



Computational approach for enzymes present in *Capsicum annuum*: A review

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Introduction

Capsicum annuum (Sweet bell pepper) is a common ingredient of staple food. In Brazil and in some other countries, the sweet bell pepper is considered one of the more important commodities in terms of production volume and commercially (De et al., 2009). There are various species from *Capsicum* genera and all are widely cultivated throughout world. Most enzymes studied have higher specific activity and protein content in green than in the red pepper (Mateos et al., 2003). It's medicinal and antioxidant properties are the main attributes to be focused on research purposes. Further, sweet bell pepper is also a good source of bioactive compounds, such as the carotenoids (Kim et al., 2004). These substances can substantially reduce the risk of

Abstract:

Capsicum annuum or sweet bell pepper is one of the more economical and agriculturally viable vegetable grown all over the world owing to its antioxidant and other medicinal properties. This review highlights the essential enzymes present and its mode of action using bioinformatics online tools viz. uniprot, swissprot and Brenda enzyme db and ExPasy protein databases. The enzymes viz. peroxidase, polyphenol oxidase, tyrosinase, catecholase, Pectin esterase, Catalase, 9-lipoxygenase, L-asparaginase, Polygalactouronase, Capsanthin and Ribulose-Phosphate 3-Epimerase contribute to its properties by various molecular mechanisms. Understanding of these mechanisms will be helpful for application of these enzymes in food processing and in the production of food ingredients. The increasing sophistication of processing industries creates a demand for a broad variety of enzymes with characteristics compatible with food processing conditions for e.g. shelf life of fruits and vegetables can be increased by decreasing the levels of peroxidase and polyphenoloxidase.

Keywords: BRENDA Enzyme DB, *Capsicum annuum*, Enzymes, ExPasy protein DB.

developing degenerative diseases such as macular degeneration in women (Moller et al., 2006). It also inhibit carcinogenic activity (Nishino et al., 2002) and reduce (50% reduced rate) posterior subcapsular cataracts in subjects with higher plasma lutein concentration (Gale et al., 2003). An inclusion complex of red bell pepper pigments with β -cyclodextrin is used as a natural colorant in yogurt (Lidiane et al., 2013). Recent trends of research is continuously shifting towards nanotechnology (Kingsley et al., 2013), computational approach. Computational approach should be applied to understand biological properties and its mechanism e.g. antimicrobial effect of garlic and cinnamon (Shivendu et al., 2012a), antibacterial effect of marigold leaves (Nandita et al., 2012), blood coagulation property of marigold leaves

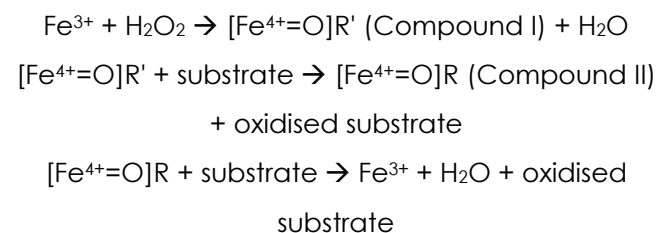
(Shivendu *et al.*, 2012b). This review provides some essential information about the enzymes present in *Capsicum annuum* retrieved from online database viz. swissprot, uniprot, ExPASy, and BRENDA ENZYME DB.

UniProt (launched on 15 December 2003) comprises of three components: Firstly, the UniProt Knowledgebase which will continue the work of Swiss-Prot, TrEMBL and PIR by providing an expertly curated database; Secondly, the UniProt Archive (UniParc) which is updated with novel sequences daily; Thirdly, the UniProt non-redundant reference databases (UniProt NREF), which provide concise views on top of the UniProt Knowledgebase and UniParc (Rolf *et al.*, 2004). Swiss-Prot is the leading universal curated protein sequence database, which contained as of November 2003 (release 42.6) contains 140,000 curated sequence entries from over 8300 different species. Being non-redundant, means that all reports for a given protein are merged into a single entry, and is highly integrated with other databases (Gasteiger *et al.*, 2001). ExPASy is the SIB Bioinformatics Resource Portal which provides access to scientific databases and software tools in different areas of life sciences including proteomics, genomics, phylogeny, systems biology, population genetics, transcriptomics etc (Panu *et al.*, 2012). BRENDA (BRaunschweig ENzyme DATabase) was created in 1987 at the German National Research Center for Biotechnology at Braunschweig and is currently being maintained by the University of Cologne (Priti *et al.*, 2003).

Peroxidase (EC number: 1.11.1)

It belongs to a large Family of Class III Plant Peroxidases i.e. Oxidoreductases. It acts on peroxide as an acceptor. Further peroxidases (POD) are haem-containing enzymes that use

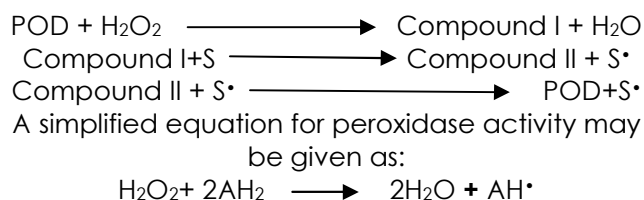
hydrogen peroxide as the electron acceptor to catalyse a number of oxidative reactions. Most haem peroxidases follow the given reaction scheme:



The enzyme reacts with one equivalent of H_2O_2 to give $[\text{Fe}^{4+}=\text{O}]\text{R}'$ (compound I). This is a oxidation/reduction reaction involves transfer of two electrons where H_2O_2 is reduced to water and the enzyme is oxidised. One oxidising equivalent resides on iron, giving the oxyferryl intermediate (Nelson *et al.*, 1994), while in many peroxidases the porphyrin (R) is oxidised to the porphyrin p-cation radical (R'). Compound I then oxidises an organic substrate to give a substrate radical (Li and Poulos, 1994).

POD mainly oxidises phenols to phenoxy radicals, which participate in reactions where polymers and oligomers are produced which are further responsible for enzymatic browning and off-flavor development (Morimoto *et al.*, 2000). It is involved in photorespiration and assimilation of symbiotically induced nitrogen in plant-specific functions. Recent postgenetic approaches in transcriptome and proteome showed that plant peroxisomes have more important roles in various metabolic processes including biosynthesis of plant hormones (Mano and Nishimura, 2005). POD can be found in plants, animals and microbes. It is one of the most thermostable enzymes performing single electron oxidation on a wide variety of compounds in the presence of hydrogen peroxide. POD reduces H_2O_2 to water while oxidizing a variety of other substrates. The catalytic process of POD occurs in a multi step

reaction. This is shown in the following scheme, where S stands for substrate and S• represents the corresponding radical. AH₂ and AH• represent a reducing substrate and its radical product, respectively (Lengauer and Rarey, 1996).



Furthermore, the related activity of PPO and POD is due to the generation of hydrogen peroxide during the oxidation of phenolic compounds in PPO-catalyzed reactions (Francisco and Juan, 2001; Khan and Robinson, 1994; Sugai and Tadini, 2006). Peroxidase is the enzyme responsible for off-flavour development, so its inactivation will inhibit any such off-flavour development (Yemenicioglu et al., 1999).

Polyphenol Oxidase (EC number: 1.14.18.1)

It also belongs to a large family of Class III Plant Peroxidases i.e. Oxidoreductases enzyme family so its mode of action is similar to that of POD i.e. acts on paired donors with O₂ as the oxidant and incorporation or reduction of oxygen. The incorporated oxygen need not be derived from O₂; or with another compound as a single donor, and incorporation of one oxygen atom into the other donor (Francisco and Juan, 2001; Khan and Robinson, 1994). Polyphenol oxidase (PPO) is a dicopper-containing enzyme which is involved in the oxidation of the polyphenols from plants. PPO shows a higher activity with diphenols (Onsa et al., 2000). Two kinds of reactions catalyzed by PPO are the hydroxylation of monophenols to o-diphenol and the oxidation of o-diphenol to o-quinone (Francisco and Juan, 2001) schematic

reaction of which is shown in Figure 1 (Prontipa et al., 2010).

The browning process can be caused by both enzymatic and non-enzymatic biochemical reactions. Polyphenol oxidase (PPO) and peroxidase (POD) are two well known enzymes involved in the browning process (Sapers, 1993; Chen et al., 2000; Deepa et al., 2007). PPO catalyzes the conversion of phenolic compounds to quinones and assists their products' polymerization in the presence of oxygen leading to the formation of undesirable brown pigments and off-flavored products. The browning of injured, peeled or diseased fruit tissues can cause undesirable changes in quality during handling, processing or storage (Yemenicioglu et al., 1999). Different forms of PPO are found in *Capsicum annum*, such as tyrosinase (Nisit et al., 2007), catecholase (Deepa et al., 2007).

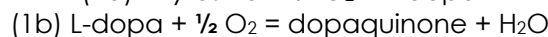
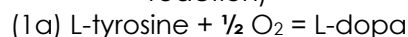
Tyrosinase/Cresolase/Phenolase (EC 1.14.18.1)

Generally known as Tyrosinase but can also be named as monophenol monooxygenase, phenolase, monophenol oxidase, cresolase, monophenolase, tyrosine-dopa oxidase, monophenol monooxidase, monophenoldihydroxyphenylalanine oxygen oxidoreductase, N-acetyl-6-hydroxytryptophan oxidase, monophenol, dihydroxy-L-phenylalanine oxygen oxidoreductase, o-diphenol oxygen oxidoreductase, phenol oxidase. Its synthetic name is L-tyrosine,L-dopa:oxygen oxidoreductase (BRENDA, 2013; ExPASy, 2013).

It is type III copper protein found in a variety of bacteria, fungi, plants, insects, crustaceans, and mammals, which is involved in the synthesis of betalains and melanin. The enzyme, which is activated upon binding molecular oxygen, can catalyze both a monophenolase reaction cycle (reaction 1) or a diphenolase reaction cycle

(reaction 2). During the monophenolase cycle, one of the bound oxygen atoms is transferred to a monophenol (such as L-tyrosine), generating an o-diphenol intermediate, which is subsequently oxidized to an o-quinone and released along with a water molecule. The enzyme remains inactive in its deoxy state and is further restored to the active oxy state by the binding of a new oxygen molecule. During the diphenolase cycle the enzyme binds to an external diphenol molecule (such as L-dopa) and oxidizes it to an o-quinone that is released along with a water molecule, leaving the enzyme in the intermediate met state. The enzyme then binds to a second diphenol molecule and repeats the process, thereby ending in a deoxy state (Rolff et al., 2011; Steiner et al., 1996).

Reaction (1)



Reaction (2)

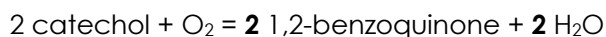


Catechol oxidase/ Catecholase (EC 1.10.3.1)

Generally known as Catechol oxidase but can additionally called as diphenol oxidase, o-diphenolase, polyphenol oxidase, pyrocatechol oxidase, dopa oxidase, catecholase, o-diphenol oxygen oxidoreductase and o-diphenol oxidoreductase, but the synthetic name is 1,2-benzenediol:oxygen oxidoreductas (BRENDA, 2013; ExPASy, 2013).

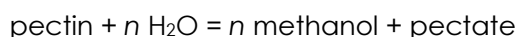
It is also a type 3 copper protein that catalyses the oxidation of catechol (i.e., o-diphenol) to the corresponding o-quinone exclusively. The enzyme also acts on a variety of substituted catechols. Unlike tyrosinase which can catalyse both the monooxygenation of monophenols and the

oxidation of catechols (Mayer and Harel, 1979; Gerdemann et al., 2002).



Pectinesterase (EC 3.1.1.11)

Pectinesterase which can also be called as pectin demethoxylase, pectin methoxylase, pectin methylesterase, pectase, pectin methyl esterase and pectinoesterase. The Systematic name is pectin pectylhydrolase (BRENDA, 2013; ExPASy, 2013). Pectin in presence of water is converted into *n* methanol and pectate with the help of enzyme pectin esterase (Figure 2).



It is involved in the regulation of the cell wall rigidity and also plays a key role in process of fruit ripening (Castro et al., 2004). Temperature stability is indicated by presence of 75% enzyme activity at 55°C, 10% activity activity activity at 75°C and 5% at 85°C, maximum stability of it is found upto a maximum temperature of 95°C (Mejia-Cordova et al., 2005).

7. Catalase (Ec 1.11.1.6)

The enzyme Catalase is also referred as equilase, caperase, optidase, catalase-peroxidase, CAT and its **systematic name** is hydrogen-peroxide:hydrogen-peroxide – oxidoreductase (BRENDA, 2013; ExPASy, 2013).

It is an oxidoreductase by classification and its mode of action is the same as others mentioned previously i.e. it reduces H₂O₂ to water (2 H₂O₂ = O₂ + 2 H₂O) (Dounce, 1983). This enzyme can also act as a peroxidase for which several organic substances like ethanol can act as a hydrogen donor. A manganese protein containing Mn^{III} in the resting state, which also belongs here, is often called pseudocatalase (Kono and Fridovich, 1983). It is found in stems, leaves, roots and developing fruits of capsicum annuum and serves to protect cells from the toxic effects of hydrogen

peroxide by reducing it to water. There are 492 amino acids present in it (Kwon and An, 2001).

Linoleate 9S-lipoxygenase /9-lipoxygenase (EC 1.13.11.58)

The above enzyme can also be termed as 9-lipoxygenase, 9S-lipoxygenase, linoleate 9-lipoxygenase, LOX1 (gene name), 9S-LOX, and the synthetic name is linoleate:oxygen 9S-oxidoreductase (BRENDA, 2013; ExPASy, 2013). It converts linoleate to 9-hydroperoxy-10,12-octadecadienoate in presence of oxygen. (Gigot et al., 2010)

Overall Reaction:

Linoleate + O₂ = (9S,10E,12Z)-9-hydroperoxy-10,12-octadecadienoate

It contains a nonheme iron and a common plant lipoxygenase that oxidizes linoleate and alpha-linolenate, the two most common polyunsaturated fatty acids in plants by inserting molecular oxygen at the C9 position with (S)-configuration. The enzyme plays a physiological role during the early stages of seedling growth (Bannenberget al., 2009).

In capsicum annum it regulates defense and cell death response to microbial pathogens. The optimum temperature for its activity is 25°C with an optimum pH of 6 ranging upto a mximum of pH 6.5 (Hwang and Hwang, 2010).

L-Asparaginase/ L-asparaginase (EC 3.5.1.1)

Its accepted name is asparaginase and can be also called as asparaginase II, L-asparaginase, colaspase, elspar, leunase, crasnitin and α-asparaginase. The synthetic name is L-asparagine amidohydrolase (BRENDA, 2013; ExPASy, 2013). It catalyzes the reaction in which asparaginase is involved in cells (Figure 3) overall reaction is as; L-asparagine + H₂O = L-aspartate + NH₃ (Narta et

al., 2007). It is responsible for asparagine degradation (Yao et al., 2005) and is involved in the interconversion of aspartate and asparagines (Falzone et al., 1988).

It is found in Capsicum annum, Datura inoxia, Pisum sativum, Solanum lycopersicum, Tamarindus indica, Vigna unguiculata, Withania somnifera etc with the function of asparatate degradation and is also involved in the interconversion of aspartate and asparagines (Oza et al., 2009).

Polygalactouronase/PG (EC 3.2.1.15)

It can also be called as pectin depolymerise, pectinase, endopolygalacturonase, pectolase, pectin hydrolase, pectin polygalacturonase, endo-polygalacturonase, poly-α-1,4-galacturonide glycanohydrolase, endogalacturonase and endo-D-galacturonase. Its synthetic name is poly (1, 4-α-D-galacturonide) glycanohydrolase (BRENDA, 2013; ExPASy, 2013). It is involved in the random hydrolysis of (1→4)-α-D-galactosiduronic linkages in pectate and other galacturonans. It splits pectin chain by adding a molecule of water and breaks the linkage between two galacturonan units. These enzymes catalyze reactions that break α-1,4-glycosidic bonds (Huang et al., 1990).

PG activity increases during ripening. Ripening specific pectin methylesterase, active in vivo, appears to enhance PG-mediated pectin ultra-degradation, resulting in cell wall dissolution and emergence of deciduous fruit traits. Some pectin methylesterase isozymes are apparently inactive in vivo, particularly in green fruit and throughout ripening in the 'Hard Pick' line, thereby limiting PG-mediated pectin depolymerization which results in moderately difficult fruit separation from the calyx (Rancibia and Motsenbocker, 2006). It is also involved in homogalacturonan degradation (Willats et al., 2001). Exo-poly-α-D-

galacturonosidase (EC 3.2.1.82) (exoPG) hydrolyzes peptic acid from the non-reducing end, further releasing digalacturonate (He and Collmer, 1990). It is found in *Capsicum frutescens* and *capsicum annum* with the similar functions of ripening (Gong et al., 2008).

Capsanthin (EC 5.3.99.8)

Its accepted name is capsanthin/capsorubin synthase and some other names are as CCS, ketoxanthophyll synthase, capsanthin-capsorubin synthase and Systematic name is violaxanthin-capsorubin isomerase (BRENDA, 2013; ExPASy, 2013). Capsanthin catalyses two reactions from substrate antheraxanthin and violaxanthin which produce capsanthin and capsorubin respectively (Bouvier et al., 1994).

This multifunctional enzyme is induced during the chromoplast differentiation in plants; the gene is specifically expressed during chromoplast development in fruits thereby accumulating ketocarotenoids but not in mutants impaired in this biosynthetic step (Bouvier et al., 1994). In *capsicum annum* it is involved in capsanthin and capsorubin biosynthesis (Al-Babili et al., 2000). It has relation with molecular genetics as *y* locus in pepper is responsible for capsanthin-capsorubin synthase which ultimately relates to the color of *capsicum annum* (Popovsky and Paran, 2000). The capsanthin-capsorubin synthase gene is activated specifically during the final stages of *Capsicum* fruit ripening (Lefebvre et al., 1998).

Ribulose-Phosphate 3-Epimerase (EC 5.1.3.1)

Its accepted name is ribulose-phosphate 3-epimerase but follows some other names such as phosphoribulose epimerase, erythrose-4-phosphate isomerase, phosphoketopentose 3-epimerase, xylulose phosphate 3-epimerase,

phosphoketopentose epimerase, ribulose 5-phosphate 3-epimerase, D-ribulose phosphate-3-epimerase, D-ribulose 5-phosphate epimerase, D-ribulose-5-P 3-epimerase, D-xylulose-5-phosphate 3-epimerase, pentose-5-phosphate 3-epimerase and Systematic name is D-ribulose-5-phosphate 3-epimerase (BRENDA, 2013; ExPASy, 2013). Enzyme ribulose-phosphate 3-epimerase is involved in the conversion of D-ribulose 5-phosphate into D-xylulose 5-phosphate as shown in Figure 4 (Thom et al., 1998)

In *capsicum* it is mainly involved in the pentose-phosphate pathway, although it has many functions like the Bifidobacterium shunt, Calvin-Benson-Bassham cycle, D-arabinose degradation II, formaldehyde assimilation II (RuMP Cycle), formaldehyde assimilation III (dihydroxyacetone cycle), heterolactic fermentation, pentose phosphate pathway (non-oxidative branch) and the ribitol degradation (Thom et al., 1998).

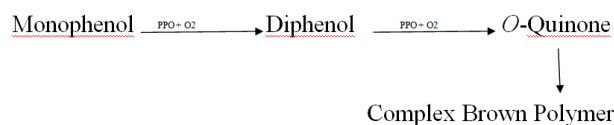


Figure 1: Hydroxylation of monophenols to diphenols and to o-quinone

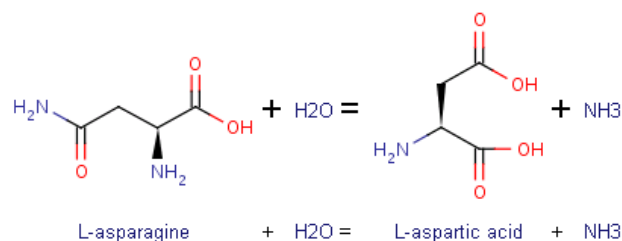


Figure 2: Overall reaction in which enzyme asparaginase is involved

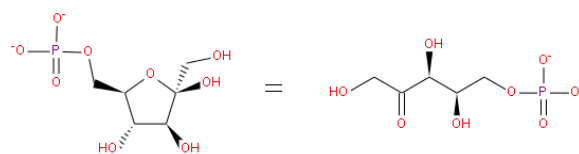


Figure 3: Overall reaction in which ribulose-phosphate 3-epimerase is involved

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