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In A. thaliana B function stems mainly from two genes, APETALA3 (AP3) and PISTILLATA (PI), both MADS-box nature. A mutation in one of these genes and causes homeotic conversion of petals into sepals and stamens carpeloides structures. 21 This is also true orthologs in A. majus , which are deficiens (DEF) and Globosa (GLO). 22 In the case of both species, the active form of DNA binding is that of a heterodimer that is, AP3 and PI or DEF and GLO,dimerize and then are able to perform its function.

In Petunia there has been a doubling of the lineages GLO / PI : thus, possesses P. GLOBOSA1 hybrida (PhGLO1 , also called FBP1) but also PhGLO2(synonymous PMADS2 or FBP3). As for the elements of function equivalent to AP3 / DEF , in Petunia is given both a gene has a sequence relatively similar, called PhDEF as a function B atypical gene, called PhTM6. According to studies of phylogeny , the first three are part of a lineage "euAP3" while PhTM6 belongs to the "paleoAP3." 24 It should be noted that the appearance of euAP3 lineage appears to be related, in terms of evolutionary history, with the radiation of dicotyledons , as representatives of class B type are present in dicots euAP3 while they are in paleoAP3 monocots and basal angiosperms, among others.

In the angiosperms eudicotiledÃ³neas floral organs, as has been previously described, are arranged in 4 whorls different, containing sepals, petals, stamens and carpels. According to the ABC model, the identity of these organs is specified by homeotic genes of class A, A + B, B + C and C, respectively. In contrast to the whorls of sepals and petals of eudicots, the perigone of many plants of theLiliaceae has two outer whorls almost identical petaloid organs with each other (tepals). To explain the flower morphology of Liliaceae, they Tunen and colleagues in 1993 proposed a modified ABC model. According to this model, class B genes are not expressed only in whorls 2 and 3 but also at 1. It follows, then, that the organs of whorls 1 and 2 express genes of Class A and Class B and thereby achieve their petaloid identity. This theoretical model is empirically tested through cloning and characterization of homologues of genes from Antirrhinum Globosa and deficiens of Lily, the Tulip(Tulipa gesneriana), which are expressed in whorls 1, 2 and 3. 26 In other species phylogenetically distant from model organisms such as Agapanthus praecox ssp. orientalis (Agapanthaceae) have also been isolated and characterized the homologs Globosa and deficiens , which were called ApGLO and ApDEF , respectively. Both contain open reading frames encoding proteins with 210-214amino acids . Phylogenetic analysis of these sequences indicated that they belong to the B gene family of monocots . The experiments of hybridization in situ revealed that both sequences are expressed in whorl 1 as well as in the 2 and 3. All these observations indicate that the mechanism of floral development in Agapanthus also follows a modified ABC model.

Near two-decade studies have suggested that there are four pathways for the genetic control of flowering time in Arabidopsis,namely:independent pathway,gibberelin pathway, photoperiod pathway and vernalization Pathway.Zheng Huiyong discoveredï¼ˆnot published dataï¼‰that the flowering time was delayed and the biological yield and seed yield greatly increased in comparison with the wildtype when a geneï¼ˆnamed as C220 temporarilyï¼‰ controlling flowering time was deleted in Arabidopsis.Therefore,this gene is valuable not only in theoretical research,but also in application.In this study,an RNA interference vector of C220 gene was constructed using the C220 homologous geneï¼ˆcDNAï¼‰previously cloned from tobacco and the Gateway technology and transferred the vector into tobacco via Agrobacterium.With PCR analysis on the total DNA and RT-PCR analysis on the total RNA extracted from the leaves of T0 transgenic plants,some transgenic plants in which the RNAi expression frame had been inserted into the genome and could express to show efficient interference effect were identified.Phenotypic investigation indicated that the length

between stem nodes of the transgenic plants was 2.32 cm on average,88.79%shorter than that of wildtype;the number of leaves of the transgenic plants is 60 on average,14 pieces more than that of wildtype;the 20-leave fresh weight and dry weight of the transgenic plants at the flowering stage were 1103g and 311g,respectively,increasing 144%and 130%compared with the wildtype;the leaf areaï¼ˆlengthÃ—widthï¼‰of the transgenic plants was 1450.20cm2 on average,increasing 148%compared with the wildtype;the flowering time of the transgenic plants under the long day condition was 117d on average,19d later than that of the wildtype; the chlorophyll content of the transgenic plants was 1.722%on average,71.5%higher than that of the wildtype.These results suggest that the tobacco C220 homologous gene has the similar function to the Arabidopsis C220 gene.Since this gene can greatly increase the leaf yield when its expression is suppressed,it may probably have important application prospect in tobacco production.

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