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A REVIEW ON COBRA-LIKE GENE FAMILY

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ABSTRACT

COBRA-like gene family is a multigene superfamily that encrypts a huge family of proteins that is merely prevailing within plants. The affiliates appertaining to COBRA-like family stay concerned with varied biotic activities associated with cell enlargement plus cell wall biosynthesis. There are 11 members in rice including OsBC1L1–9, BC1, OsBC1Lp1, 9 within maize including ZmBK2L3–9, ZmBK2, ZmBK2L1, and12 in Arabidopsis (COBRA, AtCOBL1–11). COBRA encrypts an alleged GPI-anchored protein & indispensable for oriented expansion of cell in Arabidopsis. COBRA-Like Protein also has an impact on the mechanical features of Rice plants. A COBRA-like protein operates in cellulose gathering by fastening cellulose microfibrils. Here is a review of the functions of the members of this family discovered so far.

INTRODUCTION:

COBRA-like gene family encrypts proteins only in plants. One of the main functions that it performs is their role in cell wall synthesis. Cell enlargement and cell wall biosynthesis stand as incredibly vital processes within the vivacity of plants. COBRA is amongst the genes which are extremely articulated alongside the cellulose synthase multiplex as well as incriminated to stand concerned with crystallization of cellulose[1]. The COB gene comprises a sequence theme located in proteins which stand affixed to plasma membrane appertaining to its outer plane via a glycosylphosphatidylinositol (GPI) bond. Within Arabidopsis there are eleven members of the COBRA family also supplementary COBRA-LIKE genes (COBL) got recognized in numerous monocots & dicots[2-4]. The structure appertaining to COBRA protein is extremely preserved. With rare exclusions COBRA-LIKE proteins possess a GPI anchoring motif on C terminal in addition to indicator peptide on N terminal of the gene. According to phylogenetic exploration aforementioned family stands biphyletic[2] Furthermore there is likelihood of functional severance among the distinctive genes. Also severance is additionally recommended as a result of restrictive description appertaining to physical composition of cob.

COBRA encrypts an alleged GPI-anchored protein & indispensable for oriented expansion of cell in Arabidopsis:

Diverged installation of fresh wall constituents and oriented control of cell wall addition are essential to regulate the direction of enlargement of cell. The configuration of expression of COBRA (COB) gene in roots tells that root cells within cob seem stretched additionally around an outward as compared to lengthwise dimension, sustaining cell bulk, signifying a function for COBRA in controlling the direction of cell enlargement[5]. COB encrypts an alleged GPI-affixed protein which stands contained principally along lengthwise dimension of root cells plasma membrane. Altered orientation of cell enlargement is associated with the manufacture of minor quantities of cellulose in roots by Cobra, this indicates about COB's management of positioned cell enlargement linkage with installation of cellulose. The product of COBRA gene comprises of an alleged GPI anchor which is being proposed by the sequence of its amino acid. Schindelman et al. suggested two probable representations for COB pursuit[5]. The emplacement of COB aimed at lengthwise sides of enlarging cells in an uneven manner increases the likelihood that COB operates to employee cellulose manufacturing multiplexes to distinct spots at the surface of cell, allowing lengthwise enlargement in root. On the other hand COB might perform by opposing outward wall enlargement or encouraging lengthwise wall enlargement.

According to Roudier et al.[2]glycosylphosphatidylinositol (GPI) element is accountable for the attachment of the COBRA protein towards the exterior cytomembrane leaflet. Toting up appertaining to GPI affix is accomplished at endoplasmic reticulum also suggests the separation of a C terminus peptide which is hydrophobic followed by the linkage of an already assembled GPI anchor by means of a single amide link on to the ultimate amino acid fragment. GPI linkage also permits the combined aiming of the proteins that are not related to the subregion of same membrane. On the basis of their length the COBRA Family Comprises of Two Subcategories of Alleged GPI-Affixed Proteins, proteins in one sub-category are 45% more in length than the proteins in the other sub-category. One sub-category includes the five presumed proteins COBL6, COBL5, COBL4, COBL3/2, and COBL1. Their structure resembles with COBRA, however another sub-category including COBL11, COBL10, COBL9, & COBL8 has resemblance to COBL7. All the members of COB family are noticed to be worthy nominees for GPI addition except COBL5 .The COB family proteins consist of dissimilar domains whose function is not known they depict the preservation of numerous residues including Gly, Trp and Cys. All the participants of COB family have three fields: (1).The sub-category COBL7 has a N-terminal section that has 170 amino acids corresponding towards N-terminal field within COB subcategory. (2). The CCVS field which is predominantly plentiful in Cys having a compromised N-glycosylation site, an after translation amendment often linked with GPI-attached proteins and further commonly along extracellular proteins. (3).another compromised N-glycosylation site that begins with a small region of underprivileged whole likeness and might signify an insertion section amid the compromised section prior to the GPI ω-cleavage site and CCVS field.

BRITTLE CULM1 Encrypts a COBRA-Like Protein that has an impact on the instinctive features in Rice Plants

Brittle culm1 (bc1) is a classic rice mutant which has BC1 gene. According to Li et al.[6] BC1 encrypts a COBRA-like protein which is expressed chiefly in vascular bundles of rice and emerging sclerenchyma cells. Alterations in BC1 triggers a decline in cellulose matter and the width of cellular wall however it also causes an upsurge in lignin intensity these changes signify that BC1 performs a significant character in the bio-production of the cell walls to deliver mechanical asset aimed in rice plants. BC1 holds all of the preserved traits of the COBRA family, comprising of N terminus indicator peptide sequence for emission, an extremely aquaphobic C terminal and a CCVS field, also precise traits about the ω-site prerequisite for processing. COBRA and BC1 are members of two contrary clades, suggesting that they have interrelated however dissimilar purposes. COBL4 in Arabidopsis and BC1L7 and BC1 in rice establish a monophyletic clade. BC1L7 is located on chromosomes 7 while BC1 is located on chromosomes 3 in rice.

COBRA Operates Extreme Anisotropic Enlargement by monitoring the positioning of Cellulose Microfibril:

According to Roudier et al.[1] cob-4 is a null allele which launches the crucial part of COB in monitoring anisotropic spreading out in supreme emerging body part. COB is chiefly occupied in microfibril installation in the course of hasty stretching. Through Immuno-detection analysis they showed that in stretching root cells COB was polarly directed to the longitudinal cell walls and the plasma membrane along with its replacement by a glycosylphosphatidylinositol anchor and was dispersed in a banding configuration vertical to the lengthwise region through a mechanism reliant on microtubule. COB regulates anisotropic expansion throughout plant morphogenesis by means of its engrossment in cellulose microfibril orientation. Null allele specifies COB as a crucial supervisor of anisotropic spreading out during the course of postembryonic enlargement.

COBRA like protein in Brittle stalk 2 for stalk strength

Brittle stalk-2 (bk2-ref) is an impulsive maize mutant that shows vivid decrease in the mechanical strength of tissue which is associated with rough installation of cell wall material and decrease in the quantity of cellulose in the perivascular sclerenchyma fibers and sub epidermal. *Bk2* encrypts a Cobra-like protein which is alike to the Bc1 protein in rice [7].The *Bk2* gene shows expression in the husk ,stalk, leaf tissues and root. It is highly expressed in vascular bundles. Alterations in the *Bk2* gene disturb stalk asset within maize by meddling in the cellulose installation of secondary cell wall of fiber cells.

Expression and Relative Evolutionary Analysis Of The COBRA Gene Family:

According to Brady et al. [4] Maize and Arabidopsis COB gene family affiliates display coinciding and exceptional expression configurations which are spatially and developmentally controlled at the cell and tissue level and their single subset shows response to ecological stimuli. Comparing the manifestation of COB gene family affiliates in Maize & Arabidopsis, the later one is more diversified. BRITTLE STALK 2-LIKE 3 is identified to be an alleged ortholog of AtCOB. Null alleles and fractional deficit of utility of COB display anomalous anisotropic cell expansion in the course of root growth and show inappropriate orientation and diminished levels of crystalline cellulose microfibrils. On the other hand, mutations in COB does not effect pollen development and root hair expansion

The evolutionary correlation of rice BC1,maize Bk2 & Arabidopsis COB family affiliates: AtCOBL7 to 11 and AtCOBL1 to 5 develop two major clades in the phylogenetic tree with the exclusion of ZmBk2L9, AtCOBL6 and OsBC1L p1. Two subgroups are formed in these two major clades. ZmBk2 and OsBC1 are strongly related in the clade of AtCOBL1 to 5. The rice BC1 protein is alike to AtCOBL4.Whereas the function of COBL4 in monocots might be communal in 2 co-orthologs: ZmBk2L7/OsBC1L7 and ZmBk2/OsBC1 but ZmBk2 and ZmBk2L7 do not have the same function. There are 11 members in rice, nine in maize and 12 in Arabidopsis that belong to COB gene family. BC1L rice gene was predominantly teamed up alongside a seemingly orthologous maize complement. This is predominantly marked in the COBL7 subcategory where ZmBk2L1/ OsBC1L1 and ZmBk2L8/OsBC1L8 make a monocot specific clade

COBRA-like gene articulated in the course of germination in maize:

ZmAA9-24 is a gene articulated in tissues of root. Expression of ZmAA9-24 happened previously in the course of germination if seeds are formerly osmoprimed or if the embryo axes are downed in the company of cytokinins. ZmAA9-24 has 39.6% protein sequence matching to the outcome of Arabidopsis gene COBRA. The expression of ZmAA9-24 may perhaps be controlled by the cell cycle and cell expansion during germination [8]

COBRA-Like Protein in Maize Brittle stalk2 for Tissue Flexibility at Maturity:

The maize brittle stalk2 (bk2) is a variant having brittle above ground components. The Bk2 gene encrypts a COBRA-like protein that matches to Arabidopsis COBRA-LIKE4 and rice BC1. The stalks external margin has rarer vascular bundles and the sclerids lying beneath the epidermis own slimmer secondary walls. Bk2 is extremely expressed during the course of initial development former to the commencement of the brittle conformation, Bk2 maintains organ flexibility by prefiguring of cellulose-lignin interfaces inspite of a precise part in biosynthesis of cellulose.BK2 is efficiently interrelated to Arabidopsis COBL4 and the rice BC1 having 70% identity with former and 88% identity with the later. BK2 owns a preserved region,like other COBRA, protein amongst amino acids 53 to 217 which is feature of a metal- fastening territory of plant phytochelatin synthases. [3]

COBRA IN Grass cell wall

A phylogenetic exploration of the cobra like gene family exposed a single grass particular clade signifying that genes in this clade might implement a task sole to the grasses. [9]

COBRA-like protein AND root hair elongation in Maize

The roothairless3 (hereinafter referred to as "rth3") mutant is explicitly influenced elongation of root hair. According to (Hochholdingeret al.2008)[10] rth3 gene encrypts a COBRA-like protein which presents the entire organizational attributes of a GPI anchor. COBRA family genes participate in different kinds of cell amplification & cell wall production. The rth3 gene is affiliated with a monocot-peculiar clade of the COBRA gene family. However the OsBC1L1 rice gene seems to be orthologous to rth3. rth3 shows the peak ample manifestation in primary roots mainly in the horizontal root primordia and epidermal cells establishing root hair [4]

The COBRA gene family in Populus

Yeet al. [11]scrutinized entire 18 COBRA genes (Pt COBRA) from the entirely tracked genome of *Populustrichocarpa*. The 14-affiliate Pt COBRA sub-family I proteins have extraordinary affinity to the Arabidopsis COB sub-family, and affiliates with complete length tracks were anticipated to retain notable aptitudes for a GPI- affix location. The 4-affiliate Pt COBRA sub-family II proteins are 45% lengthier as compared to subfamily. I proteins and do not have an x-addition sites on the C ambit, and are further alike to At COBL7 sub-family. Pt COBRA genes show extraordinary intensity of manifestations in young root organs and shoot tips suggesting their involvement in synchronizing cell amplification[2]

COBRA family in rice:

BRITTLE CULM1 (BC1), is a cobra like gene in rice that controls mechanical strength [12] BC1 is related to an 11-affiliate family, designated as the OsBC1L family. The OsBC1L family consists of 2 key subcategories. OsBC1L genes exposition general or particular assertion arrangements.. The OsBC1L genes discharge an array of tasks and chip in numerous developmental procedures in rice. BC1 has been button downed but the purposes of the other OsBC1Ls continue to be clarified. The rice genome consists of 11 COBRA-like genes[12]. The disintegration of the OsBC1L5 gene may trigger a bug in pollen impregnation that avoids the osbc1l5 allele to hand down to the descendants by the microgametophyte.OsBC1L4 may be engrossed in the manufacture of cellulose and cell wall in rice.OsBC1L5 is requisite for the development of pollen tube in rice.

COBRA-Like Gene in Eucalyptus:

EniCOBL4A is a COBRA-like gene in *Eucalyptus nitens* which is similar to Arabidopsis and is cited in degradation of cellulose. These genes are discriminatively articulated in lower and upper margins of xylem and huge dissimilarities in cellulose microfibril positioning and cellulose content are observed. SNP7 influences cellulose content in Eucalyptus [13]

The poplar COBL gene:

PtCOBL4 is the foremost COBL gene from *Populustomentosa*. The inferred protein sequence imparts 72.7% alikeness with Arabidopsis AtCOBL4 protein that is engaged in secondary cell wall installation. PtCOBL4 is expressed shows expression chiefly in the developed xylem region. COBRA is a multiple gene family of 11 affiliates and its every individual display dissimilar tissue-specific expression configurations. Regardless of the vital tasks performed by COBRA in cellulose production extremely less information is available about its behaving pattern in trees.PtCOBL4 is an alleged COBRA-like gene in Poplar. PtCOBL4 has a very high resemblance with Arabidopsis AtCOBL4 which signifies that PtCOBL4 has same function as that of AtCOBL4. The PtCOBL4 gene is chiefly articulated at the deferred phase of cell wall congealing in the developed xylem fiber cells however it is expressed at comparatively depleted intensities in primary tissues of immature xylem, apex and cambium. PtCOBL4 seems to be concerned with secondary cell wall installation in the stem within trees. [14]

An innovative cell wall architecture mutant of rice with malfunctioning Arabidopsis COBL4 ortholog BC1:

Cell wall architecture1 (cwa1) is an innovative rice mutant it displays culm brittleness, diminished cellulose matter in developed internodes and an uneven congealing design within secondary wall appertaining to sclerenchyma. cwa1 plant contain areas of confined accumulation in internodes in the secondary walls of the cortical fibers which display irregular thickness. Cell wall phenolic components are richly consigned at the accumulated cell wall areas within sclerenchyma which seem to be distressed due to mutation of the *cwa1* gene. cwa1 is allelic to brittle culm1 (bc1). *BC1* is recognized as a supervisor that constraints the cellulose constitution in the secondary walls of sclerenchyma and culm mechanical strength. CWA1/BC1 has an indispensable part in compiling cell wall ingredients at their suitable positions, thus assisting production of dense internodes in rice. Mutation in *cwa1* gene leads to anomalous secondary cell wall thickening. [15]

CWA1/BC1 Order Secondary Cell Wall Fabrication by means of carbohydrate binding molecule CBM:

COBRA family proteins which are GPI-anchored are anticipated to be limited to the exterior surface of the cell wall or plasma membrane. Consequently the appropriate fabrication of secondary cell wall ingredients by the CWA1/BC1 might need fastening amongst the CBM-like sequence inside CWA1/BC1 [15]. CWA1/BC1 might perform a vital part at the preliminary phase of secondary cell wall establishment and operate as a framework protein for ordering the alignment of cellulose microfibrils by fastening cell wall polysaccharides by means of the CBM-like sequence

COBRA in Tension Wood and BastFibres:

Tension wood and bastfibres are enriched with COBRA-like protein and its gene product is associated to the cell wall and cell expansion [16]

OsBC1L4 encrypts a COBRA-like protein which has an impact on cellulose synthesis in rice

Osbc1l4 (Oryza sativa brittle culm 1 like 4), encrypts a COBRA-like protein which displays distinctive organizational qualities of a GPI anchor protein. OsBC1L4 protein is chiefly situated in the cell wall and plasma membrane. The expression of OsBC1L4 is extremely interrelated with numerous primary wall-establishing cellulose synthase genes (CESAs) [17]

COBRA-like gene operating in ripening and fruit growth in tomato:

SlCOBRA-like is a tomato gene similar to Arabidopsis COBRA. The SlCOBRA-like gene is extremely articulated in asexual structures and in initial fruit growth. SlCOBRA-like gene shows a vital part in supervision of cell wall architecture in the course of fleshy fruit formation. Transgenic tomato fruits overexpressing SlCOBRA-like display pleasant initial development in physical composition including increased compactness and extended shelf life via altered COBRA expression[18]

Bioinformation analyses and Expression pattern of COBRA gene in tomato

In search of COBRA mutants *Arabidopsis*, *Oryza sativa* and *Zea mays* are also studied. The role of ortholog of COBRA in tomato remains unknown. From tomato seedling a full-length cDNA sequence which is mostly similar to other plant *COBRA* genes was identified with the help of RT-PCR. Which was named as SlCOBRA. SlCOBRA is made of 6 exons encrypting a 444-amino acid protein, containing preserved attributes of the COBRA protein, like a CCVS pattern, an N-terminus end precise attributes around the ω-site mandatory for dispensation. Amino acid sequence of SICOBRA shows 80% similarity with that of *Arabidopsis* AtCOB. Tomato *COBRA* have higher expression levels in flower, shoots, root and fruits, but only during the development of fruit when it is in green stages before the visible signs of ripening. When breaker stage start, the levels of tomato *COBRA* mRNA decline noticeably [19]

COBRA-LIKE 10:

For successful reproduction of flowering plants there is a need of relentless interaction amongst female tissues of plant and pollen tubes which are growing in plants. For swift and correctional growth of tube, female cells secrete some kind of molecules or a nutrient that is implemented by alterations of pursuits in pollen tubes. A GPI-affixed protein, COBL10, is a module of this pollen tube core system. Due to alterations in COBL10 male infertility occur, owing to the reason of diminished growth of pollen tube and conceded direction detecting in the female conveying territory. Localization of the pollen tube of COBL10 aimed on apical plasma membrane is crucial for its task and depends on appropriate GPI dispensation and its C-terminal aquaphobic deposits. COBL10 is important for oriented progression of pollen tubes advise and perform important tasks in cell-cell interactions in plants. The accountability of COBL10 in the course of signal receiving and elucidation may implicate active configuration of the pollen tube wall.[20]

ClCOBL1, COBRA-like gene, from Chinese fir (*Cunninghamialanceolata*):

COBRA genes are a crucial element for the sedimentation of cellulose and enlargement of cell. ClCOBL1 is a conifer COBRA-like gene from the xylem of plant. ClCOBL1 is articulated at a extraordinary intensity in cambium section in plant. Overexpression of ClCOBL1 shows some impacts on the development of flower and leaf. ClCOBL1 related to a arboreal plant-exclusive clade of the COBRA protein family with numerous preserved patterns. ClCOBL1 is constitutively articulated in cambium region in high level. This protein is chiefly situated in the cell wall of plant and its plasma membrane. In tobacco plants over expression of this protein transformed leaf abaxial-adaxial prefiguring and little size, puffy corolla tubes. The transformed leaf structural design in the ClCOBL1 over expressors is linked with the distinct expression of leaf abaxial-adaxial genes. ClCOBL1 is engaged to determine the dorsoventrality of leaf and anisotropic extension. [21]

COBRA-Like Protein, Brittle Culm1 Operates in Cellulose Fabrication:

Brittle Culm1 (BC1), COBRA-like protein, appear within rice and is responsible for modifying cellulose crystallinity. In BC1 a carbohydrate-binding module (CBM) appear next to its N-terminal which cooperates chiefly with crystalline cellulose and numerous aromatic deposits in this area are indispensable for binding. Three secondary wall cellulose synthases (CESAs) and BC1 and show essential part in different steps of the formation of cellulose. BC1 restrains cellulose assemblage by cooperating with cellulose and influencing microfibrilcrystallinity. [22]

COBRA-LIKE 2 insecretive cells of Arabidopsis seed cover mucilage:

COBRA-LIKE 2 (COBL2) is an affiliate of COBRA-LIKE gene family. Interruption of the COBL2 gene marks the decrease in cellulose rays that appear in seed mucilage. COBL2 functions during buildup of crystalline cellulose into diverse secondary cell wall structures during seed coat epidermal cell distinction and crystalline cellulose installation in the epidermal cells seed coat. [23]

COBRA-Like (COBL) Gene Family in Gossypium:

A 19 candidate COBL genes is identified from *G.raimondii*, 18 candidate COBL genes from *G.arboreum* and 33 candidate COBRA-Like genes from *G.hirsutum* which is acc.TM-1. COBRA-Like genes in *G.hirsutum* acc. TM-1 have varied expression designs in developing fibers, vegetative and floral tissues. COBL genes play wide range of roles in various cotton tissues. [24]

Synthesis of Cellulose in Plant Cells :

A function of COBRA (cob) mutant in direction of cell enlargement was related with a screen for Arabidopsis with defect expanded roots foremost in1993.Shortand puffed-up roots rose from mutations in the COB. GPI-proteint is obligatory for cell enlargement in Arabidopsis. COBRA triggers the cell stretching and decline in cellulose subject matter. And related to installation of cellulose microfibrils. COBRA-like gene family affiliates COBL11, COBL10, COBL9, COBL6, and COBL2 are needed for oriented crystalline cellulose accumulation in the course of growth of seed, pollen tubes and root hairs.[25]

Heveabrasiliensis COBRA Transcripts expression:

HbCOBL family shows a degree of difference in expression in *H.brasiliensis*. 2 HbCOBL transcripts (HbCOBL-P and HbCOBL-E) show noteworthy variances of expression in bark but not in latex telling that these genes may be concerned with differentiation of laticifers[26]

COBRA-LIKE 2 and seed mucilage polysaccharide matrix organization in Arabidopsis:

The synthesis of aquaphilic mucilage besides the differentiation of seed coat epidermal cell is a communal modification among angiosperms. The cobl2 has distinct features such as deficit of initial cell wall 'pyramidal' organization, ray morphology, enhanced levels of the monosaccharidesgalactose and arabinose and condensed Ruthenium red staining strength of the supporting mucilage deposit. In cobl2 the ray structure suggests a definite influence on the assemblage of the cell wall polymer-setup, needed to maintain ray form and linked mucilage column. Organic description of the influence of the cobl2 mutation on seed mucilage monosaccharide configuration exposes intricate deviations involving supervision of arabinose and galactose intensities in the supporting mucilage[27]

COBRA-LIKE protein in Sorghum:

Plant mechanical strength is vital feature in sorghum. SbBC1 is a homologue of Arabidopsis thaliana AtCOBL4 and rice OsBC1 and, encrypts a COBRA-like protein. Alteration in one nucleotide in SbBC1 leads to increased lignin content, decreased mechanical strength and decreased cellulose content. SbBC1 is chiefly spotted in vascular bundles and sclerenchyma cells in developing sorghum. SbBC1 takes part in the manufacture of cellulose in the secondary cell wall and has impact on the mechanical asset of sorghum plants, specifying supplementary genetic proof for the responsibilities of COBRA-like genes in cellulose manufacture in grasses.[28]

TABLE 1. COBRA-LIKE GENES PRESENT IN DIFFERENT PLANTS AND THEIR FUNCTIONS

COBRA-LIKE GENE NAME	ORGANISM	FUNCTION
COB GENE	Arabidopsis	Encrypts an alleged GPI-affixed protein and is indispensable for orientated enlargement of cell [5]
BC1 gene	Rice	Encrypts a COBRA-Like Protein that has an impact on the Reflex features of Rice Plants [6]
Bk2	Maize	encrypts a Cobra-like protein that provides stalk strength (Ching et al.2006), maintains organ flexibility by prefiguring of cellulose-lignin interfaces inspite of a precise part in biosynthesis of cellulose[3]
ZmAA9-24	Maize	Expressed during maize germination [8]
rth3 gene	Maize	Expressed in root hair-establishing epidermal cells and horizontal root primordia[10]
Pt COBRA	Populus	retain specific capabilities for a GPI-anchor site [11]
EniCOBL4A	Eucalyptus	The extremely powerful related marker in a quantitative trait locus (QTL) region for cellulose content [13]
PtCOBL4	Poplar	Chiefly articulated at the deferred phase of cell wall congealing in the developed xylem fiber cells. PtCOBL4 seems to be concerned with secondary wall installation in trees. [14]
cwa1 gene	Rice	Cell wall thickening [15]
OsBC1L4	Rice	Has an impact on cellulose synthesis in rice[17]
SlCOBRA-like gene	Tomato	Ripening and fruit growth in tomato[18]
COBL10	Arabidopsis	important for oriented progression of pollen tubes advise and perform important tasks in cell-cell interactions in plants[20]
ClCOBL1	Chinese fir	Expressed in differentiating xylem [21]

COBL2	Arabidopsis	functions during buildup of crystalline cellulose into diverse secondary cell wall structures during seed coat epidermal cell distinction and crystalline cellulose installation in the epidermal cells seed coat [23]
acc. TM-1	Gossypium	have varied expression designs in developing fibers, vegetative tissues and floral tissues [24]
HbCOBL	*Heveabrasiliensis*	show noteworthy variances of expression in bark but not in latex telling that these genes may be concerned with differentiation of laticifers [26]
SbBC1	Sorghum	takes part in the manufacture of cellulose in the secondary cell wall and has impact on the mechanical asset of sorghum plants [28]

Conclusion

The cobra-like gene family found in plants playes crucial roles in their life cycles. They play chief role in cell wall deposition which is very essential component of plant cell. These genes have been found in enormous plants comprising rice, maize and Arabidopsis and their indispensable roles in these plants suggest that these are essential part of plant life. Owing to their crucial roles, these genes have yet to be discovered in other plants

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References

1. Roudier, F., et al., *COBRA, an Arabidopsis extracellular glycosyl-phosphatidyl inositol-anchored protein, specifically controls highly anisotropic expansion through its involvement in cellulose microfibril orientation.* 2005. 17(6): p. 1749-1763.

2. Roudier, F., et al., *The COBRA family of putative GPI-anchored proteins in Arabidopsis. A new fellowship in expansion.* 2002. 130(2): p. 538-548.

3. Sindhu, A., et al., *Maize Brittle stalk2 encodes a COBRA-like protein expressed in early organ development but required for tissue flexibility at maturity.* 2007. 145(4): p. 1444-1459.

4. Brady, S.M., et al., *Combining expression and comparative evolutionary analysis. The COBRA gene family.* 2007. 143(1): p. 172-187.

5. Schindelman, G., et al., *COBRA encodes a putative GPI-anchored protein, which is polarly localized and necessary for oriented cell expansion in Arabidopsis.* 2001. 15(9): p. 1115-1127.

6. Li, Y., et al., *BRITTLE CULM1, which encodes a COBRA-like protein, affects the mechanical properties of rice plants.* 2003. 15(9): p. 2020-2031.

7. Ching, A., et al., *Brittle stalk 2 encodes a putative glycosylphosphatidylinositol-anchored protein that affects mechanical strength of maize tissues by altering the composition and structure of secondary cell walls.* 2006. 224(5): p. 1174-1184.

8. Cruz-García, F., et al., *Cloning and characterization of a COBRA-like gene expressed de novo during maize germination.* 2003. 13(3): p. 209-217.

9. Vogel, J.J.C.o.i.p.b., *Unique aspects of the grass cell wall.* 2008. 11(3): p. 301-307.

10. Hochholdinger, F., et al., *The maize (Zea mays L.) roothairless3 gene encodes a putative GPI-anchored, monocot-specific, COBRA-like protein that significantly affects grain yield.* 2008. 54(5): p. 888-898.

11. Ye, X., et al., *The COBRA gene family in Populus and gene expression in vegetative organs and in response to hormones and environmental*

stresses. 2009. 58(2): p. 211-223.

12. Dai, X., et al., *Molecular characterization, expression pattern, and function analysis of the OsBC1L family in rice.* 2009. 71(4-5): p. 469.

13. Thumma, B.R., et al., *Identification of a cis-acting regulatory polymorphism in a eucalypt COBRA-like gene affecting cellulose content.* 2009. 183(3): p. 1153-1164.

14. Zhang, D., et al., *Expression and nucleotide diversity of the poplar COBL gene.* 2010. 6(2): p. 331-344.

15. Sato, K., et al., *The carbohydrate-binding module (CBM)-like sequence is crucial for rice CWA1/BC1 function in proper assembly of secondary cell wall materials.* 2010. 5(11): p. 1433-1436.

16. Hobson, N., M. Roach, and M.J.R.J.o.P.P. Deyholos, *Gene expression in tension wood and bast fibres.* 2010. 57(3): p. 321-327.

17. Dai, X., et al., *OsBC1L4 encodes a COBRA-like protein that affects cellulose synthesis in rice.* 2011. 75(4-5): p. 333-345.

18. Cao, Y., et al., *Functional characterization of a tomato COBRA-likegene functioning in fruit development and ripening.* 2012. 12(1): p. 211.

19. Cao, Y., X. Tang, and Y.J.B.o.B.R. Liu, *Cloning, expression pattern and bioinformation analyses of COBRA gene in tomato (Solanum lycopersicum).* 2012. 32(3): p. 304-310.

20. Li, S., et al., *Arabidopsis COBRA-LIKE 10, a GPI-anchored protein, mediates directional growth of pollen tubes.* 2013. 74(3): p. 486-497.

21. Gao, Y., et al., *Expression of a conifer COBRA-like gene ClCOBL1 from Chinese fir (Cunninghamia lanceolata) alters the leaf architecture in tobacco.* 2013. 70: p. 483-491.

22. Liu, L., et al., *Brittle Culm1, a COBRA-like protein, functions in cellulose assembly through binding cellulose microfibrils.* 2013. 9(8): p. e1003704.

23. Ben-Tov, D., et al., *COBRA-LIKE2, a member of the glycosylphosphatidylinositol-anchored COBRA-LIKE family, plays a role in cellulose deposition in Arabidopsis seed coat mucilage secretory cells.* 2015. 167(3): p. 711-724.

24. Niu, E., et al., *Comprehensive Analysis of the COBRA-Like (COBL) Gene Family in Gossypium Identifies Two COBL s Potentially Associated with Fiber Quality.* 2015. 10(12): p. e0145725.

25. Maleki, S.S., K. Mohammadi, and K.-s.J.T.S.W.J. Ji, *Characterization of cellulose synthesis in plant cells.* 2016. 2016.

26. Putranto, R.-A. and I. Martiansyah. *Differential In Silico Expression of Hevea brasiliensis COBRA Transcripts*. in *2018 1st International Conference on Bioinformatics, Biotechnology, and Biomedical Engineering-Bioinformatics and Biomedical Engineering*. 2018. IEEE.

27. Ben-Tov, D., et al., *The role of COBRA-LIKE 2 function, as part of the complex network of interacting pathways regulating Arabidopsis seed mucilage polysaccharide matrix organization.* 2018. 94(3): p. 497-512.

28. Li, P., et al., *Brittle Culm 1 encodes a COBRA-like protein involved in secondary cell wall cellulose biosynthesis in Sorghum.* 2019. 60(4): p. 788-801.