**Biochemistry.** In the article "The chromatin unfolding domain of chromosomal protein HMG-14 targets the N-terminal tail of histone H3 in nucleosomes" by Lothar Trieschmann, Brian Martin, and Michael Bustin, which appeared in number 10, May 12, 1998, of *Proc. Natl. Acad. Sci. USA* (**95,** pp. 5468–5473), the following correction should be noted. Figs. 3 and 6 as reproduced in the issue were of very poor quality, especially Fig. 3*A*, in which the protein bands appear to be washed. Both figures and their legends are reproduced below.

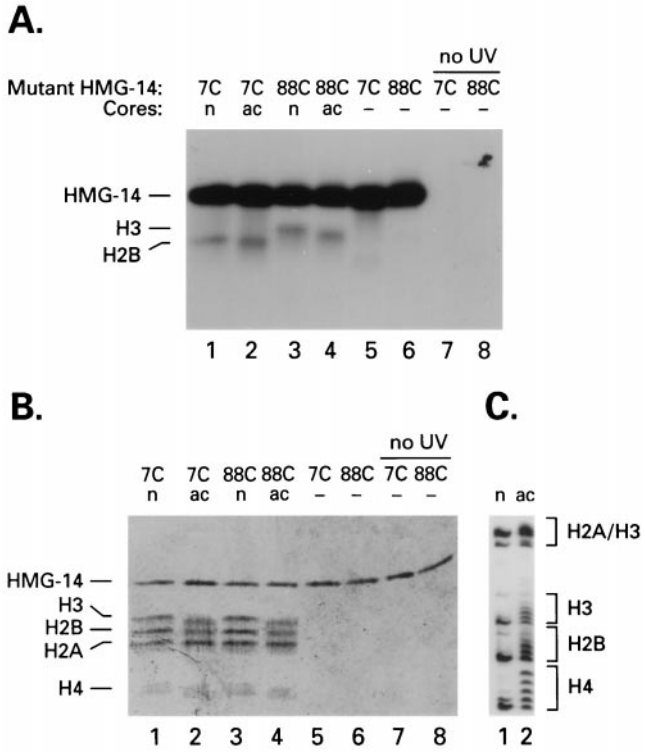


FIG. 3. Identification of the targets of the HMG-14 point mutants. Acetylated (ac) or nonacetylated (n) cores containing the $^{125}$I-labeled HMG-14 point mutants indicated at the top of the lanes were exposed to UV, treated with 2-mercaptoethanol, and analyzed by SDS/PAGE. (*A*) Autoradiograph. (*B*) Coomassie blue stain. Lanes 5–8 contained only the labeled HMG-14 mutants. Lanes 7 and 8 were not exposed to UV and therefore the radioactive label runs with the ion front. (*C*) The degree of acetylation of the histones in the nucleosome cores was assessed by Coomassie blue staining of Triton/acid/urea polyacrylamide gels (33).

**Genetics.** In the article "Evolution of rhizobia by acquisition of a 500-kb symbiosis island that integrates into a phe-tRNA gene" by John T. Sullivan and Clive W. Ronson, which appeared in number 9, April 28, 1998, of *Proc. Natl. Acad. Sci. USA* (**95,** pp. 5145–5149), the authors wish to note that, in their article, the quality of reproduction of Fig. 1 was below standard. In particular, many of the hybridizing bands appeared diffuse and the background was blotchy, making interpretation of the banding patterns difficult. The figure and its legend are reproduced below.

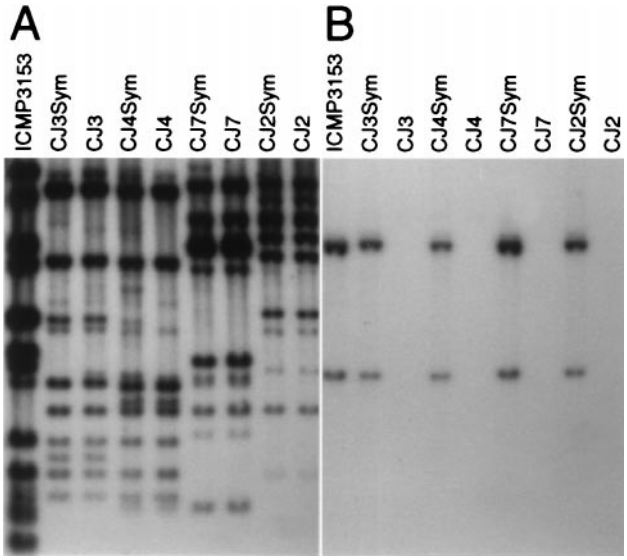


FIG. 1. Southern blot analysis demonstrating transfer of the symbiotic element to three species of nonsymbiotic mesorhizobia. Genomic DNA from the donor strain ICMP3153 and pairings of nonsymbiotic and symbiotic strains was digested with *Eco*RI and hybridized (*A*) with three random genomic *Hin*dIII fragments of ICMP3153 (18) and (*B*) with pRLnodAC containing *M. loti nodAC* genes (18).

(*Corrections continued on next page.*)

**Plant Biology.** In the article "Association of the *Arabidopsis* CTR1 Raf-like kinase with the ETR1 and ERS ethylene receptors" by Karen L. Clark, Paul B. Larsen, Xiaoxia Wang, and Caren Chang, which appeared in number 9, April 28, 1998, of *Proc. Natl. Acad. Sci. USA* (**95,** 5401–5406), the following correction should be noted. Fig. 5, accurately shown here, was damaged during the printing process.

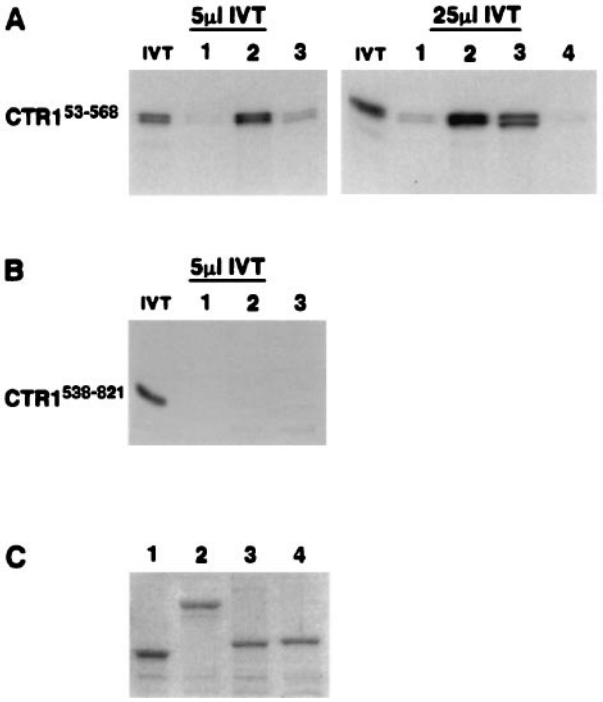


FIG. 5. *In vitro* association of radiolabeled CTR1 polypeptides with purified MBP fusions: (*i*) MBP alone, (*ii*) MBP–ETR1$^{293–610}$, (*iii*) MBP–ETR1$^{604–738}$, and (*iv*) MBP-CKI1$^{981–1122}$. (*A*) Autoradiograms showing association of the CTR1 amino-terminal domain with MBP fusions 1–4. Bacterially expressed MBP or MBP fusion was attached to amylose-containing beads, and the beads were mixed with 5 or 25 μl of *in vitro*-translated, radiolabeled CTR1 amino-terminal domain (residues 53–568) (IVT). The bead-associated proteins were separated on SDS/PAGE gels, and the radiolabeled CTR1$^{53–568}$ was visualized by autoradiography. Lane IVT contains 0.1 μl of unassociated radiolabeled CTR1$^{53–568}$. (*B*) Autoradiogram showing association of the CTR1 kinase domain with MBP fusions 1–3. Bacterially expressed MBP or MBP fusion was attached to amylose-containing beads, and the beads were mixed with 5 μl of IVT. IVT in this case is the radiolabeled *in vitro*-translated CTR1 kinase domain (residues 538–821). The bead-associated proteins were subjected to SDS/PAGE, and radiolabeled CTR1$^{538–821}$ was visualized by autoradiography. Lane IVT contains 0.1 μl of unassociated radiolabeled CTR1$^{538–821}$. The length of exposure is twice that shown in Fig. 5*A*. (*C*) Relative amounts of MBP fusions 1–4 used in Fig. 5 *A* and *B* separated on SDS/PAGE gels and stained with Coomassie blue.