

A note on the flower color polymorphism in *Hibiscus rosa-sinensis* L.

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Flower colors in many angiospermic plants are controlled by many genes. The flower colour polymorphism is related to the enzymatic components of flavonoid biosynthesis.

A wide variety of mobile elements have been identified in the *Ipomoea* genome (Morita *et al* 1999). Some of these mobile element insertions cause phenotypic changes, including those responsible for several flower color variants. Works on Japanese morning glory (*I. nil*) has provided an extensive research foundation. Considerable work has also been done on *I. purpurea*, which is a member of the same subgenus as *I. nil*. Both species appear to be quite closely related at the DNA sequence level. Molecular clock calculations indicate that the two species diverged roughly three million years ago based on synonymous divergence at DFR and CHS gene. These two closely related species provide a useful comparative framework for the analysis of genetic change over a relatively short period of evolutionary time (Clegg 2002).

The genus *Hibiscus* includes approximately 250 species distributed in tropics and subtropics of the world that are characterized by a diversity of floral pigmentation patterns. The common garden shrub *Hibiscus rosa-sinensis* L. is a native of Tropical Asia (Sharma *et al* 1993) and its innumerable cultivars have been produced through complex interspecific hybrids and their derivatives involving 8 or more different species originating from the African East Coast and islands in the Indian and Pacific Ocean.

The flower color polymorphisms is common *china rose* and is characterized by a series of colors including white, pink, purple, and red phenotypes. Recently, in authors' garden a white-flowered china-rose plant has produced pink flowers in one branch. Enquiry with the flower-growers revealed that such 'sport of nature' is quite common china-rose for flower-color and for leaf-structure in *Codiaeum variegatum* Blume.

Evidently, the development of pink colored flower on a branch under natural habitat depicted natural mutation (chimeric). To put the phenotypic variation into a biochemical context, it is useful to sketch the main outlines of the flavonoid biosynthetic pathway, which culminates in the production of anthocyanins, the main pigments responsible for flower color. The presence or absence of these pigments affects the coloration of the floral display, which attracts pollinators. The anthocyanin pigments are therefore important to reproductive success and hence to gene transmission. In addition to pigment production, several side branches of the pathway also produce compounds that are important in plant disease defense, pollen viability, microbial interactions, and UV protection (Koes & Quattrocchio 1994).

The flavonoid pathway has a pleiotropic role in plants, and one must consider that a single mutation in the pathway may have multiple phenotypic effects. The pleiotropic role of the flavonoid

pathway is a complication in the effort to link phenotype to molecular changes, but, in addition, many of the genes of the flavonoid pathway are now known to consist of small multigene families, so it is essential to associate a mutation in a particular gene with a phenotype of interest. That is, one must identify the gene family member responsible for the observed phenotype.

Genetic analysis have identified 8 genes that determined the floral colour phenotypes in *Ipomoea purpurea*; CHS, CHI, F3"H, F3"5"H, DFR, ANS, UF3GT, RT. Hence it remains to be ascertained whether the development of pink flower or *vice versa* in *H. rosa-sinensis* are results of chimeric mutation or a results of the interaction of certain gene family in their biochemical makeup. A planned experiment is required to understand the reasons for colour polymorphisim in *Hibiscus rosa-sinensis*.

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