

Structural analysis of two distinct dihydroflavonol 4-reductases in *Gerbera* Hybrids

Alberto Cassetta¹, Dorian Lamba¹, Hany Bashandy², Teemu Teeri², Stefan Martens³

¹*Institute of Crystallography, Consiglio Nazionale delle Ricerche, Trieste Outstation, Area Science Park – Basovizza, S.S. 14 Km 163.5, I-34149 Trieste, (Italy)*

²*Department of Agricultural Sciences, University of Helsinki, Finland*

³*Food Quality and Nutrition Department, IASMA Research and Innovation Centre, Fondazione Edmund Mach, Via E. Mach 1, I-38010 San Michele all'Adige, (TN), Italy*

Dihydroflavonol 4-reductase (DFR) is a key enzyme within anthocyanin biosynthesis known for its distinct substrate specificity found in various plant species (1,2). Based in the findings of enzymatic studies and *in vivo* inhibition experiments in cyanidin accumulating genotype “Clivia” two DFRs with different substrate preference were postulated. Cloning approaches with petals of “Clivia” led to the identification of a second DFR sequence sharing around 96% identity to the previously cloned DFR from pelargonidin accumulating variety “Regina” (1,3). The obtained recombinant protein shows a higher preference for dihydroquercetin (DHQ) while dihydrokaempferol (DHK) was still converted to leucopelargonidin (LPg) to a certain extent. However, the overall ratio showed a clear preference for the cyaniding branch of the pathway.

To shed light on this biochemical aspect of the anthocyanins biosynthetic pathway, we have attempted an *in silico* structure-based approach aiming to relate the specific amino acid differences in the DFRs of *Gerbera* “Regina” and “Clivia” varieties, with their molecular structures and enzyme selectivity data. The DFR models have been built using the crystal structure of the DFR from *Vitis vinifera*⁴ (PDB ID 2C29) as a template. We suggest that a residue belonging to the “specificity loop” located near the substrate “binding site” confers the observed substrate-binding specificity. Namely, Gly135 (*Gerbera* “Regina” DFR) or Val135 (*Gerbera* “Clivia” DFR) respectively, is likely to unlock or lock the orientation of the conserved residue Asn134 that in turn is engaged in hydrogen bonding interactions with 4' OH' of ring B of DHK or both 3' OH' and 4' OH' of ring B of DHQ. Interestingly the side chain orientation of Val135 (*Gerbera* “Clivia” DFR) is restricted and stabilized by hydrophobic interactions with the conserved residues Ile154 and Phe165.

Tab. 1: substrate specificity of *Gerbera* DFRs *in-vitro* with DHK and DHQ as substrates.

% conversion	heterologous expression in yeast	
	<i>Gerbera</i> „Regina“	<i>Gerbera</i> „Clivia“
DHK to LPg	30,66	10,07
DHQ to LCy	49,41	62,92
ratio LPg/LCy	0,62	0,16

As substrate a mixture of 2000 dpm [¹⁴C]-DHK and [¹⁴C]-DHQ each was used

References

1. Martens S, Teeri T, Forkmann G. (2002). Heterologous expression of dihydroflavonol 4-reductases from various plants. FEBS Lett. 531(3):453-458.
2. Smith SD, Wang S, Rausher MD. (2013). Functional evolution of an anthocyanin pathway enzyme during a flower color transition. Mol Biol Evol. 30(3): 602-612.
3. Helariutta Y, Elomaa P, Kotilainen M, Seppänen P, Teeri TH. (1993). Cloning of cDNA coding for dihydroflavonol-4-reductase (DFR) and characterization of dfr expression in the corollas of *Gerbera hybrida* var. Regina (Compositae). Plant Mol Biol. 22(2): 183-193.
4. Petit P, Granier T, d'Estaintot BL, Manigand C, Bathany K, Schmitter JM, Lauvergeat V, Hamdi S, Gallois B. (2007). Crystal structure of grape dihydroflavonol 4-reductase, a key enzyme in flavonoid biosynthesis. J Mol Biol. 368(5):1345-1357.