Erratum

In the June 2000 issue, in the article “Localization of Psoriasis-Susceptibility Locus PSORS1 to a 60-kb Interval Telomeric to HLA-C,” by Nair et al. (66:1833–1844), the authors have identified errors in five allele designations in table 2. A revised version of the table is presented here (table 2). These errors were made during preparation of the table, not in the genotypes that were used for the analysis. For risk cluster 17, the marker allele designations for M6S169, M6S200, M6S165, and M6S201 should have been 2, 4, 2, and 21, respectively (not 3, 2, 15, and 14). For cluster 19, the marker allele designation for M6S201 should have been 9 (not 10). Of these, the only errors that could yield a difference in the interpretation of the results are those affecting M6S169 and M6S200, because they produce a greater degree of similarity between cluster 17 and the remaining risk clusters. However, these two errors did not influence the determination of the boundaries of risk haplotypes 1 and 2, because that determination was based on divergences between risk clusters at M6S111 and M6S169, which persisted even after the corrections were made. The authors are in the process of sequencing the interval between risk haplotypes 1 and 2 in a collection of risk and nonrisk chromosomes. This will allow them to determine with certainty whether or not ancestral double-recombination events occurred between risk haplotypes 1 and 2.

Table 2

Haplotype Clusters (Expanded Sample) and Their Transmission to Affected Offspring

CATEGORY AND CLUSTER[a]	D6S273	M6S214	TNFB	M6S125	MICA	M6S16	**HLA-B**	M6S101	M6S151	**HLA-C**	M6S167	M6S105	M6S168	M6S178	M6S102	M6S172	M6S176	M6S145	M6S143	M6S111	M6S169	M6S200	M6S198	M6S190	M6S161	M6S160	M6S159	M6S162	M6S224	M6S179	M6S181	M6S187	M6S164	M6S163	M6S165	M6S201	T:NT (%T)	*P*
Risk:																																						
17	4	*5*	2	3	4	3	**65**	*5*	2	**8**	*13*	3	2	3	6	1	3	1	1	*9*	2	4	3	8	3	*10*	4	16	…	1	2	6	3	6	2	*21*	21:10 (67.7)	.048
19	2	*5*	*5*	3	4	6	**…**	16	3	**6**	*9*	3	2	3	6	1	3	1	1	9	3	4	3	1	2	2	2	4	*8*	2	1	4	3	*5*	3	9	16:5 (76.2)	.016
21	3	*5*	7	7	3	*5*	**13**	16	3	**6**	*15*	3	2	3	6	1	3	1	1	*9*	2	4	3	1	2	2	2	4	*16*	1	2	7	8	*9*	3	3	49:21 (70.0)	.00082
22	3	*5*	7	7	3	*5*	**13**	16	3	**6**	15	3	2	3	6	1	3	1	1	9	2	4	3	1	2	2	2	4	*16*	1	2	*4*	*5*	*12*	…	…	15:10 (60.0)	.32
23	6	*5*	*9*	*9*	3	10	**37**	*15*	3	**6**	*13*	3	2	3	6	1	3	1	1	8	2	4	3	1	2	2	2	4	*26*	1	2	4	*5*	12	8	*5*	22:9 (71.0)	.020
25	6	12	2	12	*5*	9	**57**	15	3	**6**	13	3	2	3	6	1	3	1	1	8	2	4	3	1	2	2	2	4	*20*	1	2	4	*5*	12	8	*5*	104:27 (79.4)	1.7×10^{-11}
Nonrisk:																																						
14	*6*	*5*	11	6	3	*5*	**7**	*9*	3	**7**	1	6	…	*5*	1	3	3	1	1	4	4	6	3	2	2	2	2	4	*23*	2	2	*5*	2	*5*	*3*	*5*	57:87 (39.6)	.012
26	*8*	3	2	16	3	12	**8**	7	3	**7**	15	3	*5*	3	6	1	3	1	1	10	2	4	3	6	2	1	2	4	1	1	2	7	2	6	3	*16*	53:64 (45.3)	.31
30	*5*	*5*	*5*	*12*	*5*	13	**35**	*19*	2	**4**	10	3	1	3	6	*5*	2	2	2	2	4	4	3	6	14	8	4	1	19	1	1	6	2	6	1	*10*	10:16 (38.5)	.24
44	3	4	4	16	3	13	**60**	12	2	**3**	15	3	7	6	6	*5*	2	2	4	2	1	6	3	8	2	3	2	4	11	2	1	6	2	8	4	*9*	5:15 (25.0)	.025
48	6	*9*	2	*10*	2	1	**62**	14	2	**3**	15	3	8	6	6	*5*	2	2	4	2	1	6	3	*8*	2	2	2	4	11	2	1	6	2	6	4	*11*	12:21 (36.4)	.12
54	*4*	*14*	10	6	1	10	**55**	*9*	2	**3**	13	3	*9*	7	6	*7*	2	2	4	2	1	6	3	8	2	2	2	4	11	2	1	8	2	*6*	*2*	…	11:11 (50.0)	1.00
56	4	4	*7*	7	4	*5*	**44**	3	2	**16**	*15*	3	*9*	6	6	*5*	2	2	4	2	1	*5*	3	6	2	1	2	3	20	2	1	6	3	3	3	*5*	19:22 (46.3)	.64
58	4	4	*7*	7	4	*5*	**44**	11	2	**4**	8	7	1	3	6	*5*	2	1	1	4	4	6	4	6	6	8	4	16	*18*	1	2	*5*	2	6	3	*15*	8:11 (42.1)	.49
63	*5*	*9*	6	3	3	15	**44**	*4*	2	**5**	10	3	*13*	7	3	3	1	1	1	2	4	*5*	4	8	13	*13*	4	1	…	1	2	4	2	6	1	*12*	16:27 (37.2)	.093
66	*5*	*9*	10	*17*	*5*	3	**38**	14	3	**12**	2	3	12	7	2	3	1	2	6	*9*	*5*	5	3	8	*20*	8	4	16	*8*	1	2	6	2	6	8	…	15:15 (50.0)	1.00
61	2	6	4	3	2	3	**65**	6	2	**8**	8	7	13	1	1	1	3	1	1	*5*	2	*5*	4	4	14	6	4	17	13	1	2	6	*5*	12	…	…	2:6 (25.0)	…

NOTE.—All 34 markers subjected to long-haplotype clustering are displayed, in centromeric to telomeric order, from left to right. CDSN is located in RH2, between markers M6S190 and M6S161. Ellipses (…) indicate that no allele occurred in >50% of the founder haplotypes comprising the cluster. Italicized numbers indicate that the allele shown occurred in 50–80% of the founder haplotypes comprising the cluster. Nonitalicized numbers indicate that the allele shown occurred in >80% of the founder haplotypes comprising the cluster. Only the conserved alleles of RH1 and RH2 are denoted by the left and right boxes, respectively. Alleles at HLA-B and HLA-C are indicated in boldface type.

[a] All risk clusters for which $T + NT \geqslant 10$ and the 10 most common nonrisk clusters are shown. Cluster 61 is shown for purposes of comparison with cluster 17 (see text for details). No P value is given for cluster 61, because of an insufficient number of occurrences.