ERRATUM

In the January issue of *American Journal of Perinatology*, corrections are required. The following material was omitted from the "Prolonged Neonatal Alloimmune Thrombocytopenic Purpura Associated with Anti-Bak(A)" article written by David T. Miller, M.D., Ph.D., and associates. The Publisher regrets the error.

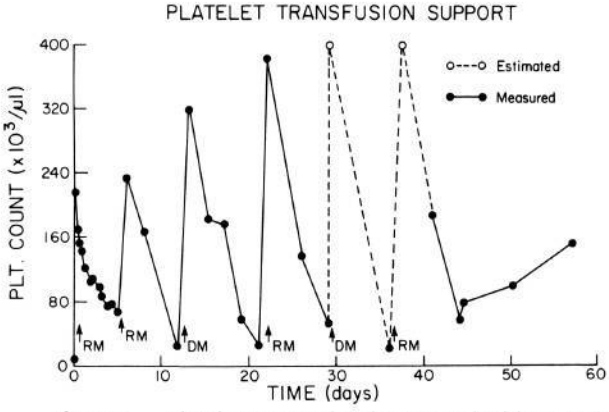

Figure 1. Platelet counts for the second sibling (SM) are plotted as a function of time for the first sixty days following delivery. Transfusions of platelet concentrate from maternal uncles (RM and DM) are indicated by arrows. Two data points were calculated from the dose of platelets given, estimated patient blood volume, and splenic sequestration of 33%.

APPENDIX

It is desirable to derive a function based on gene frequency which expresses the frequency of matings with the potential to produce offspring affected by NATP. Invoking the Hardy-Weinberg law as an approximation for autosomal, dominant inheritance, and using "p" to designate the frequency of the offending gene in the population of chromosomes, then:

p^2 = the frequency of individuals homozygous for the offending gene
$2pq$ = heterozygous individuals
q^2 = individuals homozygous for the absence of the gene

where $q = (1 - p)$. The matings types of mating that potentially could result in affected offspring may be designated as:

male	×	female
p^2	×	q^2
$2pq$	×	q^2

A function "z" may then be written for the sum of such matings. This function expresses the fraction of all matings with the potential for feto-maternal incompatibility and is termed the "incompatibility frequency."

$$z = 0.5 \times [(p^2 \times q^2) + 0.5 \times (2 \times p^2 \times q^2)] \quad (1)$$

The coefficients take into account that males can only mate with females and only one-half of the offspring of a heterozygous father are potentially affected. Using the definition of "q", the expression may be simplied to:

$$z = 0.5 \times [p - 2p^2 + p^3] \quad (2)$$

Thus given the gene frequency "p", this expression may be used to calculate the potential for feto-maternal incompatibility (Table 1).

It is also of interest to calculate the gene frequency associated with the maximum potential for incompatibility. To do this, the expression in equation (2) is differentiated with respect to "p":

$$dz/dp = 1 - 4xp + 3xp^2 \quad (3)$$

To find the maximum for the function "z", dz/dp is set to zero and the resulting quadratic equation solved. The roots of that equation are:

$$p = 0.33$$
$$p = 1.00$$

of which only $p = 0.33$ is biologically meaningful. Thus, the gene frequency associated with the maximum potential for feto-maternal incompatibility is $p = 0.33$.

Finally, parents of a previously affected child often ask about the probability that unborn siblings will be similarly affected. This question is usually asked when the gene frequency is known but the zygosity of the father is not. In the absence of effects not based on mode of inheritance, this *a priori* probability "s" is one minus the fraction of chromosomes negative for the gene in the total population of chromosomes of males who are either homozygous positive or heterozygous:

Table 1. Platelet Specific Antigens: Estimated Frequencies of Incompatible Matings and Subsequently Affected Sibs

Antigen	*Phenotype Frequency (%)*	*Gene Frequency (%)*	*Incompatibility* Frequency (%) (z)*	*Probability† (s) Affected Sibs (%)*
"Maximum"	55.1	33.0	7.4	59.9
$P1^{b}$	26.8	14.4	5.5	53.9
Bak (a)	90.9	69.6	3.3	76.7
$P1^{E2}$	5.0	2.5	1.2	50.6
$P1^{A1}$	97.6	84.5	0.9	86.6
$P1^{E1}$	99.0	90.0	0.4	90.0

*The incompatibility frequency expresses the potential for NATP in random matings as a function of gene frequency only. It is calculated as the variable "z" in the Appendix.

†The probability of affected siblings is calculated as the variable "s" in the Appendix. The value of "s" represents the probability that the parents of an affected child will have a similarly affected child with the next pregnancy. This calculation assumes that the zygosity of the father for the offending antigen is unknown.

"Maximum" is the theoretical gene frequency that produces the highest possible incompatibility frequency.

$$s = 1 - [(1 - p)/(2 - p)] \quad (4)$$

For example, for parents who have had a previously affected child involving the $P1^{A1}$ antigen ($p = 0.845$), the probability of a subsequent, affected child is $s = 0.866$ or 86.6% (see Table 1 for other antigens). It should also be noted that in the limit "p" goes to zero, the "s" goes to 0.5. In other words, the best that one may hope for is a 50% probability of an unaffected sibling.