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Biosynthesis of protein in plants under different environmental factors

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Abstract
Protein is an organic compound commonly found in living organisms. The building block of the protein is the amino acid. Protein provides energy and structural material for living system and is the essential component of the membranes. Protein is synthesized by translation of mRNA through a two-step process commonly known as the central dogma of life. It provides channels for the movement of the molecules ions across the membranes. It also provides defensive mechanism against pathogens. Some proteins are produced at specific condition like heat shock protein cold shock protein. These proteins enable the plants to cope with adverse environmental effects. Plants also preserve proteins in some storage organs like seeds. These proteins are known as seed storage protein. These proteins are directly synthesized in rough endoplasmic reticulum and accumulate in storage structure of seeds.

Keywords: Protein, protein biosynthesis, types of protein, amino acid

Introduction
Protein is the macro-biomolecules which consist of large number of polymers known as amino acid. Due to this reason, amino acid also known as the building blocks of protein. These polymers contain hydrogen, carbon, nitrogen, oxygen atoms and Sulphur. Few proteins also have additional element like phosphorus and iron.

Protein is found in almost all cells of all organisms and is the most abundant molecule found in the living system apart from water. It is believed that about 100,000 different types of protein are in found organism (Christopher, 2004) [7]. These proteins are different from each other depending on their amino acid sequences. Therefore, proteins are very significant group of molecules found in living system. They are involved in many metabolic pathways occurring in plants cells such as catalyzing reaction, replication of DNA, transporting molecules inside and outside of the cell and can be considered as building block of cell membranes.

It is known that proteins consist of several amino acids which differ from each other depending on the order and number of the amino acid, differ in molecular weight, and their function. The type of protein based on the number and arrangement of amino acid in polypeptide changes. Pierce, (2011) [28] stated that the type, structure and function of the protein happen as a result translation of genetic code on mRNA. Each genetic code links to specific amino acid so each gene is coded for a specific number of polypeptides).

Normally protein is synthesized in ribosome and rough endoplasmic reticulum, but the production of the protein is regulated by the messenger RNA (mRNA). The Messenger RNA carries messages in the form of genetic code or codon. These codes have specific information for making a polypeptide chain by binding of different type for amino acid. According to Attardi, (1967) [3] mechanism of protein synthesis consists of two steps. The first step is the transcription of DNA (deoxyribonucleic acid) into RNA (ribonucleic acid) and second step is the translation of RNA into protein. The synthesis of protein happens in ribosomes. The biosynthesis of protein starts at amino-terminal of amino acid and continues to their carboxy-terminal.

The genetic code commonly known as codon (a group of three adjacent nucleotides in the mRNA) specifies the attachment of amino acid to growing peptide chain, called polypeptide chain (Attardi, 1967) [3]. The sequence of amino acid in polypeptide chain has all information necessary for generating structure of protein molecule (Anderson *et al*. 1967) [2]. Similar mechanism of production of protein is found in plants. Protein biosynthesis plays a significant role to fulfill the energy requirement for the growth of plants (Amthor, 2000) [1]. The rate of production of protein can be assessed by investigating the quantity of ribosomes loaded in

polysomes. The environmental factors such as water deficit decrease the Polysome loading (Beilharz and Preiss, 2004) [5]. In non-stressed condition plants normally have high polysomes loading in light and have low in night (Pal *et al*. 2014) [27]. This approach specifies that plants produce maximum protein in the daytime while it is constrained in night by the rate of starch degradation and availability of carbon and energy.

Plants produce different types of the proteins to cope with environmental factors like heat shock protein, cold shock protein, protein produced during drought stress and salinity. The proteins' role and mechanism of production of them is explained in detail below (Key *et al*. 1981) [21].

Heat shock protein

The heat shock protein is synthesized in plants under heat stress conditions and hence also called stress induced protein. Heat shock protein responds to heat stress on molecular level in plants (Gupta *et al*. 2010) [13]. According to De Maio, (1999) [8] the stress initiate gene expression and biosynthesis of heat-shock proteins to cope with effect of stress. The production of heat shock protein is common phenomena in all organisms under heat stress condition (Gupta *et al*. 2010) [13]

Five classes of heat shock protein (based on molecular weight) which act as molecular chaperones are identified in plants. These five classes are as sHsps (Small heat-shock proteins) Hsp60, Hsp70, Hsp90, Hsp100, (Kotak *et al*. 2007) [22]. In a recent review, heat-shock proteins are put into families according to molecular weight i. e small Hsp family, Hsp60 family, Hsp70 family, Hsp90 family, Hsp100 family (Kotak *et al*. 2007) [22]. The heat shock proteins (Hsps) act as molecular chaperone. These molecular chaperone regulate the accumulation, localization, degradation and folding of unfolding proteins in plants (Hu *et al*. 2009) [16]

Generally, heat stress up-regulate the HSGs (heat shock genes) which encode heat shock proteins (HSPs) (Chang *et al*. 2007) [6]. Heat shock protein synthesized in the presences of heat shock elements (HSEs) which are present in the promoter region of heat shock gene. The heat shock elements activate the transcription in response to heat. The heat shock elements have 5-AGAANNTTCT-3 nucleotide sequences known as palindromic nucleotide sequences. It helps for recognition of binding site for heat shock transcription factors (HSFs) (Nover *et al*. 2001) [24].

Heat shock proteins generally regulate the thermo tolerances in plants. Under normal environmental condition, heat shock factors present as a monomer in cytoplasm associated with HSP70 but when heat increase HSFs dissociates from HSP70 and enter into nucleus and build trimmer of HSFs that bind with the HSEs (Lee *et al*. 1995) [23].

The binding of heat shock factors with the heat shock elements assists to accumulate other transcriptional components necessary for the gene expression for production of heat shock protein within minutes. As reported by Nover *et al*. (2006) [26], the all the HSGs has conserved sequence of heat shock elements. Heat shock factors activate nearly all HSGs therefore it enhances the production of heat shock protein which provides protection against heat stress.

Cold shock proteins

Like heat shock protein, Cold shock domain proteins (CSD proteins) are also found in higher plants which have vascular bundles or conducting tissues (like xylem) such as *Pinus sylevestris*) and lower plants (Non-vascular plants such as mosses and liverworts) (Karlson and Imai, 2003) [19]. Cold shock proteins are small nucleic acid binding proteins ranging from 65 to 75 amino acid length and are commonly found in plants under low temperature. Thomashow, (1998) [34] stated that the synthesis of cold shock protein enhance cold tolerance. While sufficient researches have been performed to characterize cold shock domain proteins in animals and bacteria but not that significantly yet for plants for their roles. The first functionally characterized plant cold shock domain protein is the wheat CSP (WCSP1) (Karlson *et al*. 2002) [20].

Antifreeze proteins

Antifreeze protein (AFPs) is a polypeptide chain which allows plants to survive under freezing temperature. Under freezing temperature, the process of crystallization begins in plants which could be fatal for the growth of plants. Antifreeze protein binds to ice crystal and inhibit the process of crystallization (Venketesh and Dayananda, 2008) [36]. Antifreeze protein is also observed in animals, fungi and bacteria. But the AFPs found in the plants cell are different from other organism in many ways. These proteins are commonly found in freeze resistant plants in cold regions (Griffith, 2004) [12]. It is noted that during cold acclimation AFP genes produces antifreeze protein. These proteins are activated under low temperature and enhance the production of AFP proteins (Teijo *et al*. 1999) [33]. The production of the Antifreeze protein is a complicated and tissue specific process. Harsh, (2003) [15] reported that Arabidopsis has CBF/DREB1 proteins (act as a transcription factors) which control the expression of cold-induced genes that enhances resistances in plants against freezing.

Late embryogenesis abundant (LEA) proteins

Late embryogenesis abundant protein synthesized in plants in response of desiccation in seed and leave tissues. Late embryogenesis abundant proteins belong to the glycine-rich protein family. According to (Gal *et al*. 2004) [11] the late embryogenesis abundant protein was first observed in seeds during the development of the embryo under drought stress. These proteins were first observed in cotton seed during late embryogenesis and are associated to desiccation (Gal *et al*. 2004) [11] It also protects from freezing, protect other proteins function and also stabilize the membranes (Li *et al*. 2012) [25]. The molecular mass of late embryogenesis abundant proteins ranges from 10-30 k Da, so these have low molecular weight.

Under the drought stress condition plants enhance the accumulation of mRNA which have the coding for late embryogenesis abundant protein (Hand *et al*. 2011) [14]. LEA proteins are classified into different groups based on different amino acid sequences. Finn (2010) [10] classified the Late embryogenesis abundant protein into seven groups based on their primary amino acid sequences which are LEA_1, LEA_2, LEA_3, LEA_4, LEA_5, LEA_6, and SMP (seed maturation protein) Hundertmark *et al*. (2012) [17] reported that LEA genes are commonly found in the plants genome, that are mostly expressed in seed. Battista *et al*. 2001 [4] reported 51 late embryogenesis abundant genes in Arabidopsis thaliana associated to LEA protein synthesis. About 22 LEA genes are expressed in vegetative tissues under desiccation. There are several mechanisms about working of late embryogenesis abundant protein as desiccation tolerances (Hand *et al*. 2011) [14]. Due to hydrophilicity properties of the late embryogenesis abundant proteins are thought to increase their water binding ability and decrease the water removal ability during freezing.

Multidrug and toxic compound extrusion (MATE proteins)

Multidrug and toxic compound extrusion (MATE) is very important protein produced in plants under heavy metal stress. The main function of this protein is the removal of toxic compound from the plants cell (Durrett *et al*. 2007) [9]. Multidrug and toxic compound extrusion protein (MATE protein) belongs to membrane-localized efflux proteins. The MATE type transporters were first observed in bacteria as a bacterial drug transporter and are available in almost all eukaryotes and prokaryotes and are thus one of the commonly conserved transporter families in nature. The main function of theses protein is the removal of poisons compound from the cell. FRD3 is a type of multidrug and toxic compound extrusion protein that assists in loading of iron and citrate into the root's vascular tissues. Xylem exudates from FRD3 mutant plants comprise less citrate and iron as compared to wild-type plants, whereas transgenic plants over-expressing FRD3 synthesize more citrate in root exudates. Iron-citrate complexes are essential for the translocation of iron to the leaves because iron moves via xylem in its chelated form (Durrett *et al*. 2007) [9].

Pathogenesis-related (PR) proteins

Plants also produce defensive proteins against pathogenic attack which is known as Pathogenesis-related proteins (PR proteins). The pathogenic infection activates the gene which is coded for Pathogenesis-related proteins and these genes produce PR proteins. The main role of these proteins is the protection against pathogen (Jwa *et al*. 2017) [18]. Few proteins help immune system to break down the cell wall of a fungus or bacterium while other spread signal of infection to nearby cell. Studies indicated that many proteins are found in vine (climbing plant) which acts as a defensive protein against pathogen like thaumatin and chitinases like proteins (Van-Loon, 1985) [35]. Plants produce different types of defensive proteins under pathogenic effects. During stress conditions, different types of the genes are activated. Various types of the small RNAs (50-250 nucleotides length) play a significant role in plants defense via production of defensive proteins.

Seed storage proteins

Seed storage proteins are biosynthesized in specific tissues and in specific stage of growth. The synthesis of Seed storage protein depends on nitrogen and act as a sink for extra nitrogen. However, quite a few seed storage proteins comprise methionine, cysteine and sufficient sulfur implying that these elements are also compulsory for their biosynthesis. Numerous seeds consist of distinct groups of storage proteins, some of which are enriched with sulfur amino acids while the others are not (Shewry, 1995) [32]. The seed storage proteins are classified into three groups *viz.* albumins, prolamins and globulins.

The biosynthesis of seed storage proteins is regulated in specific tissues or organs and only at specific stages during seed growth. The deposition of the storage protein in specific cells or tissues occurs largely in the absences of the cell division in seed. The young storage parenchyma cells of seeds are commonly found within cotyledons and endosperm of seed. These storage parenchyma cells help in production of various proteins such as acid hydrolases, storage proteins, and plant defense proteins (Shewry *et al*. 1999) [31].

In many seeds protein bodies act as storage vacuoles. The function of the storage vacuoles in the seeds are storage and provide site for macromolecular hydrolysis because vacuole stores several hydrolytic enzymes which are synthesized during the post-germinated step. It is also noted that not all hydrolytic enzymes are produced completely during the post-germinated stage but some are synthesized during the development of seeds. It has also been noted that seeds proteins are compartmentalized into various vacuoles based on their function (Rogers, 1998) [30]. Robinson and Hinz, (1997) [29] stated that there are many pathways of protein biosynthesis in seeds. The pathway involved in synthesis of seed storage protein in dicotyledonous seeds is the fragmentation of a huge central vacuole and storage protein accumulated into fragmented vacuoles through Golgi complex. In few cereals proteins bodies are directly synthesized from Rough endoplasmic reticulum and stored directly with in the organelles. Robinson and Hinz, (1997) [29] also reported that seed storage protein undergoes many changes during or after their synthesis such as assembly, folding, Disulphide, Protelytic processing, bond formation and glycosylation.

Conclusion

This study focused on the synthesis of different types of proteins which is the essential biological compound. It is commonly disturbed in almost all types of the organisms. Proteins differ in function and structure from each other. Some proteins are commonly found in plants which plays a structural role while others are produced under specific conditions. All these types of the protein are synthesized by ribosomes and rough endoplasmic reticulum. The mechanism of the protein synthesis is regulated by specific genes and these genes are activated by the specific circumstantial factors such as heat, cold or pathogens. Proteins also act as molecular chaperones. Some protein produced in response of stress condition such as heat shock protein, cold shock protein, MATE type of proteins, these proteins provide protection to plants against adverse effect of the environment. Few proteins are synthesized as storage protein in seeds which has a sufficient amount of nutrition for humans and animals. These proteins are known as storage proteins and commonly found in cereals grains like wheat, maize, barley and rye.

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