was fractionated, with nickel-iron and carbonaceous chondrites largely contained in the volume on the sunward side of Mars's orbit, and gases (hydrogen, helium, methane, water) and some carbonaceous chondrites in the volume from Jupiter's orbit outward[4].

Present theories on the origin of the oceans fail to account for the fact that Venus, a planet very similar to Earth in size and composition, has no surface water and only small amounts of atmospheric water. This could be explained by assuming that, early in its history, Earth collided with an ice moon approximately 900 to 950 miles in diameter, which could have furnished all the water presently on Earth. This collision, obviously a rare event, would have provided for rapid cooling of the Earth's crust, prevention of a runaway greenhouse effect by the absorption of most atmopsheric CO_2, and rapid evolution of life. This theory is also in accord with the fractionated nature of the early Solar System.

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Frequency of dizygotic twinning

SIR—From the assumption that ovulation with intercourse leads to a live birth with probability ¼ for each egg, double ovulation may be expected to lead to dizygotic twin births with probability 1/16. From that realtionship, J. Diamond (*Nature* **320**, 488; 1986) suggested that an observed frequency of 4.9% dizygotic twin births among the Yoruba implies a double ovulation frequency of 16 times 4.9, or 78%.

M. Sipser (*Nature* **321**, 570; 1986) pointed out that this suggestion is incorrect. On the simplest set of assumptions, double ovulation will lead to no birth in 9/16 of cases, to a single birth in 6/16 of cases, and to dizygotic twins in 1/16 of cases. From those relative frequencies, Sipser asserted that an observed frequency of 4.9% dizygotic twin births implies a double ovulation frequency of 7 times 4.9 or 34%.

In fact the relationship between the frequencies of double ovulation and of dizygotic twin births cannot be expressed by a constant factor. When the frequency of double ovulation is extremely low, the single births that result from double ovulation can be ignored, and the observed frequency of dizygotic twin births must be multiplied by 4 to obtain the frequency of double ovulation (single births=¼ of single ovulations; dizygotic twin births= 1/16 of double ovulations). When the frequency of double ovulations is high, the single births that result from double ovulations must be taken into account, and the factor rises. In the extreme case, if the probability of double ovualtion were 1.0, 1/7 of the births would be dizygotic twins; the factor would be 7. Sipser's comment is valid only for this case, which is of no biological significance for any known human population.

The general expression to be used is $F=T/(pT+p-T)$, where T is the fraction of dizygotic twin births, p is the probability per egg of a live birth, and F is the fraction of double ovulation. When p is assumed to be 0.25, this becomes $F=4T/(1-3T)$.

In any real case, the factor $[4/(1-3T]$ is much closer to 4 than to 7. For the dizygotic twinning frequencies that occur in the human populations tabulated in Diamond's article (0.22% to 4.9%) the appropriate factors are between 4.03 and 4.7. In the Yoruba popualtion the frequency of dizygotic twin births was 4.9%, and the estimated frequency of double ovulation, if $P=¼$, is 23%.

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How to abbreviate recombinant genes

SIR—We are all aware that recombinant DNA technologies have generated tremendous progress and spawned a literature that seems to grow exponentially. Unfortunately a custom is developing of using the abbreviation rDNA to refer to the hybrid molecules formed by uniting two or more heterologous DNA molecules; this leads to confusion, since rDNA has long been used to refer to ribosomal DNA. The abbreviation rRNA and r proteins are also in common use with r again meaning ribosomal.

To avoid confusion, I suggest the use of rt for recombinant and that editors of journals start insisting on a differentiation between rDNA and rtDNA and rRNA and rtRNA.

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A system of nomenclature for murine homoeo boxes

SIR—There is at present a considerable degree of confusion amongst workers on mammalian homoeo boxes because each group has tended to select a different system of nomenclature. It is now very difficult to follow the literature appropriately. To help avoid this confusion we would like to offer the following system.

A unifying nomenclature for murine homeo boxes should consider the chromosomal location and the number of boxes on a chromosome. Clusters of boxes should preferably be numbered consecutively and in the direction of transcription. The two known clusters are probably transcribed in one orientation only and do not contain additional boxes. Thus, at least these two would be numbered consecutively from the 5′ to the 3′ end of the cluster. The nomenclature should further allow a logical naming of newly discovered boxes.

We suggest the new prefix 'Mox', followed by two numbers: the first one giving the chromosomal location, the second identifying an individual box on the respective chromosome. This procedure leads to the following nomenclature for a selection of published murine homeo boxes:

Proposed name	Original designation	Chromosome	Ref.
Mox 1.1	Mo-en.1	1	1
Mox 6.1	m6	6	2
Mox 6.2	m5	6	3
Mox 6.3	m2	6	3
Mox 6.4	HBT-1, MH3, Hox 1.3.	6	4,5
Mox 6.5	Mo 10, Hox 1.4.	6	6
Mox 6.6	—	6	—
Mox 11.1	Hox 2.4	11	7
Mox 11.2	Hox 2.3	11	7
Mox 11.3	Hox 2.2	11	7
Mox 11.4	Hox 2.1, H24.1, Mul	11	7-9
Mox 15.1	Hox 3, m31	15	10,11

For new isolates, we suggest the following, assuming that the description of these boxes will include the information on chromosomal location and occurrence of clusters. In this case, we propose the term 'Mox', followed by the chromosome number, a period and the lowest unused number on the respective chromosome for the most 5′ box of a new cluster.

After a box has been designated in this way, the name should be kept unchanged even if new information reveals a violation of the consecutivity rule. Non-mapped isolates (from cDNAs, for example) have to obtain a preliminary designation.

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