## **Corrections**

AGRICULTURAL SCIENCES. For the article "Genetic analysis of traditional and evolved Basmati and non-Basmati rice varieties by using fluorescence-based ISSR-PCR and SSR markers," by J. Nagaraju, M. Kathirvel, R. Ramesh Kumar, E. A. Siddiq, and Seyed E. Hasnain, which appeared in number 9, April 30, 2002,

of *Proc. Natl. Acad. Sci. USA* (99, 5836–5841; First Published April 16, 2002; 10.1073/pnas.042099099), Fig. 3 appeared incorrectly. The label Karnal in *a* and *b* should read Super. The corrected figure and its legend appear below.

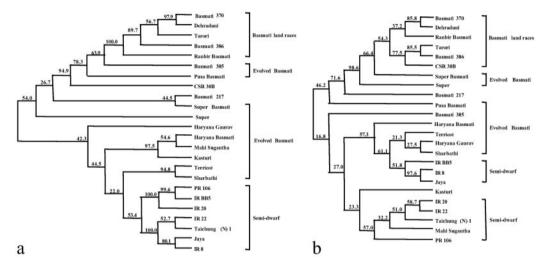


Fig. 3. Dendrograms derived from an unweighted pair group method analysis (UPGMA) cluster analysis by using Nei and Li Coefficients based on (a) ISSR markers and (b) SSR markers. Numbers on the nodes indicate the number of times a particular branch was recorded per 100 bootstrap replications after 1,000 replications.

www.pnas.org/cgi/doi/10.1073/pnas.212463799

PHYSIOLOGY. For the article "Aquaporin 1 regulates GTP-induced rapid gating of water in secretory vesicles," by Sang-Joon Cho, A. K. M. Abdus Sattar, Eun-Hwan Jeong, Mylan Satchi, Jin Ah Cho, Sudhansu Dash, Mary Sue Mayes, Marvin H. Stromer, and Bhanu P. Jena, which appeared in number 7, April 2, 2002, of *Proc. Natl. Acad. Sci. USA* (99, 4720–4724; First Published March 26, 2002; 10.1073/pnas.072083499), the authors note the following corrections to the reference numbers cited in the text. On p. 4720, in column 1, line 24 from bottom, refs. 7–15 should be 22; in line 22 from bottom, ref. 3 should be 22; in line 19 from bottom, refs. 17–21 should be 18–22; in line 9 from bottom, refs. 8–11 should be 7–13, 16, 17. On p. 4722, column 2, line 3 from bottom, refs. 9, 10, 12–15, 23 should be 12, 13, 23.

www.pnas.org/cgi/doi/10.1073/pnas.212281299

**BIOCHEMISTRY.** For the article "Cracks in the  $\beta$ -can: Fluorescent proteins from Anemonia sulcata (Anthozoa, Actinaria)," by Jörg Wiedenmann, Carsten Elke, Klaus-Dieter Spindler, and Werner Funke, which appeared in number 26, December 19, 2000, of Proc. Natl. Acad. Sci. USA (97, 14091–14096), the authors note the following. The proposed truncated form of the  $\beta$ -can is withdrawn. This correction concerns our work on the GFP homologs as CP562 and as FP595 from A. sulcata. Another group cloned a nonfluorescent red protein initially named asFP595 from another color morph of A. sulcata (1) [most likely A. sulcata var. vulgaris (2)], but changed recently to asCP/asulCP (3). This protein fluoresces with a minimal quantum yield. The cyclization mechanism for the chromophore of this protein (4) includes a cleavage of the peptide backbone and fragmentation of the protein upon denaturation. The authors reported that the truncation of the recombinant protein we suggested in our paper does not yield a functional protein.

Repeated sequencing of asCP562 revealed an error suggesting a shortened open reading frame. The sequence of asCP562 has been corrected under the published accession no. (AF322222). The sequence shows a high similarity to the sequence published by Martynov and coworkers (3) (see Fig. 1 A and B). Purified recombinant as CP562 yielded the same fragmentation pattern as asulCP. These new results indicate that asCP562 and highly fluorescent asFP595 are formed in the way described for asulCP (asFP595; ref. 1). For these reasons, the proposed truncated form of the  $\beta$ -can is not valid.

The corrected sequences were provided by B. Sundin, Department of Biochemistry, University of Washington, and G. Jach, Max-Planck-Institut für Züchtungsforschung, Köln, Germany.

- 1. Lukyanov, K. A., Fradkov, A. F., Gurskaya, N. G., Matz, M. V., Labas, Y. A., Savitsky, A. P., Markelov, M. L., Zaraisky, A. G., Zhao, X., Fang, Y., Tan, W. & Lukyanov, S. A. (2000) J. Biol. Chem. 275, 25879-25882.
- 2. Wiedenmann, J., Röcker, C. & Funke, W. (1999) in Verhandlungen der Gesellschaft für Ökologie, ed. Pfadenhauer, J. (Spektrum Akademischer, Berlin), Band 29, pp. 497-503.
- 3. Labas, Y. A., Gurskaya, N. G., Yanushevich, Y. G., Fradkov, A. F., Lukyanov, K. A., Lukyanov, S. A. & Matz, M. V. (2002) Proc. Natl. Acad. Sci. USA 99,
- 4. Martynov, V. I., Savisky, A. P., Martynova, A. Y., Savitsky, P. A., Lukyanov, K. A. & Lukyanov, S. A. (2001) J. Biol. Chem. 276, 21012-21016.

www.pnas.org/cgi/doi/10.1073/pnas.212371999

Α					
	1				50
asFP595		TTTTAAAGAA			
asCP562	51	TTTTAAAGAA			100
asFP595		GGCCACTACT			
asCP562	101	GGCCACTACT			150
asFP595 asCP562		TACGCAGGAA			
	151	TACGCAGGAA			200
asFP595		CCTTCCACAT			
asCP562	201	CCTTCCACAT			250
asFP595		AAGTA <b>T</b> GTGT			
asCP562	251	aagta <b>c</b> gtgt		_	300
asFP595		TTTTACTTGG			
asCP562	301	TTTTACTTGG			350
asFP595		CTCATCAGGA			
asCP562	351	CTCATCAGGA			400
asFP595		ATTCTTGGTA			
asCP562	401	ATTCTTGGTA			450
asFP595		AG <b>G</b> AAGATGG			
asCP562	451	AG <u>A</u> AAGATGG		_	500
asFP595		TGCGTGGACA			
asCP562	501	TGCGTGGACA			550
asFP595		ACTTGCCATC			
asCP562	551	ACTTGCCATC			600
asFP595		GAAGATGCCA			
asCP562	601	GAAGATGCCA		_	650
asFP595 asCP562		AAGTTGAGAA			
	651	AAGTTGAGAA			699
asFP595 asCP562	AGTGGGCAGG	TACTGTGATG			
asCF362	WG1GGCWGG	INCIGIGATE	CIGCICCAIC	CAAGCIIGGA	CATEACTAA
В	1				50
asFP595	MASFLKKTMP	FKTTIEGTVN	GHYFKCTGKG	EGNPFEGTQE	MKIEVIEGGP
asCP562	MASFLKKTMP	FKTTIEGTVN	GHYFKCTGKG	EGNPFEGTQE	MKIEVIEGGP 100
asFP595	LPFAFHILST	SCMYGSKTFI	KYVSGIPDYF	KOSFPEGFTW	ERTTTYEDGG
asCP562		SCMYGSKTFI			
asFP595		DGDCLVYKVK	TLGNNFPADG	PVMONKAGRW	
asCP562		DGDCLVYKVK		_	- Carlotte
asFP595	151	ALKCPGGRHL	TOUT UTTYPE	ENDY CAT NWD	200
ascP562		ALKCPGGRHL	_		_
	201		- :	232	GENE GUNKIE
asFP595		ykqyeaav <b>g</b> r		_	
asCP562	IMEEVEKGKC	ykqyeaav <b>a</b> r	YCDAAPSKLG	H <b>H</b>	

Fig. 1. (A) Nucleotide sequence alignment of the regions coding for asFP595 (ref. 1) and asCP562. Differing residues are bold and underlined. (B) Amino acid sequence alignment of asFP595 (ref. 1) and asCP562. Differing residues are bold and underlined.