differential gametic imprinting, as well as on the amount of gene product needed for biological function.

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Vielle-Calzada et al. *reply* — Our results, based on a study of 20 loci, indicate that the contributions by the maternal and paternal genome to early seed development in *Arabidopsis* are not equivalent, as evidenced by a lack of detectable paternal gene activity during the first few divisions after fertilization. As these loci are distributed throughout the genome, we inferred that early embryo and endosperm development are mainly under maternal control, but this may not be true for every locus and, as in X-chromosome inactivation[1], we would expect some loci to escape this silencing mechanism. We did not claim that maternal control is complete, but suggested that the activity of many genes during early embryo and endosperm formation could depend solely on transcription of the maternally inherited allele before and/or after fertilization.

Previously, early seed formation was thought to involve transcription from both parental copies immediately following fertilization, and maternal effects were considered rare or non-existent[2]. The time at which paternal activity can first be detected, however, is likely to vary from embryo to embryo and from gene to gene in different nuclei, as in *Drosophila*[3]. Weijers *et al.* report paternal expression of *AtRPS5A::GUS* as early as the two-cell stage, confirming that transcription in the zygote is not the rule for paternally inherited alleles, whereas transcription from maternal alleles has been demonstrated immediately after fertili-zation of the central cell[4]. We do not know what percentage of embryos show early *AtRPS5A::GUS* expression, nor the relative paternal and maternal activity, but there may also be less pronounced parent-of-origin differences.

New evidence supporting the non-equivalence of maternal and paternal genomes during early seed development is based on experiments with reporter genes[5–8] and genetic assays revealing maternal effects of genes thought to act purely zygotically[6] (S. Gilmore and C. Somerville, personal communication; J. Moore and U. G., unpublished results). Whether and at what stage expression of the paternal allele is sufficient for normal development will depend on the level of activity required for gene function. In a two-component transactivation system, no paternal activity was found during early seed development using *pOp::GUS* reporter lines with several activator lines[8]. Some early defects were evident with a *pOp::BARNASE* reporter, however, suggesting that paternal transcription is very low but is sufficient to cause *BARNASE*-induced defects in some embryos[8]. These results confirm the non-equivalence of maternal and paternal contributions to early seed development. Like imprinted genes in mammals, this difference is probably not absolute and may be due to different levels of maternal and paternal transcripts.

Our titration experiments indicated a difference in transcript levels of at least 80-fold for genes we tested by PCR. Weijers *et al.* report an expression difference in reciprocal crosses with *UAS:GUS* at the heart to torpedo stage (Fig. 1d), when we showed that both parental alleles are active at other loci we tested; indeed, this differential expression translates into an absence of detectable paternal activity at earlier stages using the *pOp::GUS* reporter system[8]. For some genes, such as *KEULE* or *KNOLLE*, low paternal expression may be sufficient for normal development, although very early defects (such as developmental delay) that are rescued by a paternal wild-type allele may be difficult to detect by scoring multinucleate embryos. Moreover, rescue of an early embryonic phenotype by a paternal wild-type allele provides no evidence against differences in parental transcript levels.

Although the exact time of paternal activation was not central to our report, most evidence so far suggests that no consistent paternal gene activity can be detected in the embryo or endosperm for several cell divisions. The results of Weijers *et al.* do not contradict our findings, but instead represent possible exceptions to a general rule. Specific genes that are important during early development (for example, those involved in cytokinesis that are distinctly regulated in the female gametophyte and the zygote[9]) may be under selection for earlier expression and be specifically activated early in development. Further investigation is required into how common early-expressing paternal genes are, and how maternal and paternal expression differs quantitatively.

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corrections

Night-time predation by Steller sea lions

G. L. Thomas, R. E. Thorne

Nature **411,** 1013 (2001)

We stated that our acoustic surveys in Prince William Sound since 1993 and infrared surveys since 2000 suggested that these sea lions "feed exclusively" on herring. However, it has been drawn to our attention that this statement is misleading. In clarification, the sea lions were selectively targeting the relatively shallow (0–50-m depth) schools of Pacific herring (*Clupea pallasi*) at night as a source of winter forage to the exclusion of relatively larger and deeper (150–250 m) concentrations of walleye pollock.

Transatlantic robot-assisted telesurgery

J. Marescaux, J. Leroy, M. Gagner, F. Rubino, D. Mutter, M. Vix, S. E. Butner, M. K. Smith

Nature **413,** 379–380 (2001)

The correct address of the third author of this communication is Division of Laparoscopic Surgery at Mount Sinai School of Medicine and Mount Sinai Medical Centre, New York 10029, USA.

Peptide antibiotics in mast cells of fish

Umaporn Silphaduang, Edward J. Noga

Nature **414,** 268–269 (2001)

The concentrations listed in Table 1 are in $\mu g\ ml^{-1}$.

erratum

Nitrate flux in the Mississippi River

G. F. McIsaac, M. B. David, G. Z. Gertner, D. A. Goolsby

Nature **414,** 166–167 (2001).

In Fig. 1 of this communication, the line referred to as "black" is in fact blue; also, in the fourth line of the third column, *P* should be greater than 0.05.