Corrections

DEVELOPMENTAL BIOLOGY. For the article “Differential regulation of midbrain dopaminergic neuron development by Wnt-1, Wnt-3a, and Wnt-5a,” by Gonçalo Castelo-Branco, Joseph Wagner, Francisco J. Rodriguez, Julianna Kele, Kyle Sousa, Nina Rawal, Hilda Amalia Pasolli, Elaine Fuchs, Jan Kitajewski, and Ernest Arenas, which appeared in issue 22, October 28, 2003, of Proc. Natl. Acad. Sci. USA (100, 12747–12752; first published October 13, 2003; 10.1073/pnas.1534900100), the authors note the following error in Fig. 5A. In the real-time RT-PCR experiments, primers against mouse Pentraxin 3 (PTX3, GenBank accession no. X83601) were used instead of primers against rat Pituitary homeobox 3 (Pitx3, a homeodomain transcription factor, GenBank accession no. RNO011005). Real-time RT-PCR with primers against rat Pitx3 (GenBank accession no. RNO011005) showed no difference in Pitx3 mRNA levels upon Wnt-5a treatment of embryonic day (E) 14.5 ventral midbrain (VM) precursor cultures for 3 days. However, Wnt-5a up-regulated mRNA levels of two other dopaminergic markers (tyrosine hydroxylase and c-ret). The corrected figure and legend appear below. The primer sequences for rat Pitx3 are as follows: forward, 5’-TTCCCGTTGCTTCAACTCG-3’; reverse, 5’-GAGCTGGGCGGTAGAATACAGG-3’.

Fig. 5. Wnts differentially control the development of DA neurons by regulating precursor proliferation and the acquisition of a DA phenotype. Wnt-5a did not affect Ptx3 mRNA expression (A), but up-regulated the expression c-ret (B) and TH (not shown) mRNA, and maintained the expression of GDNF family receptor α1 (GFRα1) mRNA (C) and NCAM mRNA (D) at 3 days in vitro, as assessed by real-time RT-PCR. (E and F) Double immunocytochemistry revealed that Wnt-5a increased the percentage of TH+/Nurr1+ cells in the VM from 50% to 90%. Wnt-1 was less efficient than Wnt-5a, and Wnt-3a actually decreased the proportion of TH+ cells from 50% to 30%. (G and H) Fz8-CRD decreased, in a dose-dependent manner, the proportion of Nurr1+ cells that acquired TH expression in E14.5 VM precursor cultures in the control condition (CP), indicating that Wnt signaling is required for the acquisition of a DA phenotype. (I and J) Treatment of rat E14.5 VM precursor cultures with Fz8-CRD decreased the percentage of TH+/Nurr1+ cells after treatment with Wnt-5a. Statistical analysis and concentrations as in Fig. 4. (J) Model of the mechanisms by which Wnt-1, -3a, and -5a regulate the development of VM DA neurons. Wnt-3a, which is mainly expressed in the dorsal midbrain, enhances the proliferation of Nurr1-expressing precursors and increases the proportion of TH+ neurons that acquire TH expression. Wnt1, probably derived from the midbrain–hindbrain organizer, controls the proliferation of Nurr1-expressing precursors and increases the number of VM neurons. Finally, Wnt-5a specifically increases the number of VM Nurr1-expressing precursors that become TH+ neurons. Note that the size of the arrows correlates with the intensity of the effects.

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COMMENTARY. For the article “An emerging consensus for telomerase RNA structure,” by Jiunn-Liang Chen and Carol W. Greider, which appeared in issue 41, October 12, 2004, of Proc. Natl. Acad. Sci. USA (101, 14683–14684; first published October 4, 2004; 10.1073/pnas.0406204101), the authors note that the uracil residue at position 769 was omitted from Fig. 2B and C. The corrected figure and its legend appear below.

![Diagram of yeast telomerase RNA core](https://example.com/figure2)

**Fig. 2.** Two possible structures in yeast telomerase RNA core. (A) Sequence alignment of regions of the proposed pseudoknot and helix V. The sequence alignment and nucleotide numbering of telomerase RNAs from eight *Saccharomyces* species are adapted from Dandjinou et al. (6). Invariant residues are highlighted in yellow. Residues that show covariation are indicated by green dots. (B) A possible secondary structure of Est2 binding domain, proposed by Lin et al. (7), consists of the stem-1, supported by one nucleotide covariation at the base pair 714G:770C. (C) An alternative structure, proposed by Dandjinou et al. (6), consists of the helix V, supported by one nucleotide covariation at the base pair 714G:731C. Potential base pairings between the loops of helix V and helix VI, as proposed by Dandjinou et al. (6), are indicated by black dots. Both structures consist of a helix called stem-2 (7) or helix VI (6).

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COMMENTARY. For the article “Mating patterns and rates of biological invasion,” by Ingrid M. Parker, which appeared in issue 38, September 21, 2004, of Proc. Natl. Acad. Sci. USA (101, 13695–13696; first published September 14, 2004; 10.1073/pnas.0405787101), the author notes that the acknowledgement in the legend of Fig. 1 was incorrect. The legend should have read, “Photograph courtesy of Janie C. Civille, University of California, Davis.”

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GENETICS. For the article “Highly efficient gene replacements in *Neurospora* strains deficient for nonhomologous end-joining,” by Yuuko Ninomiya, Keichi Irabu, Chizu Ishii, and Hirokazu Inoue, which appeared in issue 33, August 17, 2004, of Proc. Natl. Acad. Sci. USA (101, 12248–12253; first published August 6, 2004; 10.1073/pnas.0402780101), the authors note that the agent used to select for transformants was bialaphos rather than blasticidin. The word “blasticidin” should therefore be replaced by “bialaphos” throughout the text. This error does not affect the conclusions of the article or applications of the method.

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PLANT BIOLOGY. For the article “A small CDC25 dual-specificity tyrosine-phosphatase isoform in *Arabidopsis thaliana*,” by Isabelle Landrieu, Marco da Costa, Lieven De Veylder, Frédérique Dewitte, Klaas Vandepoele, Sahar Hassan, Jean-Michel Wieruszeski, Jean-Denis Faure, Marc Van Montagu, Dirk Inzé, and Guy Lippens, which appeared in issue 36, September 7, 2004, of Proc. Natl. Acad. Sci. USA (101, 13380–13385; first published August 25, 2004; 10.1073/pnas.0405248101), the authors request that Florence Corellou, Department of Plant Systems Biology, Flanders Interuniversity Institute for Biotechnology (VIB), Ghent University/VIB, Technologiepark 927, B-9052 Ghent, Belgium, be added to the list of authors between Jean-Michel Wieruszeski and Jean-Denis Faure. The online version has been corrected. The corrected author line appears below.

Isabelle Landrieu, Marco da Costa, Lieven De Veylder, Frédérique Dewitte, Klaas Vandepoele, Sahar Hassan, Jean-Michel Wieruszeski, Florence Corellou, Jean-Denis Faure, Marc Van Montagu, Dirk Inzé, and Guy Lippens

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