Red blood cell phenotype matching for various ethnic groups

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Patients requiring chronic transfusion support are at risk of alloimmunization after red blood cell (RBC) transfusion because of a disparity between donor and recipient antigen profiles. This research explored the probability of obtaining an exact extended phenotype match between blood donors randomly selected from our institution and patients randomly selected from particular ethnic groups. Blood samples from 1,000 blood donors tested by molecular method were evaluated for the predicted phenotype distribution of Rh, Kell, Kidd, Duffy, and MNS. A random subsample of 800 donor phenotypes was then evaluated for the probability of obtaining an exact match with respect to phenotype with a randomly selected patient from a particular ethnic group. Overall, there was a greater than 80 percent probability of finding an exact donor-recipient match for the K/k alleles in the Kell system. The probability ranged from 3 percent to 38 percent, depending on the ethnicity and disparities in phenotypic profiles, for the Rh, Kidd, Duffy, and MNS systems. A significant donor-recipient phenotype mismatch ratio exists with certain blood group antigens such that, with current routine ABO and D matching practices, recipients of certain ethnic groups are predisposed to alloimmunization. *Immunohematology* 2011; 27:12–19.

Key Words: alloimmunization, red cell phenotype, donor ethnicity, donors, RBC serology, blood groups, donor-recipient antigen profiles

As a premier destination medical center, the Mayo Clinic in Rochester, Minnesota, treats thousands of patients yearly. Demographic records in 2007 revealed that 78 percent of patients were from the upper midwestern area of the United States, 20 percent were from other areas of the United States, and 2 percent were international patients.[1] The majority of international patients were from the Persian Gulf States region (Saudi Arabia, Qatar, United Arab Emirates, and Kuwait) followed by patients from Canada, Europe, and South America.[1]

The 2008 population demographics of Olmsted County in southeastern Minnesota showed 86.6 percent Caucasian, 3.0 percent Hispanic/Latino, 3.8 percent Black/African American, 5.1 percent Asian, and 1.4 percent other.[2] As expected from this population demographic, blood donors at Mayo Clinic are predominantly Caucasian. In contrast, the Mayo Clinic patient demographics in the past decade show a steady increase in patients of various ethnic groups, including Somalis, Hispanics, Asians, and patients from Middle Eastern countries.

Because blood transfusion essentially constitutes a temporary transplant, there are risks of alloimmunization from exposure to foreign antigens on donor RBCs that can result in the formation of unexpected alloantibodies.[3–6] The development of RBC alloantibodies can lead to adverse complications including acute hemolytic transfusion reactions (AHTR), delayed hemolytic transfusion reactions (DHTR), and hemolytic disease of the fetus and newborn (HDFN), as well as laboratory findings such as delayed serologic transfusion reactions (DSTR) and a positive direct antiglobulin test (DAT).[3,4,6,7] Other reports have proposed that allogeneic transfusion also predisposes patients to the formation of RBC autoantibodies, which may result in the development of autoimmune hemolytic anemia (AIHA), a condition that can lead to increased hemolysis of transfused RBCs.[8,9]

The purpose of our study was to determine the degree of patient and donor matching by comparing the phenotypic distribution of Mayo Clinic blood donors, based on molecular analysis, with the published Rh, Kell, Kidd, Duffy, and MNS phenotypes of various ethnic groups. Identifying, by means of DNA analysis, the predicted donor inventory profiles that closely match certain ethnic patients who may present with unexpected antibodies will help provide the best phenotype blood for these patients as well as triage any transfusion support with faster turnaround time in obtaining compatible blood. Although interethnic RBC phenotypic disparities are well documented, this research is the first comprehensive study comparing phenotypic differences between a predominantly Caucasian donor pool and an international, multiethnic[10] group in a single report.

Materials and Methods

The results of molecular analysis of 1,000 blood donors were evaluated after approval from the Institutional Review Board. We limited molecular testing to group O and group

A donors to maximize inventory. Because D– donors were also selectively tested for inventory management purposes, the initial data showed a disproportionate 30 percent D–. To correct for the skewed D– sampling, a random subsample of 800 was selected from the initial 1,000 samples and stratified by D, such that the resulting distribution would simulate the known distribution of D phenotypes in the general Caucasian population of 85 percent D+ and 15 percent D–. These 800 samples were then evaluated for the predicted phenotype distribution of Rh, Kell, Kidd, Duffy, and MNS.

Molecular testing was performed (BioArray BeadChip wHEA, Immucor, Norcross, GA). The BioArray wHEA predicted the RBC phenotype for 28 antigens in 11 blood group systems including Rh, Kell, Kidd, Duffy, MNS, Lutheran, Diego, Colton, Dombrock, Landsteiner-Wiener, and Scianna.

DNA was extracted using Genom-6, a robotic workstation that performs rapid isolation and purification of DNA without using solvent extraction and precipitation steps. The extraction was achieved by the tendency of DNA to bind or adsorb to a silica surface of magnetic beads in the presence of a chaotropic solution.

Statistical Methods

The antigen frequencies of Rh, Kell, Kidd, Duffy, and MNS from the 800 random subsamples were estimated with percentages. For the Kell, Kidd, and Duffy groups, overall exact chi-square goodness-of-fit tests (or their Monte Carlo estimates when necessary owing to sparse data) were used to compare the overall distributions with population estimates for each ethnic group. For the Rh and MNS groups, the percentage of each individual phenotype (i.e., the percent who were DCCee vs. all others) was compared with the corresponding published data of the various ethnic groups using exact chi-square goodness-of-fit tests (or their Monte Carlo estimates when necessary). To adjust for the nine tests done per ethnicity within the Rh and MNS blood groups, the probability values from each of these individual tests were inflated by a factor of 9 (using an approximate Bonferroni methodology[11]). Further, we compared approximately 10 different ethnicities with our donor pool for each blood group. To adjust for this large number of comparisons, we considered probability values less than 0.01 to be statistically significant (overall type I error rate for a particular antigen group of 0.05/10 = 0.005; approximate Bonferroni methodology). All probability values were calculated using software (SAS version 9 software, SAS Institute, Cary, NC). A statistical summary for the different blood groups is presented in Tables 1, 2, and 3, respectively.

As a separate analysis, we also calculated the probability of getting an exact match with respect to the phenotype from a randomly selected donor from our donor pool and a randomly selected patient from a particular ethnic group within each antigen group. These calculations assumed that the observed antigen distribution from the sample of 800 donors is representative of the population of our donors. See the Appendix for details on these calculations.

Table 1. Statistical summary for the Rh blood group system

	Mayo Donors (Reference)	Caucasian[12]	East African[13]	Somali[14]	Black[12]	Chinese[15]	Thai[16]	Northern Indian[10]	Southern Indian[17]	Asian[18]	Mexican[18]	Saudi Arabian[19]
DCCee	21.4	16.0‡	0.0§	2.8§	3.0§	47.0§	55.6§	42.6§	41.6§	41.7§	27.0†	20.7*
DCcEe	11.3	14.0*	0.7§	0.7§	4.0§	30.0§	26.7§	12.1*	9.3*	34.7§	26.0§	14.8*
DccEE	2.9	3.0*	2.2*	0.3§	1.0§	6.0†	3.6*	2.6*	1.3†	7.1§	7.0‡	4.4*
Dccee	2.1	1.5*	81.9§	64.1§	42.0§	0.3§	0.6§	1.9*	1.6*	1.7*	2.0*	10.8§
DCcee	35.0	32.0*	2.9§	15.0§	26.0§	8.7§	8.7§	35.1*	32.9*	8.4§	18.0§	28.1‡
DccEe	12.4	13.0*	8.0‡	2.5§	16.0*	5.4§	1.5§	5.7§	5.3§	3.4§	8.0‡	10.3*
dccee	13.8	15.0*	2.9§	1.4§	7.0§	1.0§	0.0§	0.0§	6.0§	0.2§	3.0*	10.3*
dCcee	0.5	0.4*	0.0§	0.1*	1.0*	0.2*	0.0§	0.0§	0.8*	0.2*	0.2*	0.5*
dccEe	0.8	0.2*	0.0§	0.2*	0.0§	0.0§	0.0§	0.0§	0.0§	0.2*	0.2*	0.0§
Probability of finding same phenotype match	0.20	0.04	0.08	0.14	0.17	0.18	0.24	0.23	0.16	0.17	0.19

p-values are for comparison of the percentage of each phenotype in each ethnic group with the Mayo donor percentage.

*p-value ≥ 0.01 (not significant).

†0.01 > p-value ≥ 0.001.

‡0.001 > p-value ≥ 0.0001.

§p-value < 0.0001.

Table 2. Statistical summary for the Kell, Kidd, and Duffy blood group systems

	Mayo Donors (Reference)	Caucasian[20]	Northern Indian[10]	Southern Indian[21]	Black[20]	Somali[14]	Thai[16]	Saudi Arabian[19]	Mexican[18]	Asian[18]	East African[13]	Chinese[20]
Kell												
K–k+	**90.4**	91.0	96.0	99.0	98.0	99.0	100.0	80.0	98.0	97.8		
K+k–	**0.4**	0.2	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0		
K+k+	**9.2**	8.8	4.0	1.0	2.0	1.0	0.0	19.0	2.0	0.2		
p-value		*	§	§	§	§	§	§	§	§		
Probability of finding same phenotype match		0.83	0.87	0.90	0.89	0.9	0.9	0.74	0.89	0.88		
Kidd												
Jk(a+b–)	**27.5**	26.3	29.7	31.3	51.0	47.9	31.8	50.0	25.0	23.5		
Jk(a–b+)	**20.9**	23.4	21.7	21.3	8.0	10.3	42.8	42.0	18.0	27.1		
Jk(a+b+)	**51.6**	50.3	48.7	47.3	41.0	41.9	25.4	8.0	57.0	49.4		
p-value		*	*	*	§	§	§	§	†	§		
Probability of finding same phenotype match		0.38	0.38	0.38	0.37	0.37	0.31	0.27	0.40	0.38		
Duffy												
Fy(a+b–)	**20.9**	17.0	40.9	38.7	9.0	7.5	78.9	25.0	40.6	81.4	0.0	90.8
Fy(a–b+)	**34.5**	34.0	15.9	21.2	22.0	7.1	1.4	29.0	15.0	1.1	8.5	0.3
Fy(a+b+)	**44.5**	49.0	42.9	40.1	1.0	0.7	19.7	11.0	42.7	17.3	0.0	8.9
Fy(a–b–)	**0.1**	0.0	0.4	0.0	68.0	84.8	0.0	35.0	1.6	0.2	91.5	0.0
p-value		§	§	§	§	§	§	§	§	§	§	§
Probability of finding same phenotype match		0.37	0.33	0.33	0.10	0.04	0.26	0.20	0.33	0.25	0.03	0.04

p-value is for comparing each ethnic group with the Mayo donor distribution.

*p-value ≥ 0.01 (not significant).

†0.01 > p-value ≥ 0.001.

‡0.001 > p-value ≥ 0.0001.

§p-value < 0.0001.

Results

Results of the predicted Rh phenotype distributions of our blood donors compared with published distributions for the groups represented among our patients are summarized in Table 1. The distribution of the Rh phenotypes in our donor pool is similar to the known distribution among Caucasians, with the exception of the DCCee phenotype (21.4% for Mayo Clinic vs. 16.0% for Caucasians; p < 0.001).

The most common Rh phenotype in East Africans, Somalis, and the general Black population is Dccee, with frequencies of 81.9 percent, 64.1 percent, and 42 percent, respectively.

For Chinese and Thai people, the most common Rh phenotypes are DCCee and DCcEe, each approximately twice as frequent as donors at Mayo Clinic and Caucasians in general. For Asians of Indian descent, DCCee is the most common (42.6%), which is twice that of our donor population and Caucasians in general. However, three Rh phenotypes from Asians of Indian descent (DCcee, DCcEe, Dccee) showed no significant differences as compared with our donor pool. The predicted Rh phenotype distribution of Saudi Arabians closely resembles that of Caucasians and our donors (with the exception of Dccee, DCcee, and dccEe).

The probabilities of finding the same phenotype match for donor-recipient from our blood donors for the Rh blood groups for the various ethnic groups are presented in Table 1. The results show the probability of a random donor-recipient match ranged from 4 percent to 24 percent, depending on the ethnicity and the disparities in phenotypic profiles. For example, the chance of finding an exact Rh phenotype match between a random Mayo Clinic donor and an East African from Kampala, Uganda, is 4 percent; 8 percent for a Somali recipient, 17 percent to 18 percent for Asians of Chinese or Thai descent, 20 percent for a Caucasian recipient, and 24 percent for Asians of Indian descent.

Table 3. Statistical summary for the MNS blood group system

	Mayo Donors (Reference)	Caucasian[12]	Chinese[15]	Thai[16]	Northern Indian[10]	Somali[14]	East African[13]	Mexican[18]	Black[12]	Asian[18]
MNSs	21.2	24.0*	1.9§	7.2§	10.7§	16.9†	12.3§	17.2*	13.0§	6.0§
MNS	3.1	4.0*	0.5§	0.0§	4.6*	3.6*	5.8*	4.4*	2.0*	0.6§
MNs	23.5	22.0*	47.4§	40.3§	27.8*	30.1‡	28.3*	18.1‡	33.0§	41.2§
MSs	15.0	14.0*	3.3§	8.1§	13.3*	11.8*	10.9†	23.3§	7.0§	5.9§
MS	6.8	6.0*	0.5§	0.0§	5.5*	5.2*	2.9§	11.2‡	2.0§	0.6§
Ms	10.0	8.0*	23.9§	36.0§	22.6§	9.4*	18.1§	15.4‡	16.0§	25.9§
NSs	4.2	6.0*	1.4§	0.9§	3.5*	2.0‡	4.3*	2.6*	5.0*	2.2†
NS	0.3	1.0*	0.0§	0.2*	1.2*	0.5*	0.0§	0.7*	2.0†	0.2*
Ns	15.9	15.0*	21.1†	7.2§	9.3§	20.1*	13.0*	7.2§	19.0*	17.4*
Probability of finding same phenotype match	0.16	0.18	0.17	0.15	0.17	0.15	0.15	0.17	0.17	

p-values are for comparison of the percentage of each phenotype in each ethnic group with the Mayo donor percentage.

*p-value ≥ 0.01 (not significant).

†0.01 > p-value ≥ 0.001.

‡0.001 > p-value ≥ 0.0001.

§p-value < 0.0001.

Although DCCee (42%) is the most common published Rh phenotype among Asians of Indian descent, many Asians of Indian descent (32.9% to 35.1%; Table 1) also express the DCcee phenotype, which is the predominant phenotype (35.0%) among our donors. On the other hand, Somalis and East Africans predominantly express Dccee (64.1% and 81.9%, respectively). Therefore, greater disparities exist because of the high incidence of the Dce (R_o) phenotype and its low incidence among our donor pool (Table 1). Consequently, the large mismatched ratio and large number of donor exposures predisposes these recipients to the risk of alloimmunization to clinically significant antigens such as E and C. This large donor exposure for the mismatched antigens could be significant especially in obstetric and transfusion-dependent recipients.

Table 2 summarizes the phenotype distributions of the Kell, Kidd, and Duffy blood group systems. In the Kell system, the K+k+ phenotype among our donors (9.2%) is higher compared with that among Asians of Indian descent (4.0% and 1.0%, respectively), Somalis (1.0%), and Thai (0.0%), but significantly lower when compared with that among Saudi Arabians (19.0%). Although these discrepancies are statistically significant from a clinical standpoint (p < 0.0001), the probability of finding the same donor-recipient phenotype for the K/k alleles in the Kell blood group system, based on the observed distribution, is 74 percent to 90 percent (Table 2).

The distribution in the Kidd system is comparable between our donors and the published data for Caucasians and Asians of Indian descent. However, significant differences (p < 0.0001) exist when compared with Blacks, Somalis, Thai, Saudi Arabians, and Mexicans (p < 0.01). The Jk(a+b−) phenotype in Blacks (51.0%), Somalis (47.9%), and Saudi Arabians (50.0%) is higher than our donor pool (27.5%), whereas the frequency of Jk(a+b+) among our donors (51.6%) is higher when compared with Blacks (41.0%) and Somalis (41.9%), and 6 times higher than Saudi Arabians (8.0%). Based on our statistical calculation of the observed distribution, the probability of finding a donor-recipient phenotypic match for the Kidd blood group system ranges from 27 percent to 40 percent (Table 2).

For the Duffy blood group system, the distribution of phenotypes among our donors was found to be significantly different (p < 0.0001) when compared with all other ethnic groups, including Caucasians. The frequency of the Fy(a+b−) and Fy(a+b+) phenotypes among our donors is notable, 20.9 percent and 44.5 percent, respectively, but did not achieve statistical significance when compared with the published distribution in the general Caucasian population (17.0% and 49.0%, respectively). The Fy(a−b−) phenotype among our donors is only 0.1 percent compared with East Africans (91.5%), Somalis (84.8%), and Saudi Arabians (35.0%). The high incidence of Fy(a−b−) in Saudi Arabians is likely related to the presence of a Black and African admixture in the population of the Arabian Gulf States. The Fy(a−b−) phenotype confers resistance to certain malaria parasites and occurs predominantly among Blacks because of a genetically driven selection process.[3] From the aforementioned differences in phenotypic profiles among ethnic groups in our study, our calculation shows

the probability of a donor-recipient phenotype match for the Duffy blood group system is 3 percent to 37 percent. Given the high incidence of the Fy(a–b–) phenotype among Somalis, East Africans, and Saudi Arabians, patients from these ethnic groups can be predisposed to alloimmunization to Duffy antigens owing to the relatively high incidence of Fy(a+b+) phenotype among our donor pool. Likewise, finding phenotypically matched blood for recipients of Asian descent, such as Chinese and Thai who are predominantly Fy(a+b–) (90.8% and 78.9% respectively), could be a difficult challenge. On the basis of the phenotypic distribution of our donor pool, some recipients can be predisposed to alloimmunization to Fy[b].

The distributions for the MNS blood group system are summarized in Table 3. The most common MNS phenotypes in our donors are comparable with those of the general Caucasian population—MNs (23.5%), MNSs (21.2%), Ns (15.9%), and MSs (15.0%). However, significant differences exist when our donors are compared with the rest of the ethnic groups (probability values range from < 0.01 to < 0.0001; Table 3). For Asians (Chinese, Thai, and Asians of Indian descent), the most common phenotypes are MNs and Ms. Ns in Chinese (21.1%) is notably higher in comparison to Thai (7.2%) and Asians of Indian descent (9.3%). The MNs phenotype is most common in both Somalis and East Africans, with Ns being the second most common phenotype in Somalis (20.1%) and Ms being the second most common phenotype in East Africans (18.1%). Mexicans show a different distribution pattern, with the most common phenotypes being MSs (23.3%), MNs (18.1%), and MNSs (17.2%). On the basis of these observed phenotypic distributions, the probability of finding a donor-recipient phenotypic match is 15 percent to 18 percent for the MNS blood group system.

Discussion

RBC transfusion is a critical component of patient care, providing many benefits to those patients in need of oxygen-carrying capacity, but it also has inherent hazards. Transfusion recipients are at risk of alloimmunization owing to a disparity between donor and recipient antigen profiles. The risk associated with alloimmunization of recipients is attributable to individual and ethnic differences. These risks can be influenced by other factors, including dose, mode of exposure, and immunogenicity of the antigen.[3,7,9,22,23] The frequency of RBC-induced alloimmunization has been estimated to be between 2.6 percent and 60 percent, depending on the patient population studied and the method of study.[4–7,23] The routine practice for selection of RBCs for blood transfusion has largely been restricted to

matching for ABO and D despite lack of homogeneity of blood groups among individuals and across different ethnic groups. Exceptions include "transfusion responders" and the chronically transfused patients who are transfusion dependent and whose management sometimes dictates extended matching for other antigens because of preformed alloantibodies.[4–9,22–24] Moreover, some patient populations, such as sickle cell patients, receive extended antigen matching in advance. The effects of alloimmunization include difficulty with future management and provision of transfusion support for these recipients. The situation is further exacerbated when patients present with multiple antibodies requiring extensive serologic workup that could delay patient care.[3–9,22–25]

Although some have strongly advocated for a more proactive approach in antigen matching for transfusion, others have suggested a more balanced approach, given the logistical complexities of resource and inventory management.[5–7,22] In general, many transfusion experts support extended antigen matching for the chronically transfused patient because the frequency of alloimmunization in these patients can be as high as 60 percent. However, expert opinion varies widely with regard to prophylactic extended antigen matching in nonchronically transfused patients to mitigate or avoid alloimmunization, as not all patients have an inherent risk of RBC sensitization. Higgins and Sloan[4] reported evidence of a distinct "responder" phenotype and estimated that only 13 percent of the general patient population were responders. In addition, they reported that the risk of immunologic response attributable to alloimmunization among these patients was only 30 percent and identified only 4 percent of new alloantibodies overall, suggesting that 70 percent of the responder phenotype do not usually make antibodies. Based on these results, the authors proposed a stochastic or nonanamnestic model of RBC alloimmunization.[4] Their hypothesis implies that additional alloantibody formation is a rather random process that is not influenced by the number of preexisting patient antibodies.

However, in a 20-year multicenter retrospective study, Schonewille et al.[5] reported 21.4 percent (140 of 653) of nonhematologic alloimmunized patients in their cohort study formed additional antibodies resulting in 157 new antibody specificities. In their findings, the authors reported 33.8 percent (221 of 653) of patients demonstrated multiple antibodies, whereas 57 percent (80 of 140) of those found with additional antibodies made the antibodies after receiving just one subsequent transfusion, averaging two units per transfusion episode. The authors further noted that extended phenotype matching for C, E, c, K, Fy[a], and Jk[a] could have prevented 83 percent of the antibodies in

316 patients. Given their data, the authors recommended extended antigen matching for nonhematologic patients to avoid extensive RBC alloimmunization.

In a similar study, Schonewille et al.[6] also reported high antibody responders in previously alloimmunized hemoncology patients. Their study found that 21.7 percent (25 of 115) of previously alloimmunized hemoncology patients made additional antibodies after subsequent transfusions despite their diagnosis or compromised immune system from treatment. In essence, the findings of these two studies revealed a comparable increased ability to form additional antibodies in these two populations.

Our study explored the probability of obtaining an exact match with respect to phenotype from a randomly selected donor from our institution and a randomly selected patient from a particular ethnic group. As far as we know, our study is the first of its kind attempting to examine the probability of an exact donor-recipient match on the basis of phenotypic profiles. The probability of obtaining an exact phenotypic match from our donor pool and a random patient from various ethnic groups was calculated for Rh, Kell, Kidd, Duffy, and MNS blood group systems. These calculations assumed that the observed antigen distribution from the sample of 800 donors was representative of our donor population.

For example, the phenotype distribution of donors at our institution for K–k+, K+k–, and K+k+ is 90.4 percent, 0.38 percent, and 9.3 percent, respectively, whereas the published distribution in Caucasians is 91 percent, 0.2 percent, and 8.8 percent, respectively. If a single random Mayo Clinic donor and a single random Caucasian recipient are selected, the probability of an exact match is 83 percent. With the exception of Saudi Arabians, there is a greater than 80 percent probability of finding an exact donor-recipient match for the K/k antigens in the Kell system. However, because of the significant disparities alluded to earlier, a high risk of alloimmunization (owing to K) for a mismatch still exists for Asians, Africans/Blacks, and Hispanic groups. Patients from these ethnic groups who are alloimmunized could benefit from additional prophylactic matching for K– units.

For the Rh blood group system, the probability of a random donor-recipient match ranged from 4 percent to 24 percent, depending on the ethnicity and the disparities in phenotypic profiles. Therefore, the low probability of finding the same phenotype match can predispose certain ethnic recipients, such as Somalis and East Africans, to increased risk of alloimmunization to E and C.

In the Kidd system, there was a 27 percent to 40 percent probability of a match across all nationalities. In the Duffy system, the probabilities of a match ranged from 3 percent for Africans to as high as 37 percent for Caucasians. Given the phenotypic disparities in the Duffy system, Chinese and Thai individuals may be at risk for alloimmunization to Fy^b because these two groups predominantly express the Fy(a+b–) phenotype.

In the MNS system, the probability of a donor-recipient match ranged from 15 percent to 18 percent. For the most part, S represents the biggest risk for alloimmunization to ethnic recipients based on phenotypic discrepancies. Therefore, additional prophylactic matching for S– units should be considered for alloimmunized recipients.

In summary, dual donor-patient molecular analysis has the potential for developing comprehensive electronic genotypic profiling and matching to decrease alloimmunization caused by donor-recipient antigen disparity. Furthermore, the practice of electronic genotypic matching has the potential to eliminate the need for repeat pretransfusion testing and additional serologic testing for a majority of patients. This could result in significant financial benefits for patients, hospitals, and governments in the future. Genotypic matching will also ease or eliminate labor-intensive serologic platforms or methods, such as adsorptions or elutions, which subject patients to long delays for management. If the full genotype of a particular patient is known, the turnaround time for finding phenotypically matched donor units can be improved with a computer-assisted database management system that has the ability to query a well-characterized and comprehensive donor genotype profile.

In conclusion, our study showed a significant donor-recipient phenotype mismatch for certain blood group antigens, such that some ethnic groups are predisposed to a higher risk of alloimmunization to clinically significant antigens such as C, c, E, K, Jk^b, and Fy^a. A diversified donor pool that has been characterized genotypically to predict RBC antigen expression has the potential to enable transfusion medicine practitioners to provide individualized RBC products for recipients through extended genotypic matching.

Acknowledgments

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Appendix

Additional Details and an Example Calculation for Determining an Exact Match Using Statistical Methods

The probability of getting an exact match with respect to the phenotype from a randomly selected donor from our donor pool and a randomly selected patient from a particular ethnic group within each antigen group was calculated. These calculations assumed that the observed antigen distribution from the sample of 800 donors is representative of the population of our donors. Using the Kell group as an example, the distribution of phenotypes in our donor pool is as follows: K–k+ 90.375 percent, K+k– 0.375 percent, and K+k+ 9.25 percent. The published distribution of these phenotypes in the general Caucasian population is as follows: 91 percent, 0.2 percent, and 8.8 percent. Thus, if a single Mayo Clinic blood donor and a single Caucasian recipient are randomly selected, the probability of an exact match is equal to the chance that the following scenario occurs: (the randomly selected Mayo Clinic donor is K–k+ AND the randomly selected Caucasian patient is K–k+) OR (the randomly selected Mayo Clinic donor is K+k– AND the randomly selected Caucasian patient is K+k–) OR (the randomly selected Mayo Clinic donor is K+k+ AND the randomly selected Caucasian patient is K+k+), resulting in the following calculation:

$$
\begin{aligned}
&= P(\text{K–k+}|\text{Mayo}) \times P(\text{K–k+}|\text{Caucasian}) \\
&\quad + P(\text{K+k–}|\text{Mayo}) \times P(\text{K+k–}|\text{Caucasian}) \\
&\quad + P(\text{K+k+}|\text{Mayo}) \times P(\text{K+k+}|\text{Caucasian}) \\
&= (0.90375 \times 0.91) + (0.00375 \times 0.002) \\
&\quad + (0.0925 \times 0.088) \\
&= 0.83
\end{aligned}
$$

In general terms, this calculation uses the following probability rules: (1) if events A and B are independent, then the P(A and B) = P(A) × P(B); and (2) if events A and B are mutually exclusive, then P(A or B) = P(A) + P(B).

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