

**Plant Biology.** In the article “NEEDLY, a *Pinus radiata* ortholog of *FLORICAULA/LEAFY* genes, expressed in both reproductive and vegetative meristems” by Aidyn Mouradov, Tina Glassick, Britt Hamdorf, Lawrence Murphy, Beth Fowler, Soma Marla, and Robert D. Teasdale, which appeared in number 11, May 26, 1998, of *Proc. Natl. Acad. Sci. USA* (95, 6537–6542), the authors request that the following corrections be noted. In the *Discussion* on page 6541, the fourth, fifth, and sixth sentences should read as follows: “These domains are

variable between FLO/LFY-like proteins. The proline-rich domain is not well pronounced in NLY and PrFLL. The acidic domain of gymnosperm FLO/LFY-like proteins is not as strong as corresponding domains of angiosperm homologs. Because the proline-rich and acidic domains are located within the variable regions, they may be subject to evolutionary changes.” Also, we would like to point out that in Fig. 1, the first 44 amino acids of the PEAFL0 sequence were missing. A corrected figure and its legend appear below.

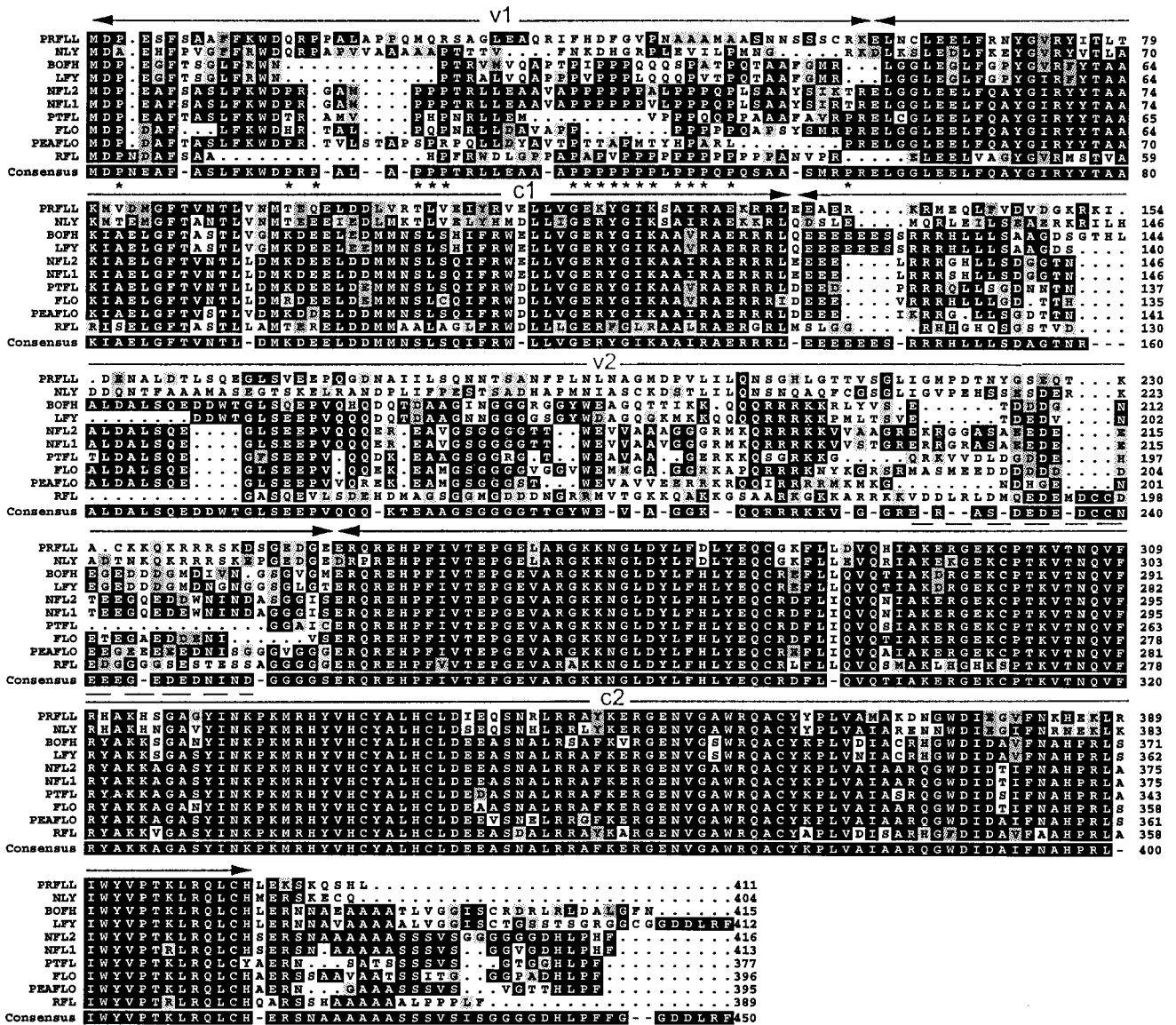


FIG. 1. Sequence comparison of FLO/LFY-like proteins (accession numbers in parentheses): PrFLL from *P. radiata* (U92008); NLY from *P. radiata* (U76757); BOFH from *Brassica oleracea* (718362); LFY from *Arabidopsis thaliana* (M91208); NFL1 and NFL2 from *Nicotiana tabacum* (U16172) and U16174, respectively); PEAFL0 from *Pisum sativum* (AF010190); FLO from *Antirrhinum majus* (M55525); PTFLL from *Populus balsamifera* (U931 96); and RFL from *Oryza sativa* (AB005620). Black boxes indicate identical amino acids, shaded boxes indicate amino acids with similar properties, and dots indicate gaps introduced to optimize alignment. c1 and c2, conserved regions; v1 and v2, variable regions. Positions of the proline residues within the proline-rich region are indicated by asterisks. Acidic domain indicated by dashed line.