 5 µg plasmid DNA, 1.5 µL each restriction enzyme (NEB), water to 50 µL. Transformation procedures occurred as described earlier. Samples were cleaned and concentrated in Zymo columns. These samples were then transformed into either the plasmid expressing VfFADX or the pB110 plasmid (Figure 2-12) allowing for the expression of DsRed fluorescence.

![Figure 2-8. Vector pB9 pBAR with the NOS promoter and terminator sequences.](image-url)
Figure 2-9. Vector pEB218 which contains VfACBP3a (seen here as Vf/mACBP) in pB50.

Figure 2-10. Vector pEB220 which contains VfACBP6 (seen here as tung soluble ACBP) in pB50.
Floral dip method for in planta transformations

Work involving in planta transformations included a floral dip method first adapted by Clough and Bent, 1998. Arabidopsis plants were grown in pots until flowering. First bolts were clipped to encourage proliferation of many secondary bolts and the plants were ready roughly 4-6 days after clipping. A strain of Agrobacterium tumefaciens (C58) was prepared to carry the
gene of interest, either ACBP3a or ACBP6, in a binary vector. A large liquid culture (600 mL) was grown at 28°C in 2XYT broth with antibiotics to select for the binary plasmid. 

*Agrobacterium* cells were pelleted by centrifugation and resuspended in 300 mL of 5% sucrose solution, containing 0.01-0.02% Silwet L-77. The above-ground parts of plants were dipped in *Agrobacterium* solution for 10 seconds, with gentle agitation. The dipped plants were placed under a dome or cover for 16 to 24 hours to maintain high humidity (plants can be laid on their side if necessary), without exposure to excessive sunlight. The plants were then watered and grown to maturity. Dry seeds were harvested afterward as will be described. Transformants were selected using a glufosinate herbicide resistance selectable marker, or a DsRed (red fluorescence protein) marker. Putative transformants were transplanted to soil and grown.

Transformed *Arabidopsis* lines followed a specific generational naming convention. Dipped parental plants: T₀; seeds that come off of those: T₁; seeds from T₁: T₂, and seeds from T₂: T₃. Stated differently, the T₁ generation breeds T₂ seeds, and the T₂ generation breeds T₃ seeds.

**Fatty Acid Methyl Ester (FAME) Analysis**

Plant tissues or dirt were separated using a 30 mesh size separating filter and seeds were placed in appropriately labeled 1.5 mL Eppendorf tubes. Approximately 30 mg of seeds were placed into 1.5 mL Eppendorf tubes along with 500 µL of hexane and steel beads and were pulverized in a bead beater for 5 minutes followed by centrifugation (13000xg/2min). 300 µL of extract was transferred to 13x100 Corning culture tubes. Seven hundred µL hexane and 400 µL sodium methoxide in methanol solution was added and the reaction incubated at room temperature for 10 minutes. Two mL hexane and 2 mL saturated NaCl solution was added and
then the tubes were centrifuged for 5 minutes in a tabletop swinging bucket centrifuge. Two mL of the top layer was transferred to 2 mL vials for gas chromatography analysis or stored at -20°C.

Gas chromatography

An Agilent Technologies (5301 Stevens Creek Blvd Santa Clara CA 95051 United States) gas chromatographer containing an autosampler along with Agilent Chemstation software was used to analyze the fatty acid methyl ester content of the aforementioned extracts. The gas chromatographer contains a Supelco SP-2380 column with helium as the carrier gas at a flow rate of 36 cm/second. The initial oven temperature is 160°C with no hold, followed by a ramp up of 4°C/minute up to 200°C and followed by a 5 minute hold. Vials were placed on the autosampler and analyzed one at a time.

Statistical analysis

Student’s t-tests were used for comparison of the fatty acid content elicited gas chromatography results (calculated using Microsoft Excel, 2007). Differences at P < 0.05 were accepted as significant. Statistical analysis of the comparison between the various plant constructs was performed using the unpaired, two-tailed t test.
Results

The elucidation of *Vernicia fordii* Acyl-CoA Binding Proteins (ACBPs)

Previously, many of the other biosynthetic enzymes of the tung lipid biosynthetic pathway were identified, cloned, and analyzed for their potential roles in the production of α-eleostearic acid in the oil bodies in seeds of the tung tree (Shockey, et al., 2006). In order to identify tung ACBPs for analysis of their roles in the tung biosynthetic pathway, it was required to obtain their full-length cDNAs as an initial step. Expressed Sequence Tag (EST) sequencing allowed for a short, transcribed cDNA sequence. Approximately 5000 randomly selected clones were chosen and utilizing homology-based comparisons, such as BLAST (http://blast.ncbi.nlm.nih.gov/Blast.cgi). These were compared to a publicly available database, GenBank (http://www.ncbi.nlm.nih.gov/genbank/), to identify two of the VfACBPs; VfACBP3a and VfACBP6. Both of the VfACBP ESTs contained entire open reading frames. The VfACBP3a open reading frame, from start codon until the stop codon, is 822 base pairs (274 amino acids) in size. VfACBP6, similar to other eukaryotic small, soluble ACBPs, has an open reading frame of 279 base pairs (93 amino acids).

The other two VfACBPs, VfACBP3b and VfACBP4, were obtained through a more contemporary technique, as compared to EST, called pyrosequencing. Pyrosequencing is a method of DNA sequencing that is based upon a principle called sequencing by synthesis (Weber, et al., 2007). It is reliant upon detection of pyrophosphate release when nucleotides are incorporated (Weber et. al., 2007).

Unlike the EST sequencing results for VfACBP3a and VfACBP6, the contigs from pyrosequencing for both VfACBP3b and VfACBP4 covered only a portion of the 3’ ends of the respective ORFs. Full-length cDNA clones for these genes were obtained by genome walking
and Rapid Amplification of cDNA Ends (RACE). Of these, only VfACBP4 has not been completely sequenced at this time. The pyrosequencing sequences yielded a 683 base pair (227 amino acids) sequence for VfACBP3b, including 341 base pairs (113 amino acids) of the 3’ UTR and 342 base pairs (114 amino acids) of coding sequence, meaning that 784 base pairs (261 amino acids) were required to reach the start methionine codon. Pyrosequencing yielded a 397 base pair (132 amino acids) sequence for VfACBP4, including 103 base pairs (34 amino acids) of coding sequence, the stop codon, and 291 base pairs (97 amino acids) of 3’ UTR, meaning that roughly 1905 base pairs (635 amino acids) will be required to reach the start codon.

**Genome walking and RACE to obtain full length open reading frames**

It was difficult to ascertain full-length cDNAs for longer open reading frames, such as the case with VfACBP3b and especially VfACBP4, due to limitations in the cDNA library synthesis of pyrosequencing. Thus, the use of the genome walking and RACE techniques were needed to produce full-length clones. As was mentioned previously, the ACBPs that were identified by EST and pyrosequencing, the genome walking and RACE products, and the full-length ORFs, were compared to a publicly available database, GenBank to identify any sequence similarity to other plant ACBPs.

VfACBP3b required to two rounds of genome walking in addition to one round of RACE in order to reach the start methionine, due to the genome walking products generating only part of the 5’ sequence up to the start methionine. VfACBP4 also required RACE after genome walking, but the remaining 5’ portion of the sequence is not completed at this time. Despite this, the partial sequence was used to perform phylogenetic analysis and to design real-time quantitative PCR primers.
After a full-length cDNA sequence was obtained from RACE PCR and genome walking for VfACBP3b, specific PCR primers (listed in Materials and Methods) were designed to obtain a full-length cDNA based on classic 3-step PCR parameters.

**Confirming the identity of 4 unique *Vernicia fordii* ACBPs**

The sequences for many of the proteins of the tung lipid pathway from the EST and pyrosequencing data were compared to online databases (GenBank, http://www.ncbi.nlm.nih.gov/genbank/) to confirm their identities. As was the case with the VfACBPs, a homology-based method from the *Arabidopsis* genome website (TAIR, http://www.arabidopsis.org/Blast/index.jsp) was used to compare the sequences borne out of the initial EST and pyrosequencing data. These cDNA sequences were compared to the TAIR10 protein database to see if any of these proteins were similar to proteins from other organisms. VfACBP6 was most similar to *Arabidopsis thaliana* ACBP6, (Representative Gene Model Number: AT1G31812.1, 1e-42, 69% identity, and 73% positives) through using the nucleotide database, TAIR10. VfACBP3a, using the TAIR10 protein database, was found to be most similar to *Arabidopsis thaliana* ACBP3 (AT4G24230.6, 1e-41, 73% identity, and 74% positives). Interestingly, VfACBP3b, using the TAIR10 amino acid database, was most similar to a *Ricinus communis* ACBP (8e-37, 73% identity, and 79% positives). VfACBP4 was most similar to *Arabidopsis thaliana* ACBP4 (AT3G05420.2).

VfACBP3a and VfACBP3b are similar to one another in sequence and to the *Arabidopsis thaliana* ACBP3. As can be seen in figure 3-1, BLAST results yielded differing best matches for either ACBP3a and ACBP3b. ACBP3a had the greatest sequential similarity with *Arabidopsis* ACBP3. ACBP3b compared most similarly to sequences of *Ricinus communis* (*E*-value of $9e^{-37}$) and *Populus trichocarpa* (*E*-values of $1e^{-31}$ and $1e^{-30}$) ACBPs. *Arabidopsis* ACBP3 was the fifth-
most similar sequence, yielding an $E$-value of $1e^{-19}$. These results indicate that these two tung ACBP3 sequences are isoforms and they are not the same protein.

Both the EST and pyrosequencing techniques provide cDNA contig sequences, and it was initially believed that $Vf$ACBP3a and $Vf$ACBP3b could actually be one protein and not two isoforms. Both of the $Vf$ACBP3s are different in size, $Vf$ACBP3a being 819 base pairs while $Vf$ACBP3b is 1125 base pairs in their respective ORF lengths. They are very similar to *Arabidopsis* ACBP3 but to differing extents. As figure 3-2 shows, $Vf$ACBP3b is related to *At*ACBP3 but is more related to other ACBPs (Parts A and B). $Vf$ACBP3b was found to be more similar to a *Ricinus communis* and a *Populous trichocarpa* ACBP (Part B) than *At*ACBP3 (Part A). The two ACBP3s from tung are not even that similar in sequence. Figure 3-1, Parts A-D, illustrates several parts of the nucleotide sequences (Parts A and B) and proteins (Parts C and D) of both $Vf$ACBP3s upon comparison. Comparing these two gives very little similarity even with the shortest word length, 16, that is possible in the BLAST program.
(A)

Score = 71.3 bits (38), Expect = 9e-16
Identities = 66/81 (82%), Gaps = 7/81 (8%)
Strand=Plus/Plus

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(B)

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Identities = 35/39 (90%), Gaps = 0/39 (0%)
Strand=Plus/Plus

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<td></td>
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(C)

Score = 36.6 bits (83), Expect = 8e-07, Method: Compositional matrix adjust.
Identities = 26/71 (37%), Positives = 38/71 (54%), Gaps = 9/71 (12%)

<table>
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<table>
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<td>64</td>
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<td>EKLVEVFHSE</td>
</tr>
<tr>
<td></td>
<td>71</td>
<td></td>
</tr>
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</table>

(D)

Score = 137 bits (345), Expect = 3e-37, Method: Compositional matrix adjust.
Identities = 63/109 (58%), Positives = 81/109 (75%), Gaps = 1/109 (0%)

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</tr>
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Figure 3-1. BLAST comparisons of VfACBP3a and VfACBP3b. Parts A and B: BLASTn results of VfACBP3a (Query) against VfACBP3n (Subject) illustrate that these two VfACBPs are not very similar in their nucleotide sequences. Parts C and D: BLASTp results of VfACBP3a (Query) against VfACBP3b (Subject) illustrate that these two VfACBPs are not very similar in their protein sequences.

So, not only are the two proteins different lengths, but they do not share very much identity. These data illustrate that there are two isoforms of VfACBP3; VfACBP3a and VfACBP3b. This discovery of VfACBP3b is interesting because of both an absence of an ortholog in Arabidopsis thaliana and its presence as an ortholog in Ricinus communis and Populous trichocarpa. This presence in Ricinus communis shows the shared Euphorbiaceae lineage of tung and castor.

(A)

| Query: | 602 YGCGGCPFGTAKVXARRKLAGRGLNNPFTVADYVAGVYLAVP693GST DNGKF 503 |
| Subject: | 602 YGCGGCPFGTAKVXARRKLAGRGLNNPFTVADYVAGVYLAVP693GST DNGKF 503 |

BLAST AGAINST ALL TAIR PLANT PROTEINS

(B)

| Query: | 502 SSTXAA----NHSGAL---FEBSTY---SSHBPYITTEK R116 |
| Subject: | 227 SEMETGVLPPFES23LEDPTMVLTTGVDSE23XIVGGER 236 |

The AtACBPs have highly conserved binding domain residues (Xiao and Chye, 2009). Perhaps the most important property of ACBPs is their specific binding to acyl-CoA and as such, it is critical that they contain certain residues that constitute a binding domain (Xiao and Chye,
There are 8 critical binding domain amino acid residues in the acyl-CoA binding domain of *Arabidopsis thaliana* ACBP6: F5, K35, D40, F47, K54, W58, A69, and Y73. Figure 3-3, part A illustrates the critical residues of tung ACBP3a as compared to *At*ACBP6. *Vf*ACBP3a has a match of 7 of the 8 critical residues for acyl-CoA binding, while *Vf*ACBP3b (not pictured) also matched 7 of the residues, but the difference was that the 4th critical residue, P (proline), was different (proline in *Arabidopsis* changed to serine in tung), while the difference for *Vf*ACBP3a was at the second residue, K (lysine) changed to a Q (glutamine) in tung. Interestingly, proline being changed to serine is a nonpolar to polar uncharged change. Lysine to glutamine is a basic polar to polar uncharged change. The implications of these changes are unknown. Tung ACBP6, on the other hand, matched 6 of these 8 residues (figure 3-3, part B). This illustrates the conservation of critical binding domain residues.

![A](image1)

![B](image2)

Figure 3-3. Tung ACBP6 and ACBP3a critical binding residues in the acyl-CoA binding domain. Red arrows represent amino acid changes while black represent no changes. Part A: Seven of the eight residues believed to be critical in the binding of acyl-CoA are direct matches in *Vf*ACBP3a (query) of tung as compared to *At*ACBP3 (subject). Part B: Six of the eight residues believed to be critical in the binding of acyl-CoA are direct matches in *Vf*ACBP6 (query) as compared to *At*ACBP6 (subject).
The structure of the highly conserved, soluble bovine ACBP

Through NMR studies, the three-dimensional structure of bovine ACBP has been determined (Andersen, et. al., 1991). This ACBP is similar to all other ~10 kDa ACBPs found throughout many eukaryotes, including *Arabidopsis* and *Vernicia fordii* ACBP6. Through these studies, and since there is a high amount of conservation between these ACBPs, it is possible to observe some of the features that may be present in these ACBPs, and is thus relevant to tung ACBP6. The bovine ACBP has been shown to be an up-down-down-up four-K-helix bundle (A1 through A4) with an overhand loop connecting two helices (Andersen, et. al., 1991). This bundled arrangement of ACBP is unique amongst other known four-helix folds (Andersen, et. al., 1991). The arrangement is skewed, since one of the helices is disjointed from two other helices, which results in only four helix-helix interfaces, as opposed to the typical six interfaces as seen in the well-known four-helix bundles (Andersen, et. al., 1991). All of the interaction angles between helices in the bovine ACBP were calculated using the program, PRONTO (Andersen, et. al., 1991). The residues at the nearest contact in the four helix interfaces are Ala9 and Tyr31, within helices A1-A2, Phe5 and Ile74, in helices A1-A4, Ala34 and Ala69, in helices A2-A4, and Ser29 and Trp58, in helices A2-A3 (Andersen, et. al., 1991). All of the central residues of bovine ACBP were determined from calculations using a set of structures of ACBP using the program XPLOR (Andersen, et. al., 1991). All of the central residues, aside from Ser29, are highly conserved in the sequences of ACBP (Andersen, et. al., 1991). It is also apparent that many of the residues that make up the interfaces are conserved throughout evolution (Andersen, et. al., 1991). The most conserved interface is between helices A1 and A4, and the least conserved between helices A2 and A4 (Andersen, et. al., 1991). The edges of the interfaces are where the most dramatic differences in structure are located, which are possibly
compensated for by similar changes or by an increased dynamic structure (Andersen, et. al., 1991). Therefore, it is of a high probability that the four-helix bundle architecture is conserved throughout many different species, including *Arabidopsis* and tung ACBP6 (Andersen, et. al., 1991).

**Quantitative Real-Time Polymerase Chain Reaction (qPCR) revealed dynamic expression patterns for VfACBPs**

After each of the VfACBPs was cloned and analyzed, the testing and analysis of their expression patterns was performed. Ultimately, qPCR was used to determine and analyze tissue specific expression patterns of the tung ACBPs and compare these results with enzymes that have known functions in tung. This was done to determine if there is any function(s) the VfACBPs may have in tung. Quantitative real time PCR (qPCR) was used to amplify and quantify targeted DNA molecules. The principal difference between classic PCR and real time PCR is that the reaction is observed in real time as opposed to the detection of a product at the end of the amplification process.

![Figure 3-4. qPCR: tissue-specific expression patterns of VfDGAT2 and VfFADX, two components with known roles of the tung lipid biosynthetic pathway.](image-url)
Figure 3-5. qPCR: tissue-specific expression patterns of VfACB3a.

Figure 3-6. qPCR: tissue-specific expression patterns of VfACB3b.
Figure 3-7. qPCR: tissue-specific expression patterns of VfACBP4.

Figure 3-8. qPCR: tissue-specific expression patterns of VfACBP6.
Each of the dates shown in figures 3-4 through 3-8 are representative of the weeks after flowering. June 23rd is the date in seeds that is 8 weeks after flowering (WAF) with each subsequent date being one week after that. The range shown here is from 8 to 18 WAF.

Referring to figure 3-4, the expressions of both DGAT2 and FADX had a very distinct pattern. Tung express these enzymes, along with several others, at a greater rate when the production of α-eleostearic acid in seed oil bodies stored in triacylglycerols (TAGs) was increased. This corresponds to mid to late summer, with little expression in leaf and flower tissues. Both VfDGAT2 and VfFADX exhibit a bimodal expression pattern, with an increase in expression in mid-summer, followed by a subsequent decrease, and then another increase. Neither expressed highly, or at all, in leaves and flowers.

All 4 VfACBPs had expression levels that correlated with VfDGAT2 and VfFADX expression levels except that there was higher expression in leaf and flower tissues by the VfACBPs. Each of the VfACBPs had an expression pattern that was low at the early weeks after fluorescing (WAFs), rose in mid-summer, lowered again, then rose closer to the fall. In contrast to VfDGAT2 and VfFADX, the VfACBPs expressed at higher levels in leaf and flower tissues. Despite the common bimodal expression pattern, the levels of expression of each VfACBP were very different from one another and VfDGAT2 and VfFADX. VfACP3b expressed at the highest levels as compared to every other protein. There was a dramatic difference between the very high levels of expression of 7/14, 7/21, and 9/1 for VfACP3b compared to the other VfACBPs and VfDGAT2 and VfFADX. Clearly, VfACP3b was expressed much higher at WAFs in the seeds of tung. In addition, compared to itself, it expressed in low amounts in leaf and flower tissues; however, these amounts are comparable to the other VfACBPs but in greater amount than VfDGAT2 and VfFADX, which showed very little expression. Like VfACP6,
VfACBP3a exhibited its highest expression in leaf tissues. VfACBP3a also appeared to have less difference in expression between each of the WAFs where it was expressed in leaf and flower. VfACBP4 expressed at its highest at 9/1 and like the pattern exhibited by VfACBP3b, it had a low level of expression in leaf tissues. VfACBP6 was very similar in overall expression as VfACBP3a, except its initial rise in expression occurred later (peaks at 7/28 as opposed to 7/21 in VfACBP3a).

<table>
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<tr>
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<th>6/30</th>
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<td>1.7</td>
<td>9.5</td>
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<td>1.3</td>
<td>1.8</td>
<td>4.3</td>
<td>1.9</td>
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Figure 3-9. Normalized fold expression data of the VfACBPs and VfDGAT2 and VfFADX. Each value is normalized to the reference gene, tung ubiquituing ligase.

Previously, tung DGAT2 and FADX, two components with known roles in the tung metabolic pathway, were analyzed by qPCR (figure 3-4). The expressions of these were shown to coincide with the peak of TAG accumulation (Shockey, et. al., 2006). Each VfACBP also exhibited unique patterns and levels of expression, as seen in Figure 3-9. One aspect of their expression that is commonly seen amongst each of them, however, is that they generally have increased expression in mid-summer months, first in July and then later in late August. Essentially, in a sequential manner, each of the VfACBPs are expressed at low levels in the earliest days of summer then, expression rises in mid-summer, lowers again, and rises closer to the fall. These results show that the VfACBPs are specifically expressed at certain times, and this expression can be lowered or raised. What this means for the potential roles of each VfACBP is
unknown, but the relevance of the expression pattern is consistent with peak TAG accumulation. One interesting result is the expression patterns of each $Vf$ACBP in the leaf and flower tissues. Both $Vf$DGAT2 and $Vf$FADX are not expressed in these tissues. Thus, these data show a unique expression pattern for $Vf$ACBPs.

Overall, this data shows unique expression patterns of the $Vf$ACBPs. They express differently, not only amongst themselves, but when compared to $Vf$DGAT2 and $Vf$FADX. The general levels of expression are also markedly different between each $Vf$ACBP and $Vf$DGAT2 and $Vf$FADX. These data show that each $Vf$ACBP is expressed at differing levels but have specific WAFs in seeds that they are expressed high or low. Likewise, each exhibits unique levels of expression in leaves and flowers perhaps suggesting that each may have a unique biological function.

**Split-Ubiquitin Yeast Two-Hybrid Analysis: qualitative plate assays**

Each of the $Vf$ACBPs was expressed in all tissues, including seeds, and with some interesting differences and some interesting similarities. If they are expressed in seeds, they may participate in complex lipid synthesis. So, split ubiquitin yeast two-hybrid analysis was performed using the $Vf$DGATs. Previous studies in our lab showed that each $Vf$DGAT, $Vf$DGAT1 and $Vf$DGAT2, is targeted to different subdomains of the ER membrane (Shockey, et. al., 2006). They have different affinities for eleostearic acid containing substrates when expressed in yeast, and are therefore expected to perform different biological roles in planta. In each of those different subdomains, there might be different complexes of protein isoforms to carry out those specific tasks. It is possible that some of the $Vf$ACBPs could be a part of one or both protein complexes, and this can be tested through protein:protein interactions by split ubiquitin. In addition, since the $Vf$ACBPs are expressed in seeds (just not seed specific), and
interact with the VfDGATs, they were expressed in the seeds of transgenic plants to study the effects of vfACBP expression on seed lipid fatty acid content.

A split-ubiquitin-based membrane yeast two-hybrid assay was performed in order to examine the interactions of the three of the tung ACBPs with themselves, one another, and two enzymes known to be involved in tung lipid biosynthesis, DGAT1, and DGAT2. This assay is similar in principle to the classic two-hybrid assay in yeast cells, with the exception that the protein-protein interactions can take place anywhere in the yeast cell, including in cellular membranes, as opposed to the nucleus only, a situation that may greatly improve the fidelity of measuring protein-protein interactions of membrane-bound proteins (Snider et al., 2010).

Despite the potential to fuse the ACBPs with either NubG to the N terminus and Cub-LexA to the C terminus or NubG to the C terminus and Cub-LexA to the N terminus, it was observed that fusing ACBPs with NubG to the N terminus and Cub-LexA to the C terminus was needed to avoid false negative results (Dyer, personal communication).

![Figure 3-10. Example of two split-ubiquitin SD-LT and SD-LTHA plate results. Dilutions are increased from left to right. The left-most parts of figure 3-7 represent SD-LT plates, which serve as positive controls for growth. The right-most parts of figure 3-7 show SD-LTHA plates, which select for interactions. VfACBP6 does not interact with VfACBP3a but does interact with VfDGAT2.](image-url)
### (A)

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### (D)

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<td>DGAT2-Cub-LexA</td>
<td>NubG-ACBP6</td>
<td>Interaction Observed</td>
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Figure 3-11. Split ubiquitin interactions of the VfACBPs. All of the VfACBPs interact with VfDGAT1, VfDGAT2, and the positive control bait (pCCW-Alg5-Cub-LexA) but not with other VfACBPs or themselves. This positive interaction only occurs if NubG is attached to the N-terminus of VfACBPs. VfACBPs with Cub-LexA fused to its C-terminus (results not shown), VfACBPs with Cub-LexA fused to its N-terminus (results not shown), or VfACBPs
with NubG fused to its C-terminus (results not shown), did not show interactivity with any preys or baits respectively, including positive controls.

Because each of the ACBPs interacted with both VfDGAT1 and VfDGAT2, two enzymes with known functionality in the tung lipid biosynthetic pathway, ACBPs may provide a role in the incorporation of eleostearic acid into complex lipids such as triacylglycerols. Due to the transient nature of the protein fusions as discussed above, it was difficult to discern if there would be any significant interaction between any of the ACBPs with one another. As it stands, it would be difficult to determine what role this would even provide. The aim of this study is to identify any influences tung ACBPs have, or what general roles they play, not just those involved in eleostearic acid channeling and accumulation. Clearly, these results show that VfACBPs interact with VfDGAT1 and VfDGAT2 in a qualitative manner. Beta-galactosidase assay were performed to quantitatively determine the interactivities seen here.

**Split-Ubiquitin Yeast Two-Hybrid Analysis: quantitative beta-galactosidase assays**

More specifically, β-galactosidase assays were performed to confirm and quantify the results attained from the serial plate dilution assays. Indeed, the β-galactosidase correlated very well with those of the plate dilution assays.

The enzyme β-galactosidase cleaved lactose to glucose and galactose for the usage as a carbon or energy source. The result was the production of a yellow color in solution, which can be used to determine enzyme concentration. Afterward, spectrophotometric measurements were made to determine optical densities of the solution. These OD readings were used in a formula to calculate enzyme activity, expressed in Miller units.
Figure 3-12. β-Galactosidase Assay results for the VfACBPs and their respective interacting Baits.
The results presented in the above figures confirm what was summarized previously in the plate dilution assay results section. It illustrates the strong interactivity of the VfACBPs with VfDGAT1 and VfDGAT2, along with the positive control, Alg5-Cub-LexA. The interaction of the VfACBPs with themselves is as weak as the negative control, Cub-LexA. This suggests that the VfACBPs do not form dimers or any other form of homopolymers. It does not, however, eliminate the possibility of self-interaction. Thus far, the tung ACBPs appear to perform their functions independently of one another.

The interactions were very similar in strength across all VfACBPs, with the exception of the VfACBP6 and its interaction with VfDGAT2. Interestingly, VfACBP6 has a weaker interaction with VfDGAT2 as compared to all of the other VfACBPs.

**Fatty Acid Methyl Ester (FAME) Analysis and Gas Chromatography (GC) does not reveal any seed specific biosynthetic functions of ACBPs**

Since qPCR showed that each VfACBP is expressed in seeds, and split ubiquitin analysis demonstrated that they interact with the VfDGATs, the VfACBPs were expressed in the seeds of transgenic plants to study the effects of VfACBP expression on seed lipid fatty acid content.

One of the primary goals of this project and the culmination of other projects on the tung pathway is to produce α-eleostearic acid in high amounts in a transgenic system. “High amounts” is defined as a sizeable percentage of α-eleostearic acid versus all other fatty acids produced. As mentioned earlier, the oil of tung consists of approximately 80% eleostearic acid (wt/wt total fatty acids). Genes involved in the production of this fatty acid were placed into transgenic plants due to its useful drying properties and industrial applications. Fatty acid methyl esters (FAME) were created by alkali catalyzed reactions between fatty acids and methanol through transesterification. The fatty acid content in the seeds of transgenic *Arabidopsis* lines was
analyzed. Essentially, there were two main approaches to expressing tung ACBPs in transgenic *Arabidopsis*. The first was to analyze the potential role of VfACBPs, when co-expressed with VfFADX in *fad3/fae1*, to determine whether these proteins increased the eleostearic acid content in seed lipids compared to the expression of VfFADX alone.

These constructs contained the *fad3/fae1* double mutant which completely diverts the tung biosynthetic pathway toward α-eleostearic acid production via a diverged desaturase, FADX. Otherwise, linolenic acid would be produced if FAD3 were available for use. FAD3 would act as a competitor for linoleic acid substrate of FADX (Dyer, et. al., 2002) and the product of FAD3, linoleic acid, is toxic when produced in the same tissues as eleostearic acid. FAE1 is an elongase; thus deleting it is expected to prevent production of very long-chain fatty acids. Also, this absence of the enzyme reduces the use of oleic acid, which could be in turn be used FAD2 to make more linoleic acid.

![Figure 3-13](image)

Figure 3-13. Bulk T<sub>2</sub> generation scatter plots of VfACBP3a and VfACBP6.

Figure 3-13 illustrates T<sub>2</sub> generation scatter plots of both VfACBP3a and VfACBP6 co-expressed with VfFADX in *fad3/fae1* versus plants expressing VfFADX alone. As the data shows,
there are no real “boosters” of eleostearic acid content when the VfACBP are introduced. So, it was imperative to investigate the effects of VfACBP co-expression on any other fatty acids in seeds.

(A)

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Avg. 6.4935 3.14025 5.02775

Std. Dev. 0.161628 0.09942 0.331329

versus

| V/FADX + VfACBP6 T$_2$ #2 | 7.231 | 2.621 | 5.932 |
| V/FADX + VfACBP6 T$_2$ #19 | 7.615 | 2.911 | 4.547 |
| V/FADX + VfACBP6 T$_2$ #24 | 7.312 | 2.789 | 5.511 |
| V/FADX + VfACBP6 T$_2$ #3  | 7     | 2.863 | 4.339 |
| V/FADX + VfACBP6 T$_2$ #4  | 6.965 | 2.783 | 4.28  |

Avg. 7.2246 2.7934 4.9218

Std. Dev. 0.263595 0.11014 0.751615

(B)

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<th>Significantly Different</th>
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Figure 3-14. Transformed lines with binary plasmid carrying VfFADX (driven by the seed-specific beta-conglycinin promoter) as compared to VfACBP6 co-expressing VfFADX T$_2$ plants with similar eleostearic acid values. Part A: Analysis of the average 16:0 and 18:0 values as compared to constructs lacking VfACBP6 to see if there was a significant difference. Individually and on average, these VfACBP6 constructs have lower 18:0 percentage values while higher 16:0 percentage values as compared to plant lines lacking VfACBP6. Part B: Student’s t-test to examine the significance of the average 16:0 and 18:0 values of VfACBP6 plants co-expressing VfFADX as compared to VfFADX lines lacking VfACBP6.

78
(A)

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**versus**

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<tr>
<td>V/FADX + V/ACBP3a T2 #30</td>
<td>7.789</td>
<td>2.937</td>
<td>6.731</td>
</tr>
<tr>
<td><strong>Avg.</strong></td>
<td><strong>7.33825</strong></td>
<td><strong>2.84775</strong></td>
<td><strong>8.02575</strong></td>
</tr>
<tr>
<td><strong>Std. Dev.</strong></td>
<td><strong>0.409827</strong></td>
<td><strong>0.078771</strong></td>
<td><strong>1.398388</strong></td>
</tr>
</tbody>
</table>

(B)

<table>
<thead>
<tr>
<th>Student's T-test</th>
<th>16:0</th>
<th>18:0</th>
<th>Eleostearic acid</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>P-values</strong></td>
<td>0.006699341</td>
<td>0.031673901</td>
<td>0.688888577</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th></th>
<th>Significantly Different</th>
<th>Slightly Significantly Different</th>
<th>Not Significantly Different</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>16:0</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>18:0</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Figure 3-15. Transformed lines with binary plasmid carrying V/FADX (driven by the seed-specific beta-conglycinin promoter) as compared to V/ACBP3a co-expressing V/FADX T2 plants with similar eleostearic acid values. Part A: Analysis of the average 16:0 and 18:0 values as compared to constructs lacking V/ACBP3a to see if there was a significant difference. Individually and on average, these V/ACBP3a constructs have lower 18:0 percentage values while higher 16:0 percentage values as compared to plant lines lacking V/ACBP3a. Part B: Student’s t-test to examine the significance of the average 16:0 and 18:0 values of V/ACBP3a plants co-expressing V/FADX as compared to V/FADX lines lacking V/ACBP3a.

Student’s t-tests were performed in order to observe any statistical significance of the results from the transgenic Arabidopsis lines that were produced. The results from both Figures 3-14 and 3-15 illustrate the differences in the 16:0 and 18:0 saturated fatty acid content of seed oil from transformed Arabidopsis V/FADX lines containing tung VfACBP6 and VfACBP3a co-expressing V/FADX as compared to V/FADX lines without VfACBP with similar eleostearic acid
values. All of the 16:0 fatty acid percentages were higher individually and collectively on average for both VfACBP6 and VfACBP3a versus FADX lines without VfACBPs. All of the 18:0 fatty acid percentages were lower individually and collectively on average for both ACBP6 and ACBP3a as compared to VfFADX plants not co-expressed with VfACBP. There was a statistically significant difference in the 16:0 and 18:0 content (P < 0.05) despite the lack of significant difference in eleostearic acid content in both constructs. Clearly, these two VfACBPs affect the 16:0 and 18:0 fatty acid content in seeds. So, these two VfACBPs have an effect on the fatty acids in tung.

Of important note is that these lines are selected by Basta herbicide resistance, and therefore it is not so simple to sort out homozygous T₃ lines. Unfortunately, there is such a small sample size produced form these lines that it is difficult to ascertain any specific information with regard to the influence of VfACBPs on eleostearic acid content in seeds. However, acyl-CoA is used in a very large number of reactions in the cell and not just in lipid synthesis. For example, they are involved directly in the Kennedy Pathway (GPAT, LPAT, and DGAT), and indirectly as in LPCAT (Yurchenko, et. al., 2009). So, it is difficult to predict based on this preliminary analysis what its role may be in lipid metabolism in tung seeds. But, there are some statistically significant differences with 16:0 and 18:0, so it seems to be altering the size and content of at least one pool of acyl-CoAs in the seeds.

The second approach to expressing tung ACBPs in transgenic Arabidopsis involved analyzing the effects of VfACBP expression on entire normal metabolism of seed FAs in general. This was accomplished by expression in wild type Arabidopsis thaliana (ecotype Columbia) which makes a number of fatty acids that are not seen in fad3/fae1 constructs. Plants were grown with either VfACBP6 or VfACBP3a expressed. Since wild type Arabidopsis does not produce
eleostearic acid, the analysis of the seed oils in these plants was used to monitor comprehensive fatty acid profile changes and composition when expressing a tung ACBP. In direct opposition to the Basta screening in the \textit{VfFADX} expressing lines, these lines used \textit{DsRed} screening used for selection, making the identification of homozygous \(T_3\) lines much easier. Essentially, all seeds chosen in the identification of homozygous lines were visualized as bright red fluorescing seeds. This is a clear-cut method that is much easier than the Basta selection method.

In figures 3-16 and 3-17, those lines that are highlighted, ACBP3a + DsRed \(T_2\) #1 and ACBP6 + DsRed \(T_2\) #2, were chosen to produce \(T_3\) lines, since their seeds were brightly red fluorescing. Seeds that were obviously fluorescent were chosen over seeds that were not as brightly red fluorescing. Figures 3-16 and 3-17 illustrate the effects of inserting \textit{VfACBP3a} and \textit{VfACBP6} into wild type \textit{Arabidopsis} plants. Looking at each line, there are several differences in the individual fatty acid contents and overall composition of \textit{VfACBP3a} and \textit{VfACBP6} as compared to the averages of wild type plants. These differences clearly illustrate that introducing \textit{VfACBP3a} and \textit{VfACBP6} has an effect on comprehensive fatty acid profiles.
<table>
<thead>
<tr>
<th>Wild type Columbia</th>
<th>16-018-0</th>
<th>18-1</th>
<th>18-2</th>
<th>18-3</th>
<th>20-1</th>
<th>20-2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Std. Dev.</td>
<td>±0.095</td>
<td>±0.089</td>
<td>±0.511</td>
<td>±0.306</td>
<td>±0.392</td>
<td>±0.327</td>
</tr>
</tbody>
</table>

Construct

<table>
<thead>
<tr>
<th>Construct</th>
<th>ACBP3a + DsRed T$_2$ #1</th>
<th>6.686</th>
<th>2.987</th>
<th>14.137</th>
<th>28.003</th>
<th>17.253</th>
<th>20.043</th>
<th>1.832</th>
</tr>
</thead>
<tbody>
<tr>
<td>ACBP3a + DsRed T$_2$ #2</td>
<td>6.829</td>
<td>2.913</td>
<td>13.205</td>
<td>27.972</td>
<td>17.850</td>
<td>19.892</td>
<td>1.987</td>
<td></td>
</tr>
<tr>
<td>ACBP3a + DsRed T$_2$ #6</td>
<td>8.362</td>
<td>3.399</td>
<td>11.773</td>
<td>30.017</td>
<td>15.847</td>
<td>17.170</td>
<td>2.497</td>
<td></td>
</tr>
<tr>
<td>ACBP3a + DsRed T$_2$ #10</td>
<td>8.889</td>
<td>3.167</td>
<td>12.563</td>
<td>32.213</td>
<td>15.360</td>
<td>15.858</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ACBP3a + DsRed T$_2$ #12</td>
<td>6.874</td>
<td>2.977</td>
<td>14.170</td>
<td>29.076</td>
<td>16.531</td>
<td>20.122</td>
<td>1.639</td>
<td></td>
</tr>
<tr>
<td>ACBP3a + DsRed T$_2$ #13</td>
<td>8.125</td>
<td>3.479</td>
<td>11.843</td>
<td>29.450</td>
<td>16.148</td>
<td>17.517</td>
<td>2.467</td>
<td></td>
</tr>
<tr>
<td>ACBP3a + DsRed T$_2$ #17</td>
<td>8.036</td>
<td>3.231</td>
<td>13.011</td>
<td>30.283</td>
<td>15.012</td>
<td>17.506</td>
<td>2.467</td>
<td></td>
</tr>
<tr>
<td>ACBP3a + DsRed T$_2$ #18</td>
<td>8.226</td>
<td>2.959</td>
<td>13.151</td>
<td>30.707</td>
<td>15.495</td>
<td>17.128</td>
<td>2.542</td>
<td></td>
</tr>
</tbody>
</table>

ACBP3a + DsRed T$_3$ #1-18 | 6.673 | 2.619 | 13.583 | 29.246 | 16.775 | 20.662 | 1.994 |
| ACBP3a + DsRed T$_3$ #1-196.618 | 2.609 | 13.436 | 27.800 | 18.168 | 20.848 | 1.980 |
| ACBP3a + DsRed T$_3$ #1-236.532 | 2.664 | 13.138 | 27.858 | 17.869 | 20.952 | 2.144 |
| ACBP3a + DsRed T$_3$ #1-246.650 | 2.687 | 13.672 | 29.411 | 16.538 | 20.861 | 1.861 |
| ACBP3a + DsRed T$_3$ #1-256.673 | 2.692 | 13.045 | 27.989 | 17.918 | 21.081 | 1.972 |
| ACBP3a + DsRed T$_3$ #1-267.711 | 3.536 | 12.569 | 28.976 | 15.989 | 19.111 | 2.384 |

Figure 3-16. Wild type *Columbia Arabidopsis thaliana* plant lines expressing VfACBP3a, in the T$_2$ and T$_3$ generations, as compared to plant lines lacking VfACBP3a. Each plant line shown above is representative of lines that differ markedly in fatty acid content from plant lines lacking VfACBP3a. This difference is determined by comparing the individual 16-0, 18-0, 18-1, 18-2, 18-3, 20-1, and 20-2 values of each T$_2$ and T$_3$ plant line to the individual average values of the plant lines lacking VfACBP3a.
Wild type *Columbia* 16-018-0 18-1 18-2 18-3 20-1 20-2

<table>
<thead>
<tr>
<th>Construct</th>
<th>ACBP6 + DsRed T3</th>
<th>ACBP6 + DsRed T3</th>
<th>ACBP6 + DsRed T3</th>
<th>ACBP6 + DsRed T3</th>
<th>ACBP6 + DsRed T3</th>
<th>ACBP6 + DsRed T3</th>
<th>ACBP6 + DsRed T3</th>
<th>ACBP6 + DsRed T3</th>
<th>ACBP6 + DsRed T3</th>
<th>ACBP6 + DsRed T3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Averages</td>
<td>7.3043±0.089</td>
<td>28.504±0.051</td>
<td>16.877±0.306</td>
<td>19.722±0.392</td>
<td>2.389±0.327</td>
<td>1.09±0.127</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Std. Dev.</td>
<td>± 0.095±0.089</td>
<td>± 0.051±0.306</td>
<td>± 0.306±0.392</td>
<td>± 0.327±0.127</td>
<td>± 0.112±0.127</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

ACBP6 + DsRed T3 #1 17.700 3.154 13.400 29.064 16.028 18.527 2.451
ACBP6 + DsRed T3 #2 7.360 2.921 11.843 28.272 17.269 19.789 2.628
ACBP6 + DsRed T3 #3 7.429 2.619 11.337 28.774 17.670 20.362 2.637
ACBP6 + DsRed T3 #4 6.777 2.878 12.417 27.242 17.417 21.608 2.408
ACBP6 + DsRed T3 #5 7.135 3.119 12.597 27.065 16.963 21.353 2.583
ACBP6 + DsRed T3 #6 7.046 3.142 12.871 27.300 16.756 21.388 2.494
ACBP6 + DsRed T3 #7 6.546 2.616 18.064 26.735 14.322 17.952 1.898
ACBP6 + DsRed T3 #8 7.280 3.180 12.650 27.407 16.986 20.624 2.531
ACBP6 + DsRed T3 #9 7.281 3.138 13.106 27.622 16.988 21.120 2.465

ACBP6 + DsRed T3 #2-16.713 2.839 13.809 27.272 18.428 20.820 1.629
ACBP6 + DsRed T3 #2-26.738 2.819 14.565 27.786 17.757 20.128 1.839
ACBP6 + DsRed T3 #2-47.139 2.808 12.664 27.720 17.918 21.260 2.197
ACBP6 + DsRed T3 #2-76.767 2.889 13.553 27.375 18.613 20.807 1.499
ACBP6 + DsRed T3 #2-96.692 2.797 14.281 27.823 18.191 20.130 1.893
ACBP6 + DsRed T3 #2-106.843 2.681 13.831 26.809 19.683 20.100 1.782
ACBP6 + DsRed T3 #2-116.649 2.812 13.754 27.500 18.347 20.475 2.021
ACBP6 + DsRed T3 #2-156.324 2.401 13.793 27.026 19.532 20.612 1.899

Figure 3-17. Wild type *Columbia Arabidopsis thaliana* plant lines expressing VfACBP6, in the T2 and T3 generations, as compared to plant lines lacking VfACBP3a. Each plant line shown above is representative of lines that differ markedly in fatty acid content from plant lines lacking VfACBP6. This difference is determined by comparing the individual 16-0, 18-0, 18-1, 18-2, 18-3, 20-1, and 20-2 values of each T2 and T3 plant line to the individual average values of the plant lines lacking VfACBP6.

Figures 3-16 and 3-17 contain small arrows illustrating the changes in individual saturated or unsaturated fatty acid contents in each construct. This helps to display, in more detail, the effects that VfACBP3a and VfACBP6 have on the comprehensive fatty acid profiles upon their expression in wild type *Arabidopsis* plants.

The VfACBP3a T2 constructs in figure 3-15 appear to vary considerably; however, 18:2 fatty acid content seems to increase with the introduction of VfACBP3a, with the exception of two constructs. The T3 plants, with the exception of 18:2 and 18:3 fatty acids content, exhibit uniform changes. There is a decrease in 16:0, 18:0, and 20:2 content with an increase in 18:1 and 20:1 fatty acids as compared to the wild type plants lacking VfACBP3a. The introduction of
VfACBP3a shifts 16:0, 18:0, and 20:2 production to the production of 18:1 and 20:1 fatty acids in the T₃ generation.

In the case of VfACBP6 T₃ constructs, there is a uniform change in each construct from the wild type plants not containing VfACBP6. All VfACBP6 constructs’ 16:0, 18:0, 18:2, and 20:2 content decreased from the wild types not containing VfACBP6, while the 18:1, 18:3, and 20:1 content increased. Introducing VfACBP6 appears to shift the production of 16:0, 18:0, 18:2, and 20:2 to the production of 18:1, 18:3, and 20:1 in the T₃ generation. The T₂ constructs vary considerably in 18:0, 18:3, 20:1, and 20:2, while 16:0, 18:1, and 18:2 content shows the same change as the T₃ plants (decrease, increase, and decrease).

Comparing the results of VfACBP3a and VfACBP6, with the exception of 18:3 in the constructs for VfACBP3a, either VfACBP appeared to shift the production of fatty acids toward the 18:1 and 20:1 unsaturated fatty acids. Both VfACBP3a and VfACBP6 shifted saturated fatty acid production to produce certain unsaturated fatty acids. This clearly shows the shift toward the production of certain unsaturated fatty acids as compared to the wild types not expressing VfACBPs. Since tung produces α-eleostearic acid (18:3), the shift upon the introduction of VfACBP6 was especially intriguing.
Wild Type

<table>
<thead>
<tr>
<th>Columbia</th>
<th>16-0</th>
<th>18-0</th>
<th>18-1</th>
<th>18-2</th>
<th>18-3</th>
<th>20-1</th>
<th>20-2</th>
</tr>
</thead>
</table>

VfACBP3a T2

<table>
<thead>
<tr>
<th>16-0</th>
<th>18-0</th>
<th>18-1</th>
<th>18-2</th>
<th>18-3</th>
<th>20-1</th>
<th>20-2</th>
</tr>
</thead>
</table>

VfACBP3a T3

<table>
<thead>
<tr>
<th>16-0</th>
<th>18-0</th>
<th>18-1</th>
<th>18-2</th>
<th>18-3</th>
<th>20-1</th>
<th>20-2</th>
</tr>
</thead>
</table>

VfACBP6 T2

<table>
<thead>
<tr>
<th>16-0</th>
<th>18-0</th>
<th>18-1</th>
<th>18-2</th>
<th>18-3</th>
<th>20-1</th>
<th>20-2</th>
</tr>
</thead>
</table>

VfACBP6 T3

<table>
<thead>
<tr>
<th>16-0</th>
<th>18-0</th>
<th>18-1</th>
<th>18-2</th>
<th>18-3</th>
<th>20-1</th>
<th>20-2</th>
</tr>
</thead>
</table>

---

**Figure 3-18.** Average values of VfACBP3a and VfACBP6 T2 and T3 lines expressed in wild type *Columbia* plants as compared to wild type *Columbia* plants lacking VfACBP3a and VfACBP6.

Additionally, on average (Figure 3-18), T2 plants showed an increase in 18:1 and 20:1 with a decrease in 16:0, 18:0, 18:2, 18:3, and 20:2 content. The T3 plants showed an increase in 18:1, 18:3, and 20:1, with a subsequent decrease in 16:0, 18:0, 18:2, and 20:2. Again, the T3 plants showed similar changes as illustrated in the individual statistical measurements (Figure 3-17), that being a shift to one very long chain monounsaturated fatty acid and two long chain unsaturated fatty acids.

Another interesting test involved the analysis of the amounts of red seeds produced in the T2 and T3 generations of the wild type *Arabidopsis* constructs expressing VfACBP3a and VfACBP6. In figure 3-19, VfACBP6 had a total of 64 brown seeds seen in a pool of 270 seeds total (24%). A single transgene insertion should result in T2 seed pools with 75% red seed, and 25% brown. Two copies would be seen at 94% (15/16) red, and 6% brown. This is consistent with a single transgene insertion of VfACBP6. Figure 3-20, on the other hand, illustrates VfACBP3a as having 70 brown seeds out of a pool of 180 seeds (39%). This is a very large...
amount of brown seeds seen in the T₂ generation. This anomaly was probably due to subjectivity of the perceived lack of sensitivity of the light source and filter combination that was used in the procedure. A new type of green light flashlight and red filter goggles that is much more powerful has recently been purchased and these results will be re-evaluated.

<table>
<thead>
<tr>
<th>VfACBP6</th>
<th>Brown/Total</th>
<th>Homozygous (100% Red Seeds)</th>
<th>Notes</th>
</tr>
</thead>
<tbody>
<tr>
<td>T₂ #2</td>
<td>64/270 (24%)</td>
<td>T₃ 2-1</td>
<td>Y</td>
</tr>
<tr>
<td></td>
<td></td>
<td>T₃ 2-2</td>
<td>N</td>
</tr>
<tr>
<td></td>
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<td>T₃ 2-3</td>
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<td>T₃ 2-4</td>
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<td>T₃ 2-5</td>
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<td>T₃ 2-15</td>
<td>Y</td>
</tr>
<tr>
<td></td>
<td></td>
<td>100% Red/Total 11/15 (73%)</td>
<td></td>
</tr>
</tbody>
</table>

Mostly brown

Figure 3-19. Brown and red seeds observed in T₂ and T₃ seeds of VfACBP6.
<table>
<thead>
<tr>
<th>VfACBP3a</th>
<th>Brown/Total</th>
<th>Homozygous (100% Red Seeds)</th>
<th>Notes</th>
</tr>
</thead>
<tbody>
<tr>
<td>T2 # 1</td>
<td>70/180 (39%)</td>
<td>T3 1-1</td>
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</tr>
<tr>
<td></td>
<td></td>
<td>T3 1-2</td>
<td>Y</td>
</tr>
<tr>
<td></td>
<td></td>
<td>T3 1-3</td>
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<td>T3 1-4</td>
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<td>T3 1-22</td>
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<td></td>
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<td>T3 1-23</td>
<td>N</td>
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<td>T3 1-29</td>
<td>N</td>
</tr>
<tr>
<td>100%</td>
<td>Red/Total</td>
<td>7/29 (24%)</td>
<td>Mostly brown</td>
</tr>
</tbody>
</table>

Mostly brown

Figure 3-20. Brown and red seeds observed in T2 and T3 seeds of VfACBP3a.

It would be expected for all of the T3 seeds to be 100% red homozygous if a T2 line is chosen that has been shown to contain (statistically) a single insertion. Each T3 line was measured in the same way as the singular T2 line that was chosen to plant the T3 generation. A pool of seeds was analyzed for red seeds versus brown ones. These pools of seeds were analyzed to see if every seed in the pool was bright red fluorescent with no brown seeds present. So, any row labeled with a Y (for yes) represents a pool of seeds that is 100% red. Unfortunately, based
on the results shown in both figures 3-17 and 3-18, the production of completely red homozygous seeds from the chosen T₂ lines did not produce 100% homozygous seeds. The T₃ generation of seeds in VfACBP6 chosen from the second line of T₂ seeds, shows 73% homozygous red seeds, and a set of seeds (2-10) were seen as containing mostly brown seeds. Likewise, only 24% VfACBP3a constructs contained 100% red seeds. Again, re-evaluation using a more sensitive light source and filter is necessary in the near future. In addition, Southern blots may be performed to confirm or deny the possibility of the single insertion events that were statistically shown here in the T₂ seed pools.
Discussion

Overview

Acyl-CoA Binding Proteins (ACBPs) have been analyzed in many eukaryotic systems for approximately 25 years and have been shown to play a variety of roles as described above. These analytical processes reveal that an analysis of components with the presumed abilities of ACBP should be sought after in the tung lipid metabolic pathway. Many other components within this pathway have been investigated (Shockey, et. al., 2006). Coenzyme A has an established role in the synthesis and oxidation of fatty acids and other lipids; thus, a protein capable of binding long chain acyl coenzyme A esters is relevant to analyze since it may participate in several aspects of seed lipid metabolism.

Regardless of the category of biological study, whether it includes cell biology, biochemistry, or molecular biology, there have been major advances that have come from extensive studies of biological membranes. These membranes not only create a barrier to the outside of the cell, but also delimit the various subcellular organelles contained within the cell. The fractionation of subcellular organelles along with the investigations of biochemical compartmentalization of enzymatic functions (deDuve, et al., 1965) along with the propagation of the fluid mosaic model (Singer and Nicholson, 1972) have illustrated the importance of proteins in membranes.

In one classic example, the enzyme ATPase, which catalyzes the decomposition of adenosine triphosphate (ATP) into adenosine diphosphate (ADP) and a free phosphate ion. It requires a lipid bilayer environment for its activity. It has now become apparent through several recent studies that many other enzymes demand the proper lipid environment to provide their function(s) (Ohlrogge and Browse, 1995). For example, E. coli glycerol-3-phosphate
acyltransferase is inactive in a homogeneous state, but re-attained its activity upon the addition of *E. coli* phospholipids, mixtures of phospholipids, or pure phospholipids (Scheideler and Bell, 1989).

Due to their increasing role as a major raw resource for the production of food and non-food products, vegetable oils have become one of the more industrially important resources in the chemical industry (FAOSTAT, 2007). Some of the more prominent sources of vegetable oils for industrial applications include sunflower, rape, soybean, and oil palm. Moreover, the lipids that compose their seeds constitute ≥40% of the dry weight of the seeds (FAOSTAT, 2007, Biermann et al., 2000). More than 500 fatty acids, combined into an untold number of natural triglycerides have been identified in plant species (Aitzetmüller, et. al., 2003). These findings, along with the highly utilized sources of plant lipids, make it evident that there is a great importance in the genetic engineering of plant lipids. Unfortunately, one of the major obstacles in putting the information on genetic engineering of plant lipids into practical application is the understanding of the biochemical pathways involved in the production of the lipids, and in the temporal and tissue specific expression of the genes. Finally, the enzymes in the pathways must also channel fatty acids into their necessary destination(s).

Little information is available regarding the structures of many of the enzymes involved in complex lipid biosynthesis in part due to the problems encountered in purifying membrane-bound enzymes (Browse and Sommerville, 1991). One of the approaches involved in countering this, however, is generating mutants of lipid metabolism (Browse and Sommerville, 1991). For example, mutants with alterations in membrane lipid composition have been used to study the structural and adaptive roles of lipids (Browse and Sommerville, 1991). In addition, gene probes that are derived from soluble proteins can be used to clone membrane-bound counterparts of
fatty acid synthesis, since the crucial reactions of fatty acid synthesis are conserved (Heinz, 1993). Thus, it stands to reason that certain requirements of fatty acids in the biosynthetic process can be tested through mutational and/or transformational studies. An example of this comes from an experiment performed for trans Δ3-hexadecanoic acid, through the determination of a mutation at a single locus, \( fadA \). The carriers of this mutation lack trans-16:1 (Hugly, et. al., 1991). This is an acyl chain that performs a role in an aspect of photosynthesis; however, its loss did not appear to have an effect on the function of chloroplasts.

Transformational and mutational studies can also be extended to examine the functional importance of particular lipid classes. Also, the transcriptional regulation of genes involved in the lipid classes can be studied due to the availability of cDNAs and clones for fatty acid synthase components of plants. Unfortunately, there are many complications at the biochemical level, such as the interactions of fatty acid synthase components \( \textit{in vivo} \) (if there are even any), the nature of substrate entering and the product produced from the plastid, and several other unresolved issues (Browse and Sommerville, 1991). It is imperative that the major unanswered questions be addressed so genetic engineering of lipids, including those processes involved in the storage of lipids, like the tung biosynthetic pathway, can provide important applications in industry.

\textbf{An in-depth look at acyl-CoA binding proteins and their potential influence(s) in tung}

The most predominant form of acyl-CoA binding protein (ACBP) as has been observed in various eukaryotes, is a highly conserved, approximately 10 kDa cytosolic protein (Chye, 1998, Gersuk, et al., 1995, McDonough, et. al., 1992, Mogensen, et. al., 1987). It was initially identified and analyzed in mammals as a neuropeptide that is capable of inhibiting diazepam, a drug that is used for treating a variety of ailments, including insomnia and anxiety, by binding to
the GABA (γ-aminobutyric acid) receptor (Gersuk, et. al., 1995). Following this observation, many subsequent studies have identified ACBP as binding to long-chain acyl-CoA esters, those of length from 12 to 22 carbons, with both high specificity and affinity (Ivell, et. al., 2000, Kragelund, et. al., 1993). A wide array of evidence has indicated that ACBP performs as an intracellular acyl-CoA transporter and an acyl-CoA pool former (Faergeman, et. al., 2007). Yeast ACBP has been identified, and is essential for the elongation of fatty acids, synthesis of sphingolipids, sorting of proteins, and vesicular trafficking (Schjerling, et. al., 1996). The evidence provided by these studies in addition to many others demonstrate a crucial role for ACBP in binding and transporting acyl-CoA (Faergeman, et. al., 2007).

Previously, it was determined that bovine ACBP’s structure, as examined by NMR, was a four α-helix bundle protein (Kragelund et. al., 1993, Faergeman, et. al., 1996, Andersen et. al., 1991). Several chordate ACBP proteins have been analyzed to reveal a substantial number of conserved residues that are either hydrophobic or are found to be involved in binding of an acyl-CoA ester within its binding site (Faergeman, et. al., 1996, Andersen et. al., 1991). A majority of the conserved hydrophobic residues engage in the propagation of three mini-cores within the structure of the ACBP, producing a network of interactions between the helixes of the ACBP (Andersen et. al., 1991). Whether this structure shares any similarity to tung ACBP6 has yet to be determined, but it provides a basic framework from which to work, especially when deciphering the binding preferences, and how or if these preferences influence the role(s) of tung ACBP6.

The presence of large gene families within a single species encoding different functional paralogs of ACBP has been noted. In mammals, in addition to the protein initially identified as ACBP, which was initially identified in the human liver (L-ACBP), homologous unique ACBP-
like cDNAs have been characterized in the testes (T-ACBP) and brain (B-ACBP) (Taskinen, et. al., 2007. Two unique ACBP-like genes have been determined specifically in Digitalis lanata (Metzner, et. al., 2000), and six in Arabidopsis (Chye, 1998). Also, multiple inactive ACBP pseudogenes have been characterized in various genomes of mammals, including those in rat and human (Taskinen, et. al., 2007).

In addition to ACBP occurring as an independent protein, many ACBP-like domains have been characterized in several large, multifunctional proteins found in various eukaryotic species. These proteins include large membrane-associated proteins with N-terminal ACBP domains, multifaceted enzymes containing both ACBP and peroxisomal enoyl-CoA and 2-enoyl-CoA isomerase domains, and proteins containing an ACBP domain along with ankyrin repeats (Taskinen, et. al., 2007, Burton, et. al., 2005, Chye, et. al., 2008).

In humans, long chain acyl-CoAs (LCACoA ) were initially considered to be an intermediate in lipid metabolism; however, recent studies have indicated that LCACoA have become increasingly recognized as modulators of a large range of functions in cells. The properties involved in regulation necessitate a strict control of the concentration of intracellular LCACoA in a manner that simultaneously allows much variation in the lipogenesis rate and β-oxidation and a sufficient supply of LCACoA for specific purposes such as the acylation of proteins. Despite many intracellular proteins having been reported to bind LCACoA, including liver fatty acid binding protein (L-FABP) and sterol carrier protein 2 (SCP2), currently, ACBP is characterized as the primary intracellular acyl-CoA binding protein (Taskinen, et. al., 2007). Since many of the ACBPs found in eukaryotic systems provide various functions to their specific organisms, it is reasonable to hypothesize that ACBPs may also have some influence on not just seed specific lipid metabolism in tung, but other functions as well. ACBPs can be hypothesized...
to play a role in the regulation, bindings, and transportation involved throughout cellular metabolism. The information provided here provides strong reasons to pursue the study of ACBPs in tung.

Much of molecular biology involves comparing sequences, structures, and functions of genes and the proteins they encode. This information is then used to compare genes and proteins from one organism to another. Many of the lipid metabolic functions of ACBPs are conserved in other organisms, such as in *Arabidopsis thaliana* (Chye, et. al., 1998). These functions may or may not be similar in tung, but it would be reasonable to investigate any potential functions given the importance of ACBPs in other organisms’ lipid metabolic pathways. Although, not every ACBP will perform the same function(s) in one organism as it does another, the structures and functions of previously characterized ACBPs are still relevant. At the very least, tung ACBPs can be experimented upon in similar manners to other ACBPs to observe if the results attained are in any way similar.

**Identification of Acyl-CoA binding proteins in *Vernicia fordii***

Scientists around the globe are working diligently to sequence and assemble the genomes of a multitude of organisms, for a variety of crucial reasons. Obtaining a sequence of a genome and identifying a complete set of genes are often two necessary goals of sequencing projects; however, the most crucial set of information revolves around an understanding of gene expression. The understanding of when a gene is expressed allows for the examination of its expression under both normal and altered conditions.

An Expressed Sequence Tag (EST) is representative of a portion of a complete cDNA which can be utilized to aid in the identification of unknown genes and in the mapping of their positions in a genome (Mount, 2004). As EST technology continues to improve, the time
necessary to locate and describe a gene in great detail quickly declines. ESTs allow researchers a relatively cheap and fast path to the discovery of unique genes. With this discovery comes the information provided to analyze gene expression and regulation, along with the construction of genomic maps.

The ease of access and use as a gene discovery tool produced by ESTs is due to the organization provided via a searchable database that can also provide access to certain genome data. This utility, along with the speed and cost of generating data, provides the generation of hundreds of thousands of ESTs available for public use. Upon the generation of an EST, researchers may submit their tags to a database called GenBank, which is the NIH sequence database in operation by NCBI.

As mentioned in the results section, two of the tung ACBPs were identified from EST sequencing project: VfACBP6 and VfACBP3a. Initially, these ACBPs were known as a soluble ACBP (VfACBP6) and simply a larger, possibly membrane-associated ACBP (VfACBP3a). The nomenclature provided by Chye and her colleagues, through various experiments on Arabidopsis thaliana ACBPs, has identified 6 unique ACBPs (Chye, 1998). The tung ACBPs were named using Chye’s nomenclature.

As mentioned, the other two ACBPs from tung were identified from data analysis via pyrosequencing, a more contemporary counterpart to EST. Upon the completion of the process, the nucleotide sequence can be determined from a Pyrogram trace by visualizing signal peaks (Weber, et. al., 2007, Yang, et. al., 2010).

The data from these two processes, EST and pyrosequencing, was received in the form of a large Microsoft Word document. The data provided is used to search and compare the
sequences in this file to those in an online database, such as GenBank. In addition, the BLAST tool is used to compare sequences and make reasonable judgments of the sequences on-hand.

As was described on pages 68-71 and Figures 3-1 and 3-2 of the Results section, VfACBP3a and VfACBP3b are not very similar in their nucleotide or protein sequences. The two proteins are also of different lengths. They were both found to be sequentially similar to AtACBP3. VfACBP3b, however, was most similar to *Ricinus communis* (castor) ACBP, showing the shared Euphorbiaceae (spurge) lineage of tung and castor. This shows that orthologs of VfACBP3b do exist in other plants. This presence in castor but absence in *Arabidopsis thaliana* of an orthologous ACBP3b suggests that the gene duplication event that gave rise to ACBP3a and ACBP3b came about after the split of the forbearers of *Arabidopsis* and tung.

Rapid Amplification of cDNA Ends (RACE) and genome walking to obtain full length Open Reading Frames (ORFs) of VfACBPs

Part of the sequences of each VfACBP were found through EST and pyrosequencing. Genome walking and RACE techniques were used to provide the sequence of an RNA transcript from these known sequences to complete the ORFs. Using DNA of interest, genome walking constructs pools of uncloned, adaptor-ligated genomic DNA fragments, termed libraries. RACE, on the other hand, produces a cDNA copy of an RNA sequence of interest, via reverse transcription, followed by amplification of cDNA copies. These cDNA copies were sequenced afterward. If these sequences are long enough, they may map to a full-length mRNA that has been already described.

The initial step in 5’RACE was to use reverse transcription which generated a cDNA copy of a region of an RNA transcript. An unknown end portion, in this case the 5’ end, of a transcript was copied utilizing a known sequence from within the transcript. The copied region
was bounded by the known sequence, at the 5' end. From this point, mRNA was used as a template in cDNA synthesis. The principal difference between 3’RACE and 5’RACE, aside from the 3’end of the sequence in question, is that 3’RACE takes advantage of the poly(A) tail of mRNA.

As was mentioned, 5’RACE was performed using 3’RACE parameters, including SuperScript™ III reverse transcriptase. Perhaps the higher rate of success using the SuperScript™ III reverse transcriptase as opposed to the SuperScript™ II reverse transcriptase lies in some of the principal performance differences provided by the different enzymes. Fidelity and processivity of the two enzymes were shown to be no different from one another, but the specific activity is 25% higher in SuperScript™ III reverse transcriptase, the half-life of SuperScript™ III reverse transcriptase is 35-fold longer, and SuperScript™ III reverse transcriptase produces very strong bands in similar reactions that SuperScript™ II reverse transcriptase has catalyzed that only produce faint bands (http://tools.invitrogen.com/content/sfs/productnotes/F_071215_Superscript%20III%20Enzyme%20RD-MKT-TL-HL.pdf). Thus, it stands to reason that the SuperScript™ III reverse transcriptase provided a much greater advantage in catalyzing the 5’RACE first strand synthesis reaction.

Both of the enzymes are a point mutant of Moloney murine leukemia virus RT (M-MLV RT). Much like M-MLV, they are DNA polymerases that synthesize complementary DNA strands from single stranded DNA, RNA, or RNA:DNA hybrids; however, compared with wild type RTs, the SuperScript RTs deliver higher yields of full-length cDNA. Both have been engineered to reduce RNase H activity and provide an increase in thermal stability. The enzymes are best used to synthesize cDNA at a temperature range of 42 to 55°C. Because they are not
significantly inhibited by ribosomal and transfer RNA, they produce first-strand cDNA from total RNA preparations (http://tools.invitrogen.com/content/sfs/productnotes/F_071215_Superscript%20III%20Enzyme%20RD-MKT-TL-HL.pdf).

**Tissue specific expression of VfACBP through quantitative real-time PCR**

Quantitative real-time polymerase chain reaction (qPCR) is a technique based on classic PCR, which amplifies and quantifies a DNA molecule of interest at the end of the reaction. qPCR allows for simultaneous detection and quantification (as the absolute number of copies or relative amount upon normalization to a DNA input or additional normalizing genes) of one or more target sequences in a DNA sample. There are two methods used in qPCR, but the method applied in this research was through the use of a fluorescent dye, SYBR Green, that intercalates with any double-stranded DNA (dsDNA).

In this study, qPCR was used to provide quantitative measurements of tung ACBP transcript abundance and to determine how the expression of these ACBPs change over time in seed development and other tissues. These data were used to compare the expression patterns of the VfACBPs to other known components of the tung lipid metabolic pathway that exhibit specific expression patterns. Comparing known components to the VfACBPs allows for an understanding of some of their functions.

Previously, tung DGAT2 and FADX, two components with known roles in the tung metabolic pathway, were analyzed by qPCR (figure 3-4). The expressions of these were shown to coincide with the peak of TAG accumulation (Shockey, et. al., 2006). Each VfACBP also exhibited unique patterns and levels of expression, as seen in Figure 3-9. One aspect of their expression that is commonly seen amongst each of them, however, is that they generally have
increased expression in mid-summer months, first in July and then later in late August. Essentially, in a sequential manner, each of the VfACBPs are expressed at low levels in the earliest days of summer then, expression rises in mid-summer, lowers again, and rises closer to the fall. These results show that the VfACBPs are specifically expressed at certain times, and this expression can be lowered or raised. What this means for the potential roles of each VfACBP is unknown, but the relevance of the expression pattern is consistent with peak TAG accumulation. One interesting result is the expression patterns of each VfACBP in the leaf and flower tissues. Both VfDGAT2 and VfFADX are not expressed in these tissues. Thus, these data show a unique expression pattern for VfACBPs.

In a 2002 study, a contrapuntal network of gene expression was observed during Arabidopsis seed filling. In this case, contrapuntal refers to two peaks of activity from different sets of proteins and enzymes during Arabidopsis seed development; one early and one late. cDNA microarrays were used to examine changes in gene expression during Arabidopsis seed development and to compare wild-type and mutant wrinkled1 (wri1) seeds that have an 80% reduction in oil. Between 5 and 13 days after flowering, a period preceding and including the major accumulation of storage oils and proteins, ~35% of the genes on the array changed at least twofold, but a larger fraction (~65%) showed little or no change in expression. Genes whose expression changed most tended to be expressed more in seeds than in other tissues. Genes related to the biosynthesis of storage components displayed unique temporal expression patterns. For example, a number of genes encoding core fatty acid synthesis enzymes showed a bell-shaped expression 5 and 13 days after flowering. In contrast, the expression of storage proteins, oleosins, and other known abscisic acid–regulated genes increased later and remained high. Genes for photosynthetic proteins followed a pattern very similar to that of fatty acid synthesis
proteins, implicating a role in CO₂ fixation and the supply of cofactors for oil synthesis. Expression profiles of key carbon transporters and glycolytic enzymes reflected shifts in flux from cytosolic to plastid metabolism. Despite major changes in metabolism between wri1 and wild-type seeds, ~1% of gene expression levels differed by more than twofold, and most of these were involved in central lipid and carbohydrate metabolism. Thus, these data define in part the downstream responses to disruption of the WRI1 gene (Ruuska, et. al., 2002).

In summary, there were two peaks of activity from different sets of proteins and enzymes during Arabidopsis seed development; one early and one late. The tung ACBPs as shown here by qPCR have two peaks of expression during seed development. Perhaps, there is a contrapuntal gene expression pattern occurring and VfACBPs may be examples of genes that are expressed during both waves.

Looking at Figure 3-9, VfACBP3a is similar to VfACBP6 in that it is expressed at its highest in leaf and exhibits some expression in flower as well. Again, like all of the other proteins analyzed in figures 3-4 through 3-8, it exhibits a bimodal expression pattern, with a rise in expression around mid-July, with a subsequent decrease, followed by an increase near the fall. Also, like each VfACBP, it expresses in leaf and flower tissues, which is unique from VfDGAT2 and VfFADX.

Interestingly, VfACBP3b exhibits the greatest differences in expression levels as compared to every other protein analyzed via qPCR. In some cases, it expresses upwards of over 30 times as much as other VfACBPs. For example, at July 14th, July 21st, and September 1st, it is expressed at a higher level than any other VfACBP, VfDGAT2, or VfFADX at any point in time. This means that VfACBP3b can be the highest expressing VfACBP, and can also express much higher than VfDGAT2 and VfFADX. Despite this, it expresses at very low levels in other times,
especially at June 23\(^{\text{rd}}\), June 30\(^{\text{th}}\), and July 7\(^{\text{th}}\). \(Vf\)ACBP3b is expressed anywhere from 16 to 30 times less at these points than July 14\(^{\text{th}}\), July 21\(^{\text{st}}\), and September 1\(^{\text{st}}\). Clearly, there is a need to increase the expression of \(Vf\)ACBP3b in a dramatic fashion and then decrease in a similar scale; however, the reason for this is unknown. It does not express very highly in leaf or flower tissues as compared to the times it is expressed highly. Again, there is a dramatic difference in expression levels. It is, however, expressed comparably in flower tissues to all of the other \(Vf\)CBPs. There is just a huge change in expression levels as compared to the other tissues its expressed in. It is similar to the expression in leaf and flower tissues as \(Vf\)DGAT2 and \(Vf\)FADX in that those tissues are among the lowest \(Vf\)ACBP3b is expressed.

\(Vf\)ACBP4 exhibits high expression in flower and low in leaf as compared to its own expression levels. It expresses at its highest in the late summer days, especially September 1\(^{\text{st}}\). Its initial rise in expression appears to come about a little earlier than the other \(Vf\)ACBPs, with its two highest points being at July 7\(^{\text{th}}\) and July 14\(^{\text{th}}\). It is also expressed at low levels in leaf tissues.

\(Vf\)ACBP6 has a high expression, relative to its overall expression in other tissues, in leaf tissues. It is not expressed highly in flowers. Its initial onset of expression is the latest of the \(Vf\)ACBPs, with its highest expression at July 28\(^{\text{th}}\) in the first “peak” of the bimodal pattern exhibited by all the \(Vf\)ACBPs and \(Vf\)DGAT2 and \(Vf\)FADX. \(Vf\)ACBP6, as presented in various other organisms, is known to play a variety of roles. Perhaps its versatility is exhibited in tung as well, but it is clear that its time of expression is specific. It is, like the other \(Vf\)ACBPs, expressed in leaves and flowers though, illustrating its general tissue expression pattern.

In summation, each of the \(Vf\)ACBPs is expressed at differing levels at specific times. They are all expressed, however, in leaves, flowers and seeds. Despite the lack of tissue
specificity, they are all expressed at different levels in these tissues, each displaying unique expression patterns.

**Split ubiquitin as a sensor of protein interactions: qualitative plate assays**

Split ubiquitin yeast two-hybrid analysis is a technique used to discover protein:protein interactions by testing for physical interactions between two proteins. These protein:protein interactions are used as a way of learning role(s) of one protein by observing if it rubs up against another protein with a known role.

Positive controls for these experiments were designed so that a protein is expressed as a fusion with the wild-type Nub sequence, NubI. NubI has a high affinity for Cub and the reconstitution of ubiquitin is not reliant upon the physical interaction of two fusion proteins being analyzed. On the other hand, fusion of a protein with the mutated version of Nub, NubG, resulted in a fusion protein that has a low affinity for Cub. The Cub and NubG domains stay separated unless they are brought in close proximity by two fusion proteins interacting. This allows for the interaction of Cub and NubG which reconstitutes ubiquitin thus allowing release of the reporter protein LexA for reporter gene activation.

The interactions shown in the results section indicate interactions between all tung ACBPs and the two isozymes of VfDGAT: DGAT1 and DGAT2. Both VfDGAT1 and VfDGAT2 catalyze the formation of triglycerides from diacylglycerol and acyl-coA (Shockey, et. al., 2006). Even though both isozymes catalyze similar reactions, they have no sequence homology to one another (Shockey, et. al., 2006). These results show an interaction between VfDGAT and the VfACBPs, but how the interaction occurs and in what orientation is not clear. It is unknown what role, if any, this interaction has in the plant. Normally, the quadruple knockout plates in the dilution assay are allowed to grow at 30°C for 72 hours and then the plates’ pictures are taken
and recorded. Interestingly, the interactions between the VfACBPs and the VfDGATs were so strong, that the plate dilution assays showed cell growth after only 24 hours on quadruple knockout plates and the spots of cell growth did not dramatically increase in diameter after that amount of time. All non-interacting combinations did not show any cell growth at all even after 72 hours. This strength and weakness of interactivity was also seen later in the β-galactosidase assays, through the rapid yellowing of the solution, which is representative of a positive interaction.

As seen in some of the Arabidopsis ACBPs, like ACBP4 and ACBP5 that contain kelch motifs allowing for protein-protein interactions, it is difficult to hypothesize how VfACBPs and VfDGATs would interact based upon the different components comprising the different proteins. Both (His)6-AtACBP4 and (His)6-AtACBP5 bind [14C]oleoyl-CoA with high affinity, [14C]palmitoyl-CoA with lower affinity and do not bind [14C]arachidonyl-CoA. Hence, these AtACBPs with kelch motifs have functional acyl-CoA-binding domains that bind oleoyl-CoA. Their predicted cytosol localization suggests that they could maintain an oleoyl-CoA pool in the cytosol or transport oleoyl-CoA from the plastids to the ER in plant lipid metabolism (Chye, et. al., 2004). Likewise, regarding the larger ACBPs from tung, there exists a possibility of an additional component that drives interactivity.

In addition, some DGATs have suspected acyl-CoA binding motifs (Weselake, et. al., 2000). In the 2000 study by Weselake, et. al., the fragment, BnDGAT1(1-116)His6, interacted with [1-14C]oleoyl-CoA, suggesting that the N-terminal region of BnDGAT1 may have a role in binding cellular acyl-CoA. Also, some residues in Saccharomyces cerevisiae ACBP have been mapped to the area near the thioester bond (Knudsen, et. al., 1994). There is a possibility that these two areas, the N-terminal region that binds acyl-CoA on BnDGAT and the residues near
the thioester bond in ScACBP, may interact. Future experiments would include making split ubiquitin constructs containing only these regions in VfDGATs and VfACBPs. The process seen in the studies presented above could then be repeated, but with these new constructs to further identify binding capabilities of VfDGATs and VfACBPs.

When paired with one another, the VfACBPs did not produce any cells on quadruple-knockout plates. This illustrates that dimerization or any other form of homopolymerization doesn’t occur with these particular ACBP proteins. It does not, however, eliminate the possibility of self-interaction. Thus far, the tung ACBPs appear to perform their functions independently of one another.

It was consistently observed that fusion proteins containing Cub-LexA linked to the N-terminus of an ACBP protein yielded strong positive reporter gene activation when paired with the Alg5-NubI control protein. Fusion proteins containing Cub-LexA linked at the C-terminus of ACBP, however, produced a significant decrease, or complete absence, of reporter gene activation when paired with Alg5-NubI. The basis for this effect is currently unknown, but these results were consistently observed with many different Cub/Nub fusion proteins, and similar results have been reported in the literature (Deslandes et al., 2003; Obrdlik et al., 2004). As such, results were not included from reciprocal testing of NubG and Cub on both the N and C termini of ACBP proteins.

**Split ubiquitin: β-galactosidase assays as a quantification tool for the interactions of VfACBPs**

The lacZ gene of the lac operon in *E. coli* encodes the β-galactosidase enzyme, which is a roughly 120 kDa and 1000 amino acid tetrameric protein. The function provided by the enzyme is to cleave lactose to glucose and galactose so they may be utilized as energy sources. A yellow color is produced upon the recognition and cleavage of the artificial substrate o-nitrophenyl-β-D-galactoside (ONPG) yielding galactose and o-nitrophenol. The production of o-nitrophenol per
unit time is proportional to the concentration of β-galactosidase when ONPG is in excess over the enzyme in a reaction. Due to this, the enzyme concentration can be determined based on the production of yellow color (Gietz, 1997).

The β-galactosidase assays were performed to quantify and confirm the interactions that were observed in the serial dilution plate assays. For a detailed list of interactions between the tung ACBPs and other components, please see pages 73-76 in the Results section and Figures 3-11 and 3-12. Indeed, the results attained from β-galactosidase assays correlated well with the interaction strengths observed in the serial dilution plate assays. The Miller Units indicate strength of interaction, and as can be seen in Figure 3-12, and VfACBP3a, VfACBP3b, and VfACBP6 either interact strongly or not at all with other proteins. Due to the strength of interactivity and the strong results obtained from the positive and negative controls, VfACBP3a, VfACBP3b, and VfACBP6 interact with both VfDGAT1 and VfDGAT2. This was first observed in the plate dilution assays and correlated with β-galactosidase assays. Again, as stated with the plate dilution assays, there was an immediate response in the experiment, for the β-galactosidase assays, showing positive interactions between the VfACBPs and VfDGATs. Normally, the component solutions involved in the process are incubated at 37°C for as long as it takes for the solution to turn yellow. The positive interaction combinations frequently started turning yellow even before they were placed in the incubator, usually within seconds of preparing the solution. This is an correlation with the fast growth on the quadruple knockout plates, illustrating the strength of the positive interactions. The two VfDGAT proteins are involved in tung lipid metabolic processes, and if there is interaction between the them and the VfACBPs, perhaps there are some role(s) for VfACBPs in metabolic processes involving VfDGAT1 and VfDGAT2. These interactions would have to be qualified since the VfACBPs may have unique localizations and possible specific binding affinities to certain fatty acyl-CoAs. As alluded to earlier, both of the VfDGATs use acyl-coA in their role for the production of TAG from DAG. If there is a
role for any of the VfACBPs in the production of TAGs in tung, perhaps one of the functions is involved at the step for providing the VfDGATs with acyl-CoA.

**Fatty Acid Methyl Ester (FAME) Analysis in the derivatization of tung seed oil for analysis by gas chromatography**

One of the most vital methods for analyzing lipids involves the preparation of methyl esters of fatty acids for analysis by chromatographic means. The transesterification of fatty acids commonly involves two methods; one using an acidic reagent as a catalyst or another using a basic reagent as a catalyst, the latter being used in this research. The transesterification of triglycerides and phospholipids occurs rapidly in anhydrous methanol in the presence of a basic catalyst, such as sodium methoxide, which allows for the exchange between methanol and glycerol. The required methyl esters are shortly obtained in quantitative yield.

\[
\text{OCH}_3
\]

\[
\text{RCOOR'} + \text{CH}_3\text{OH} \leftrightarrow \text{RCOOC}_3 + \text{R'}\text{OH}
\]

Sodium methoxide in methanol reacts very quickly with a glycerolipid. For example, the complete transesterification of triacylglycerols and phospholipids occurs in a few minutes at room temperature in a glass tube. Using these conditions, there is usually no isomerization of double bonds in polyunsaturated fatty acids, though it is possible that alterations to fatty acids can occur. For example, prolonged or careless use of the reagents involved in the procedure can lead to degradation. Using basic reagents, aldehydes are not liberated from the plasmalogen forms of phospholipids, as opposed to when acidic conditions are applied. This may provide an advantage in simplifying the interpretations of gas chromatography traces (Christie, 1993).

Interestingly, the use of sodium methoxide and its counterpart prepared with potassium are often used for catalyzing the large-scale production of biodiesel. Sodium methoxide initiates an anionic addition polymerization with ethylene oxide. This leads to the formation of a
polyether with a large molecular weight. Animal fats or vegetable oils (fatty acid triglycerides) are transesterified with methanol to produce fatty acid methyl esters (FAMEs) (Christie, 1993).

FAMEs were prepared from total lipid extracts of transgenic *Arabidopsis* seeds, followed by gas chromatography (GC) to analyze the fatty acid content. GC is a type of partition chromatography which employs a gas as the mobile phase and a liquid as the stationary phase. The identification of all of the methyl esters in the samples from the extracted oil of the transformed *Arabidopsis thaliana* plants was made by comparing the retention times, which is the interval between the instant of injection and the detection of the component, of standard fatty acid methyl esters.

**Statistical analysis of the seed oil content as attained from transgenic *Arabidopsis thaliana* expressing tung ACBPs**

In 2009, there was a study conducted on the overexpression of *Brassica napus* ACBP, which is similar to ACBP6 of tung and *Arabidopsis*, in developing seeds of *Arabidopsis thaliana*. It was revealed that there was a significant increase in the polyunsaturated fatty acids 18:2cisΔ^9,12^ and 18:3cisΔ^9,12,15^ at the expense of very long monounsaturated fatty acid 20:1cisΔ^11^ and saturated fatty acids in T2 and T3 generations of *A. thaliana* seeds. In addition, recombinant *B. napus* ACBP (rBnACBPP) increases formation of phosphatidylcholine (PC) in the absence of added lysophosphatidylcholine in microsomes from yeast expressing *A. thaliana* lysophosphatidylcholine acyltransferase cDNA or in microsomes from cultures of *B. napus* L. cv. Jet neuf. Also, either recombinant *Brassica napus* ACBP or bovine serum albumin were observed to be critical for *A. thaliana* lysophosphatidylcholine acyltransferase catalysis of the transfer of an acyl group from PC into acyl-coA. Taken together, this data implies that the *B. napus* ACBP affects the equilibrium between metabolically active acyl-coA and phospholipid
pools involved in modifications of fatty acids and triacylglycerol assembly. ACBP overexpression during seed development may provide a valuable biotechnological approach in the alteration of fatty acid composition in seed oils (Yurchenko, et. al., 2009).

The results attained by Yurchenko, et. al., provided inspiration to test VfACBP6 in a similar manner. As stated earlier, constructs were created to analyze the effects of VfACBP expression on the entire normal metabolism of seed FAs in general by their expression in wild type Columbia plants. DsRed screening used for selection, making identification of homozygous T3 lines much easier. The VfACBP6 construct is more directly comparable to the data presented above by Yurchenko, et. al. This is because VfACBP6 is an ortholog of BnACBP6 and there is no known orthologous VfACBP3a in Brassica napus. The increase in 18:2cisΔ9,12 and 18:3cisΔ9,12,15 in T2 and T3 lines transformed with BnACBP, coming at the expense of very long monounsaturated fatty acid 20:1cisΔ11 and saturated fatty acids, wasn’t completely observed in any of the constructs listed in Figure 3-18 or Figure 3-17 for VfACBP6.

Individually (Figure 3-17), VfACBP6 T2 constructs vary considerably in 18:0, 18:3, 20:1, and 20:2, while 16:0, 18:1, and 18:2 content shows the same change as the T3 plants (decrease, increase, and decrease). These results do not compare to the BnACBP6 results. For the T3 plants, introducing VfACBP6 appears to shift the production of 16:0, 18:0, 18:2, and 20:2 to the production of 18:1, 18:3, and 20:1. This is somewhat similar to the results attained for BnACBP6, except for the increased production in very long chain monounsaturated fatty acids (20:1). There is not a complete shift of production to long chain unsaturated fatty acids.

Additionally, on average (Figure 3-18), T2 plants show an increase in 18:1 and 20:1 with a decrease in 16:0, 18:0, 18:2, 18:3, and 20:2 content. The T3 plants showed an increase in 18:1, 18:3, and 20:1, with a subsequent decrease in 16:0, 18:0, 18:2, and 20:2. Again, the T3
plants showed similar changes as illustrated in the individual statistical measurements (Figure 3-17), that being a shift to one very long chain monounsaturated fatty acid and two long chain unsaturated fatty acids. Both the T$_2$ and T$_3$ generations exhibit different changes in the fatty acid profile as compared to the results observed for BnACBP6.

Overall, while there appears to be some similarities, not every change is comparable. This is not too surprising as even though they are orthologous, BnACBP6 is different from VfACBP6, which might have different acyl-CoA or membrane phospholipid binding affinities. In addition, the constructs created for VfACBP6 include the presence of a myc tag, which will have to be removed in future experiments. Also, different promoters are used in the vector constructs for VfACBP6 from BnACBP6. It is interesting how introduction of VfACBP6 in both statistical measures showed an increase in very long chain monounsaturated fatty acids (20:1). There appears to be a channeling of the production of saturated fatty acids to specific long chain and very long chain fatty acids.

Individually, the T$_2$ plants of VfACBP3a, as seen in Figure 3-16, varied too much to surmise what effects VfACBP3a had on the changes to fatty acid content. The T$_3$ generation exhibited a decrease in 16:0, 18:0, and 20:2 content with an increase in 18:1 and 20:1 fatty acids as compared to the wild type plants lacking VfACBP3a. Again, as seen with VfACBP6, there appears to be a shift from saturated fatty acids to specific unsaturated fatty acids and interestingly, to a very long chain monounsaturated fatty acid.

Figure 3-18 illustrates the average changes in fatty acid content that VfACBP3a introduction produced. In the T$_2$ generation, there was an increase in 16:0, 18:0, 18:1, and 18:2, with a decrease in 18:3, 20:1, and 20:2. This is different from any result attained thus far, as there is an increase in saturated fatty acid content with a decrease in both very long chain fatty acids
and 18:3. The T3 generation exhibited an increase in 18:2, 18:3, and 20:1, and decrease in 16:0, 18:0, 18:1, and 20:2. These results are not consistent from one generation to the next. T3 plants showed a decrease in saturated fatty acids as compared to the wild type, which is also a decrease from the T2 generation. Like VfACBP6 (T3), on average, there was an increase in 18:3 and 20:1 fatty acids; however, 18:2 content increased in the T3 generation of plants expressing VfACBP3a. VfACBP6 T3 plants showed an increase in 18:1. Still, both constructs displayed an increase in specific long chain and very long chain unsaturated fatty acids at the expense of saturated fatty acids and other unsaturated fatty acids in the T3 generation on average.

The over-expression of ACBPs in various animal systems and yeast has been shown to increase acyl-coA pool size, due to an increase in specific acyl-coA species, and the rates of glycerolipid synthesis (Mandrup et al., 1993; Huang et al., 2005). The information presented in these studies gives reason to hypothesize that manipulating VfACBP expression in Arabidopsis can influence size and composition of the cellular acyl-coA pool.

As stated on pages 76-80, the potential role of VfACBP when co-expressed with VfFADX in fad3/fae1 was analyzed. They were compared to plants expressing VfFADX alone, and as Figure 3-13 indicates, there was no significant increase in eleostearic acid content. Again, the effects of VfACBP co-expression on any other fatty acids in the seeds was analyzed (Figures 3-14 and 3-15), and 16:0 and 18:0 content, but not eleostearic acid content was changed. This clearly indicates that introducing VfACBP3a or VfACBP6 affects saturated fatty acid content in seeds.

The method of selection for determining which seeds will be planted in subsequent generations for transgenic Arabidopsis wild type Columbia lines was through the use of a modified form of Discosoma sp. red fluorescent protein (DsRed) (Cahoon, et. al., 2007). Use of
DsRed produces bright red fluorescent seeds representative of successful transformations, which, after harvesting, can be picked from brown seeds to be planted and produce future generations. Referring to Figures 3-19 and 3-20, the fad3/fae1 double mutants expressing VfACBP3a in T2 lines elicited 70 brown seeds out of 180 total seeds (~39% brown seeds). This is a high amount of brown seeds, but is more than likely a single insertion. The results will be re-evaluated upon the receipt of a more sensitive light source and filter used to screen for red seeds.

In addition, the generation of transgenic plants through Agrobacterium-mediated transformation can result in one or more inserts of the T-DNA. A common problem in the generation of transgenic plants is that Agrobacterium T-DNA-mediated transformation may result in the integration of more than one copy of foreign DNA, for instance as tandem or inverted repeats (Meza, et. al., 2002).

Using DsRed selection at times can be subjective due to the process of selecting red seeds. It is up to the viewer to determine which seeds to choose in order to plant the T3 lines. Unfortunately, it is easy to accidentally pick a brown seed, whether it be attached to a red seed or even subjectively believed to be red when it is really brown, and plant future generations using that seeds. As stated, the red seeds are representative of successful transformations, and picking a brown seed would produce a plant that does not contain the transgene (VfACBPs). Also, the selection of red seeds is accomplished in the dark, so as to take advantage of a filter that removes extraneous low-levels of non-specific red emission background to determine fluorescence. Obviously, searching for red seeds in the absence of light creates a difficulty in selecting red seeds based on the individual performing the search. At this time, there is no specific plan to re-transform these lines, but in future, the issue has to be resolved. An approach to the resolution would be to perform a Southern blot to check if there is 1 or 2 loci in the genome.
In future experiments, the top two eleostearic acid producing lines coexpressing *Vf FADX* plus either *VfACBP6* or *VfACBP3a* will be planted for the production of T4 generation plants. One set of each of the constructs will be sprayed with a glufosinate-based herbicide to get an estimate of gene copy number. Another set of each construct will be grown out to maturity and seed fatty content will be analyzed by gas chromatography. In addition, plant lines expressing constructs containing *VfACBP3b* or *VfACBP4*, either alone or in conjunction with *Vf FADX* will be generated, but time constraints eliminated the possibility of these lines being produced in time for this publication.

**Final Thoughts**

This research primarily involved elucidating any functions of *VfACBP* s. The initial goal was to identify *VfACBP*, clone, and sequence them. There has been extensive research on various ACBPs throughout many different organisms, many of which perform unique functions. This is especially true for the highly conserved ACBP, *VfACBP6* as its counterpart, with homologues that were identified in all four eukaryotic kingdoms, Animalia, Plantae, Fungi and Protista, in addition to eleven species of eubacteria (Yurchenko, et. al., 2009, Xiao, et. al., 2009, Mogensen, et. al., 1987, Schjerling, et. al., 1996, Taskinen, et. al., 2007, Burton et. al., 2005).

The *VfACBP* s, as a whole, were found to be orthologous to several ACBPs from many different organisms. There was, however, a unique ACBP, *VfACBP3b*, in that its best-matched orthologs were found in *Ricinus communis* and *Populus trichocarpa*, both members of the Spurge family (Euphorbiaceae), which is the same family as *Vernicia fordii*. Many of the orthologs for the *VfACBP* s were found in *Arabidopsis thaliana*, which is a member of the Brassicaceae family. So, this research provided a unique discovery through the elucidation of *VfACBP3b*.
In addition to the discovery of four VfACBPs, it is clear that VfACBP3a and VfACBP6 affect general fatty acid metabolic profiles, causing a shift in the production of specific fatty acids to the production of others. The VfACBPs are expressed at different times as well and may be contrapuntal in their gene expression patterns. They were also found to strongly interact with VfDGAT1 and VfDGAT2 both qualitatively and quantitatively.

These data provide a firm knowledge base for VfACBPs and allow for the creation of future experiments that will be completed in the coming months. The determination of acyl-CoA binding specificity is one such experiment. This will be performed through the use of a modified chromatographic procedure.

Yurchenko, et. al., also demonstrated through *in vitro* assays that recombinant *B. napus* ACBP strongly increases the formation of phosphatidylcholine in the absence of added lysophosphatidylcholine in microsomes from yeast expressing *A. thaliana* lysophosphatidylcholine acyltransferase (*AtLPCAT*) cDNA or in microsomes from microspore-derived cell suspension cultures of *B. napus* L. cv. Jet Neuf. They also showed that BnACBP or bovine serum albumin (BSA) were crucial for *AtLPCAT* to catalyze the transfer of an acyl group from PC into acyl-CoA *in vitro* (Yurchenko, et. al., 2009). VfMBOAT1, likely a lysophosphatidylcholine acyltransferase, has recently been cloned into split ubiquitin vectors, much like the VfACBPs and VfDGATs. VfACBP3a and VfACBP6 split ubiquitin constructs will be paired with these VfMBOAT1 constructs. This will be a direct way to address the question of whether the LPCAT enhancement shown by Yurchenko, et. al., might also be occurring in tung seeds as well.

One possible source of concern is that the plant constructs created for VfACBP3a and VfACBP6 that were used for statistical analysis after FAME analysis, all have a *myc* tag. It is
possible that adding a myc tag could alter acyl-CoA binding or protein:protein interactions of either VfACBP3A or VfACBP6, and could affect (assumed) extracellular targeting of VfACBP3A. Some of the seed-specific expression work may be repeated using untagged protein constructs and in the case of expressing VfACBPs by themselves, will be expressed in whole plants using constitutive promoters like CaMV35S.

This research puts forth a better understanding of the current VfACBPs with many more experiments to come. ACBPs in general have been clearly shown to provide a variety of integral roles throughout various organisms. It is imperative that there be a continued effort in the analysis of these VfACBPs so as to enhance the knowledge of fatty acid metabolism. The furthering of the knowledge base of ACBPs can only help to enhance the studies for not just tung but other organisms as well.
References


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Vita

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