

# The Tyrosinase Protein Families

Chem184

May 13, 2008

**How can you identify a member?**

**Is protein sequence information enough?**

**Is catalytic activity enough?**

**What reaction(s) can tyrosinases catalyze?**

**What reaction(s) do tyrosinases catalyze *in vivo*?**

**Do all tyrosinases catalyze the same reaction(s)?**

# *Agaricus bisporus*

**White button, brown button, Portobello**



*Agaricus bisporus* Tyrosinase:

- isolated in 1858 (Shoenbein)
- purified in 1938 (Kibowitz)

# Enzymatic Browning in Plants/Fungi

- Polyphenol Oxidases: Tyrosinase and Laccase
- Laccases
  - also a type 3 copper enzyme
  - activity against ortho- and para-phenols and are inactive against monophenols
  - Different pH optima than tyrosinase
  - Different susceptibility to inhibitors
  - No significant laccase in *A. bisporus* (makes our life easier)
- Peroxidases
  - Oxygen from  $\text{H}_2\text{O}_2$  not  $\text{O}_2$

# Homologs: Two genes descended from a common ancestor

- Two genes with high sequence identity/similarity are usually *assumed* to be homologs.
- Sequence similarity is **not** essential (hemocyanin and tyrosinase)
- Similar structure is pretty much essential (same general folds)
- Similar/Identical function is not essential (hemocyanin and tyrosinase)

## Isoforms, isoenzymes, glycoforms, allozymes

ISOFORMS: most general term, same or different gene, different splicing, different proteolysis, different glycosylation, different phosphorylation

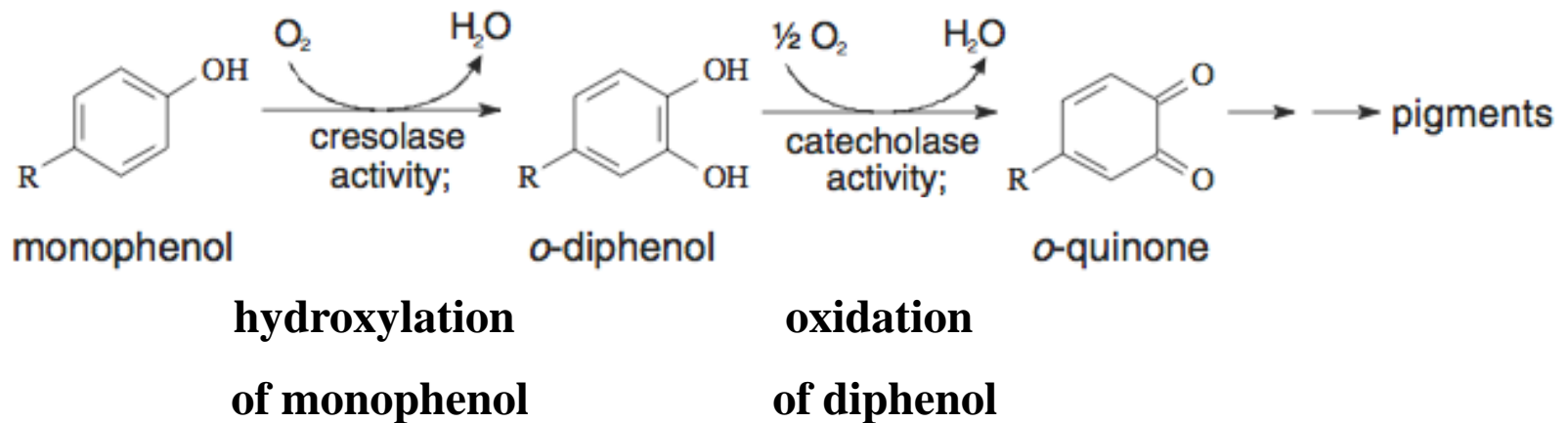
ISOENZYMES: different genes, same reaction (tend to have different  $K_M$ ) ??

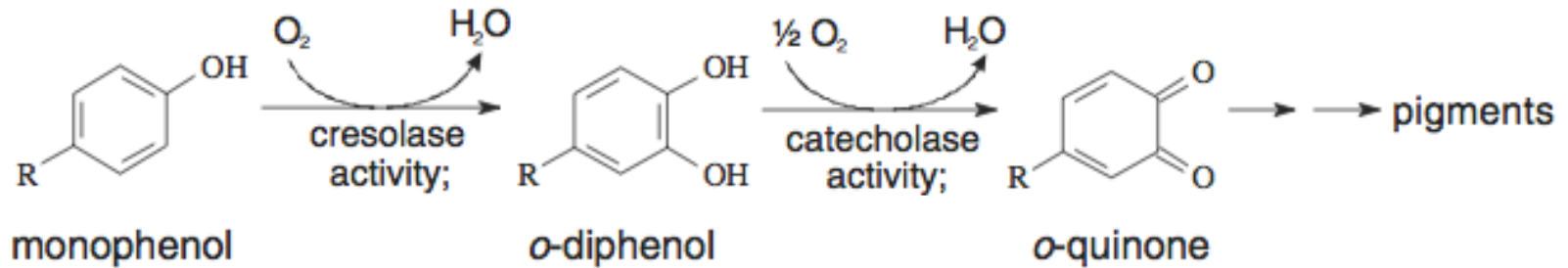
GLYCOFORMS: different glycosylation pattern

ALLOZYMES: products of different alleles of the same gene

# Tyrosinase

- Involved in the synthesis of melanins and other polyphenolic compounds.
- Able to (1) insert an oxygen in a position ortho- to an existing hydroxyl in an aromatic ring and (2) oxidizes the resulting diphenol to the quinone
- Molecular oxygen is used





**hydroxylation  
of monophenol**

**oxidation  
of diphenol**

CATECHOL OXIDASE  $\neq$  TYROSINASE

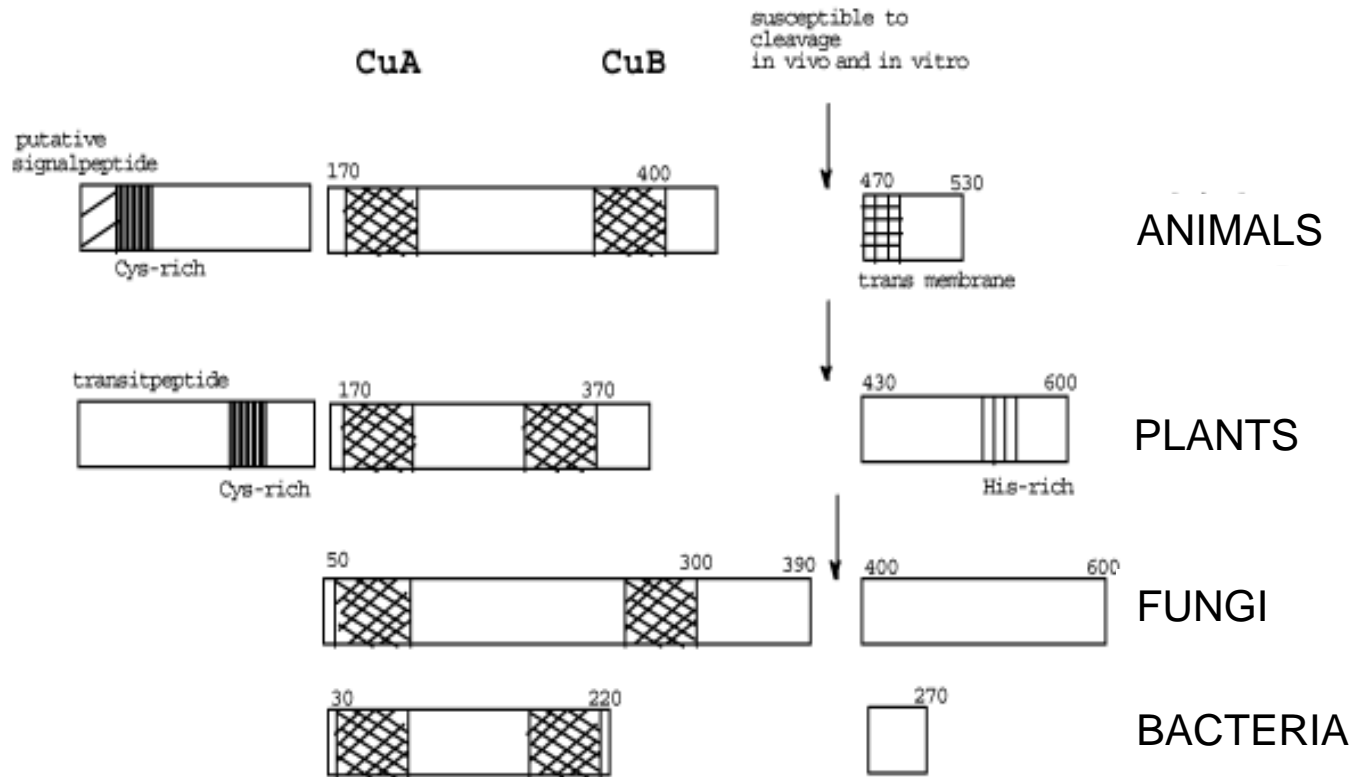
*BUT SEE LATER ...*

# Tyrosinase: Nearly ubiquitous

- Bacteria, plants, animals, fungi
- Higher similarity within groups than between
  - No common structure
  - Differ with respect to sequence (20%), primary structure, glycosylation pattern, activation characteristic

## **Similarities:**

- **Binuclear type 3 copper center in active site**
- **All have 2 conserved regions CuA and CuB**





tyrosinase

<i>Agaricus bisporus</i> PPO1	White button mushroom (& portobello)
<i>Agaricus bisporus</i> PPO2	
<i>Lentinus edodes</i>	Shitake
<i>Podospora anserina</i>	Other fungi
<i>Polyporus arcularius</i>	
<i>Aspergillus fumigatus</i>	
<i>Aspergillus oryzae</i>	
<i>Neurospora crassa</i>	
<i>Streptomyces avermitilis</i>	Streptomyces (gram + soily bacteria; neosporin)
<i>Streptomyces coelicolor</i>	
<i>Streptomyces glauscesens</i>	
<i>Mus musculus</i>	Mouse
<i>Homo sapiens</i>	
<i>Helix pomatia</i>	Human
<i>Panulirus interruptus</i>	Snail
<i>Vicia faba</i>	Spiny lobster
<i>Lycopersicon esculentum</i>	Fava bean
	Tomato

haemocyanin

catecholase

*Agaricus bisporus* PPO1  
*Agaricus bisporus* PPO2  
*Lentinus edodes*  
*Podospora anserina*  
*Polyporus arcularius*  
*Aspergillus fumigatus*  
*Aspergillus oryzae*  
*Neurospora crassa*  
*Streptomyces avermitilis*  
*Streptomyces coelicolor*  
*Streptomyces glauscesens*  
*Mus musculus*  
*Homo sapiens*  
*Helix pomatia*  
*Panulirus interruptus*  
*Vicia faba*  
*Lycopersicon esculentum*

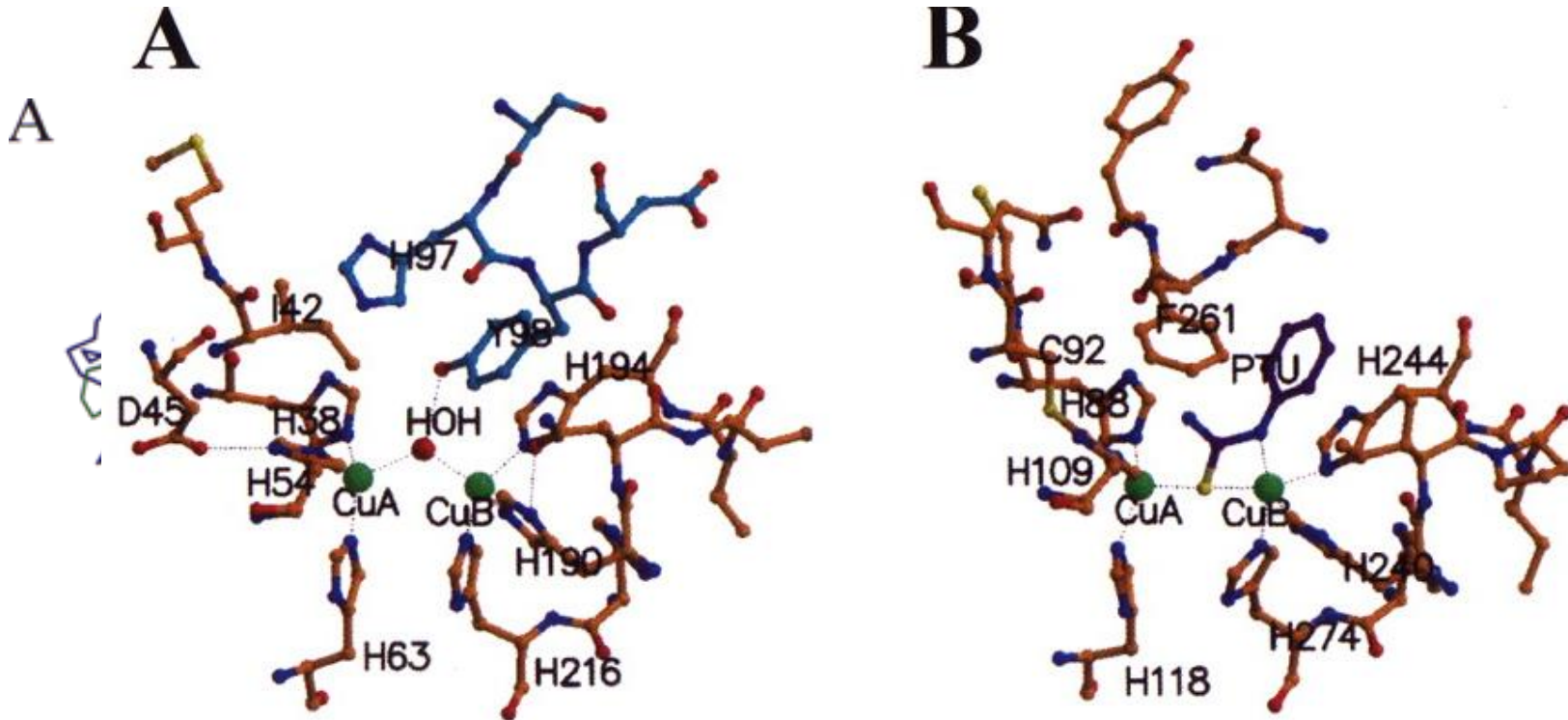
	CuB
VHDDIHVMVGYGKIEG-----HMDHPFFAAFDPFI FWLHHTNVDRLLSLWKAINPI	
IHDNIHVLVGG---NG-----HMSDPSVAPFDPI FFLH HANVDRLIALWSAIRYI	
IHDSVHVDVGG---NG-----QMSDPSVAGFDPI FFMH HAQVDRLLSLWSALNPI	
VHNEIHDRTGG---GG-----HMSSLDVSSFDPLEFWFHHTNVDRLLWAIWQDLNPI	
IHDGIHVAVGG---NG-----HMSDPSVAAFDPFI FFLH HCQVDRLLALWSALNPI	
IHNNVHNWVGGTDYLGDPSPKPDQAGHMSSVPVAAFDPFI FWLYHNNVDRLTAIWQVLNPI	
PHNDMHLAIGGVQIPGFNVQYAGANGDMGENDTASFDPFI FYFH HCFIDYLFWTWQTMHKI	
VHNEIHDRTGG---NG-----HMSSLEVSADFPLFWLH HVNVDRLLWSIWQDLNPI	
NHNRVHRWVGG-----HMVSG-ASVNDPVFWMH HAFVDLLWSRWQQRHQ-	
NHNRVHRWVGG-----AMVGG-ASVNDPVFVWLH HAFIDLQWSRWQARHR-	
LHNRVHVWVGG-----QMATG-MSPNDPVFVWLH HAYVDKLWAEWQRHP-	
MHNALHIFMNG-----IMSQVQGSANDPI FLLH HAFVDSIFEQWLRRHRI	
MHNALHIYMNG-----TMSQVQGSANDPI FLLH HAFVDSIFEQWLRRHRI	
SHNAIHSWTGGQSPYG-----MSTLEYTAYDPLFLLH HSNVDRQFAIWQALQKI	
LHNTAHVMLGRQGDPHG---KFNLPVGVMEHFETATRDPS FFRLLHKYMDNIFKKHTDSFPI	
PHAPVHTWTGDN-----TQTNIEDMGI FYSAADPI FYSH HSNVDRLLWYIWKTLGGI	
PHSPVHIWVGTRR-GSVLPVVKISNGEDMGNFYSAGLDPLEYCH HSNVDRMWNENKATGGI	

# Tyrosinase structure

- All tyrosinases and catechol oxidases and hemocyanins have a binuclear type 3 copper center
- Each copper atom is coordinated with three histine residues
- Both a catechol oxidase from sweet potato and a tyrosinase from *Streptomyces castaneoglobisporus HUT 6202* have been crystallized and the structure solved
- Steptomycetes structure has “caddie” protein
- Pymol

# Tyrosinase, catechol oxidase, and octopus hemocyanin

seq catechol oxidase and tyrosinase (25%), tryosinase and hemocyanin (-)

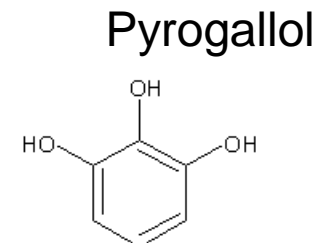
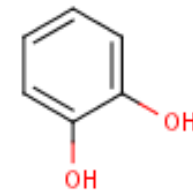
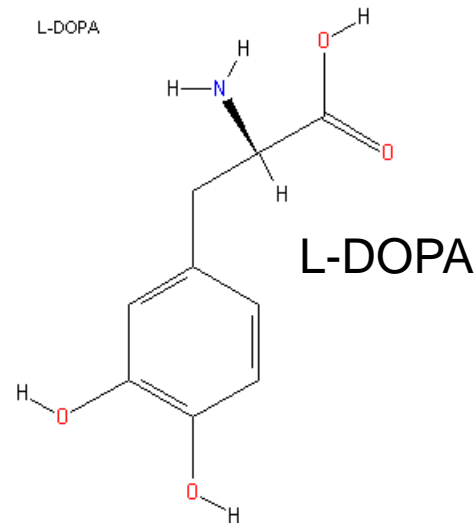


**A** tyrosinase (blue from caddie), **B** catechol oxidase (notice the phe F261) - PTU is inhibitor

(hemocyanin shield blocks active site)

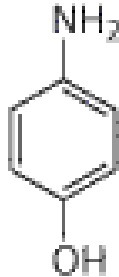
# Mushroom Tyrosinase

- Different isoforms have different activities. None show significant tyrosine hydroxylation. Monophenol oxidase activity is lower (almost nonexistent) than diphenol oxidase activity
- Ex. Cap skin – highest to lowest. **THIS IS A MIXTURE OF MANY ISOFORMS!**
  - Catechol
  - 4-methylcatechol
  - L-dopa
  - Pyrogallol

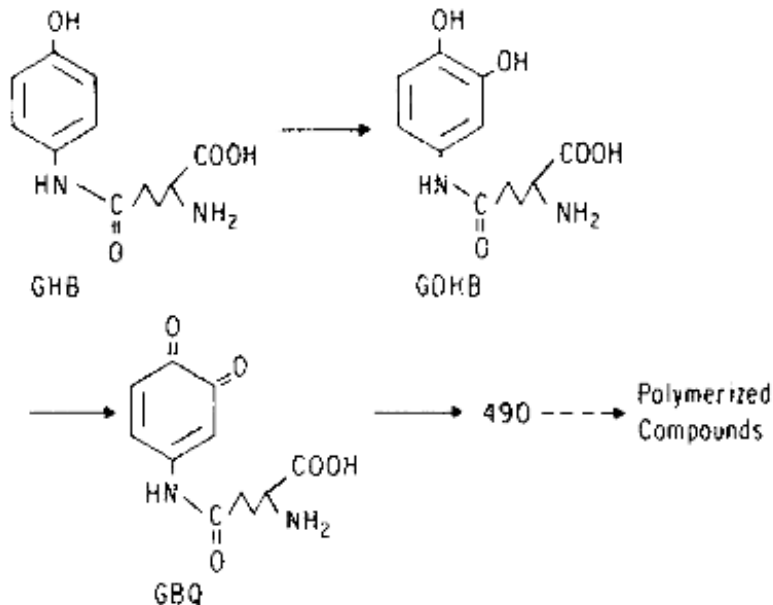


# Mushroom tyrosinase: *putative* substrates *in vivo*

- p-aminophenol



- glutaminyl-4-hydroxybenzene (GHB)



Browning seems to be controlled by decompartmentalization

# Mushroom Tyrosinase Sequence

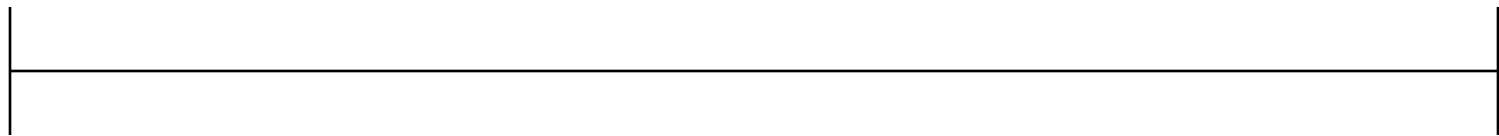
- Wichers et al. (2003) Appl. Microbiol. Biotechnol 61: 336-341
- Two genes AbPPO1 and AbPPO2 (*notice safe use of PPO*)
- Proteolysis
- Many glycosylation and phosphorylation sites
- Protein produced in *E.coli* is recognized by antibody but is NOT active
- 90% certainty no other PPO genes

# Glycosylation

- 10 bands on IEF gel ?? (Flurkey)
- Low pI bands are due to glycosylation - review
- Quick review of glycosylation:
  - 2 types N-linked and O-linked
  - **N-linked**: N-acetylglucosamine is linked to the amide nitrogen of asparagine (asp-X-thr or asp-X-ser), more moieties are bound to the glucosamine (VARIABLE)
  - **O-linked**: moieties are linked to ser or thr, 1 - 1000 moieties  
VARIABLE
  - **MICROHETEROGENITY**
  - NO GENERALIZATIONS REGARDING FUNCTION
  - **Any takers?**

# Final thought:

- Should we rename the lab “Characterization of catechol oxidase from mushroom” ?
- Tyrosinase vs. catechol oxidase
  - Black, white or gray?



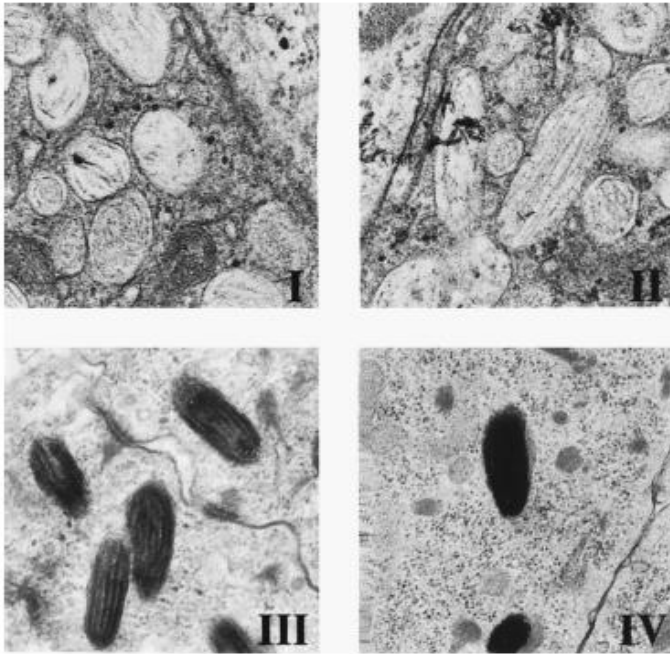
*tyrosinase*

*Catechol oxidase*

Anybody want to try a site-directed mutagenesis approach?



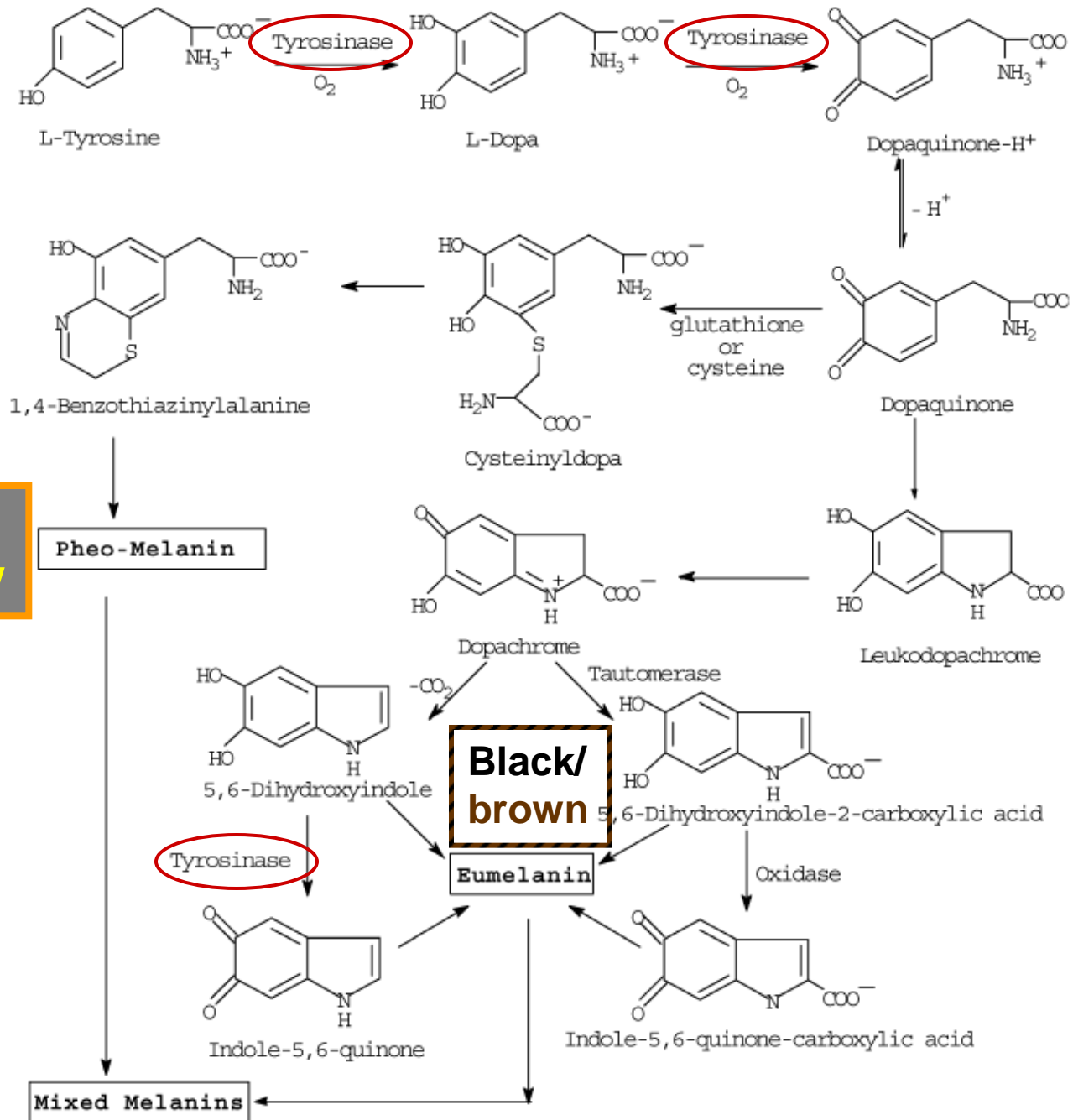
# Human Tyrosinase



- Tyrosinase is a critical enzyme in melanin production
- It catalyzes the hydroxylation of tyrosine and DOPA
- Hydroxylation of tyrosine is the rate-limiting reaction in melanin biosynthesis
- After DOPAquinone is formed melanin synthesis is spontaneous *in vitro*.
- All enzymes are membrane bound

**Melanocytes synthesize melanin in melanosomes and transport the mature melanosomes to keratinocytes.**

Scheme 1. Pathway of Melanogenesis (13, 16, 17)



# Human Tyrosinase Family

- The human tyrosinase gene family has three members: tyrosinase (TYR), tyrosinase related protein 1 (TRP1), and tyrosinase related protein 2 (DCT, TRP2).
- They bind different divalent metal cations and have different catalytic properties. They act in a complex. DCT1 (trp2) binds zinc, tyrosinase binds copper, and it is unclear which cation is bound by TRP1.
- Trp1 and tyrosinase share 40% AA identity. Dct and tyr share 32% identity; both were identified because they are recognized by tyrosinase antibodies.
- SEE NEXT SLIDE FOR TRP2 CONFUSION. MIGHT BE MORE IMPORTANT IN COMPLEX STABILIZATION.
- All three are involved in melanin biosynthesis.
- They do NOT have detectable levels of each others enzymatic activity.

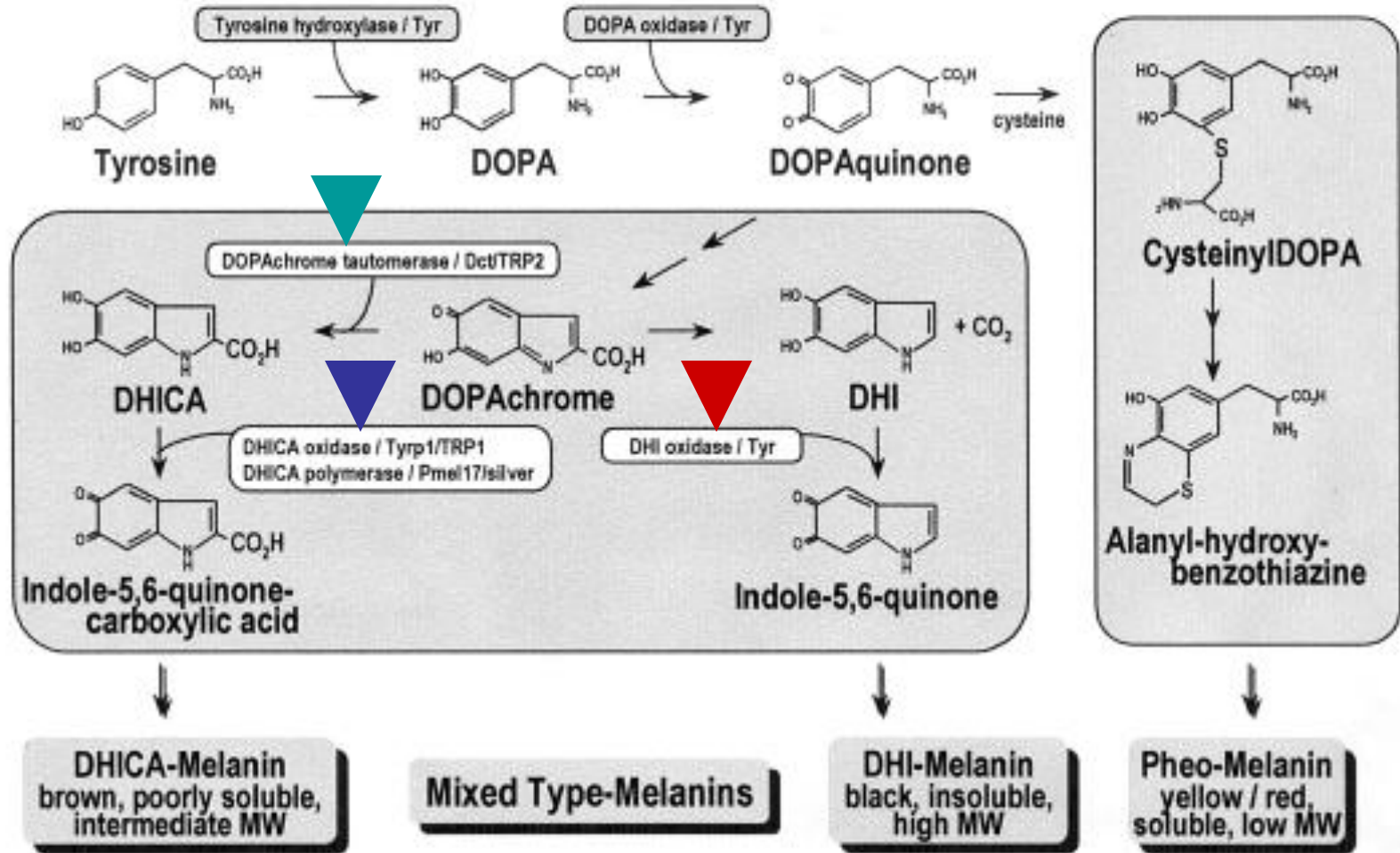
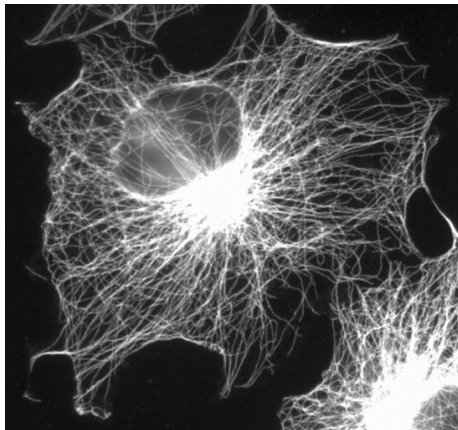


Fig. 220-4 Melanin biosynthetic pathway. The melanin pathway presents a summary of the known reactions and regulatory enzymes in eumelanogenesis and pheomelanogenesis.

Dopa is a required cofactor for tyrosinase hydroxylation. Mouse tyrosinase can hydroxylate DHI but not DHICA, BUT human tyrosinase can use DHICA. Mouse Trp1 can use DHICA BUT human cannot! (99%)

# Fishy Melanosome Movies (Borisy lab)

- Melanosomes are vesicles filled with melanin
- All the enzymes are in the membrane with the enzymatic subunit inside
- Melanosomes are moved along the microtubule tracks by kinesin (towards the outside) and dynein (towards the center)
- Caffeine inhibits dynein - MOVIE 1
- Melanosomes are moved along actin filaments by myosins; actin filaments
- Lantrunculin disrupts the actin network



**Nomenclature Committee of the International Union of Biochemistry  
and Molecular Biology (NC-IUBMB)**

**EC 1.14.18.1**

**Accepted name:** monophenol monooxygenase

**Reaction:** L-tyrosine + L-dopa + O<sub>2</sub> = L-dopa + dopaquinone + H<sub>2</sub>O

**Other name(s):** tyrosinase; phenolase; monophenol oxidase; cresolase; catechol oxidase; polyphenolase; pyrocatechol oxidase; dopa oxidase; chlorogenic oxidase; catecholase; polyphenol oxidase; monophenolase; *o*-diphenol oxidase; chlorogenic acid oxidase; diphenol oxidase; *o*-diphenolase; tyrosine-dopa oxidase; *o*-diphenol:oxygen oxidoreductase; polyaromatic oxidase; monophenol monooxidase; *o*-diphenol oxidoreductase; monophenol dihydroxyphenylalanine:oxygen oxidoreductase; *N*-acetyl-6-hydroxytryptophan oxidase; monophenol, dihydroxy-L-phenylalanine oxygen oxidoreductase; *o*-diphenol:O<sub>2</sub> oxidoreductase; phenol oxidase

**Systematic name:** monophenol,L-dopa:oxygen oxidoreductase

**Comments:** A group of copper proteins that also catalyse the reaction of [EC 1.10.3.1](#) catechol oxidase, if only 1,2-benzenediols are available as substrate.

**Nomenclature Committee of the International Union of Biochemistry  
and Molecular Biology (NC-IUBMB)**

**EC 1.10.3.1**

**Accepted name:** catechol oxidase

**Reaction:**  $2 \text{ catechol} + \text{O}_2 = 2 \text{ 1,2-benzoquinone} + 2 \text{ H}_2\text{O}$

**Other name(s):** diphenol oxidase; *o*-diphenolase; phenolase; polyphenol oxidase; tyrosinase; pyrocatechol oxidase; Dopa oxidase; catecholase; *o*-diphenol:oxygen oxidoreductase; *o*-diphenol oxidoreductase

**Systematic name:** 1,2-benzenediol:oxygen oxidoreductase

**Comments:** A group of copper proteins that act also on a variety of substituted catechols, and many of which also catalyse the reaction listed under [EC 1.14.18.1](#) monophenol monooxygenase; this is especially true for the classical tyrosinase.

## References

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**Read about mechanism & biological function!**