Clinical pathology selected abstracts

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RH genotype matching for transfusion support in sickle cell disease

January 2019—In patients with sickle cell disease, Rh alloimmunization remains a challenge, despite the transfusion of serologic Rh C, E, and K antigen-matched red cells. The rates of alloimmunization are due to the complexity of the Rh blood group system, which includes more than 50 antigens defined at the serologic level, encoded by the *RHD* and *RHCE* genes. The degree of *RH* genetic diversity is higher in African populations than in Europeans, who represent the majority of blood donors. Approximately 85 percent of African-American patients with sickle cell disease carry at least one *RH* allele that differs from that commonly found in white blood donors, causing some patients to recognize donor antigens as foreign. *RH* genotype matching may be used to mitigate the risk of alloimmunization, but its feasibility is unknown. The authors evaluated the efficacy of serologic matching, compared *RH* allele frequencies between patients with sickle cell disease and African-American donors, and created a model of *RH* genotype matching. They found that during the four-year period of 2013 through 2016, 105 of 550 (19 percent) patients who received at least one blood transfusion using serologic testing with units selected primarily from African-American donors developed antibodies. Their analysis suggested that 50 percent of these cases may result from D-, C-, and E-like cross-reactive epitopes stimulated by African-American donor cells—a rate that may be mitigated by providing genetically matched red cells at the *RH* loci. The authors also compared *RH* allele diversity between their patient population (n = 857) and African-American donors (n = 587) and found it to be comparable, with 29 percent of *RHD* and 53 percent of *RHCE* alleles altered in sickle cell disease patients and African-American donors. They modeled four matching strategies: serologic DCEK matched; serologic DCEK with extended antigens matched; *RH* genotype and K matched; and *RH* genotype, K, and extended antigen matched. Their model showed that Rh matching based on *RH* genotype and K status met 95 percent of their patients' needs if twice as many African-American donors were collected each weekday. A much smaller increase in donors is necessary if less restrictive genetic matching is employed. For each of the four algorithms, a donor pool consisting primarily of African-Americans is necessary to avoid depleting D− units. In summary, *RH*-genotype–matched red cells may reduce rates of alloimmunization in patients with sickle cell disease and may be feasible from an inventory perspective. While African-American donor recruitment may be a challenge, the authors point out that strategies used by some blood centers have been successful. They also note that the cost of *RH* genotyping may be prohibitive, but this factor is likely to resolve as sequencing approaches continue to improve.

Chou ST, Evans P, Vege S, et al. *RH* genotype matching for transfusion support in sickle cell disease. *Blood*. 2018;132(11):1198–1207.

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Changes in prevalence of health care-associated infections in U.S. hospitals

Health care-associated infections are a major risk factor for patients in U.S. hospitals. The rates of hospital-associated infections are national metrics that are used by governmental agencies and consumer-related groups to assess health care quality in hospitals. The National Healthcare Safety Network of the Centers for Disease Control and Prevention tracks state and national data on the prevention of health care-associated infections in thousands of U.S. health care facilities. Point-prevalence surveys complement the network's location- and infection-specific data and allow public officials and health care leaders to periodically assess health care-associated infections for future consideration of tracking and prevention. A point-prevalence survey performed in 2011 showed that four

percent of patients had a health care-associated infection. The authors, all investigators for the CDC's Emerging Infections Program Hospital Prevalence Survey Team, repeated the survey in 2015 to assess changes in the prevalence of health care-associated infections. They recruited up to 25 hospitals in Emerging Infections Program site areas in 10 states, prioritizing hospitals that participated in the 2011 survey. Each hospital selected one day to randomly sample patients identified for assessment. Trained staff then compared the percentages of patients with health care-associated infection and performed multivariable log-binomial regression modeling to evaluate the association of survey year with the risk of health care-associated infection. In 2015, 12,299 patients in 199 hospitals were surveyed, compared with 1,282 patients in 183 hospitals in 2011. Patients' risk of having a health care-associated infection was 16 percent lower in 2015 than in 2011, largely due to reductions in the prevalence of surgical-site and urinary tract infections. These results were statistically significant. The most common health care-associated infections identified in the survey were pneumonia; gastrointestinal infections, primarily due to *Clostridium difficile*; and surgical-site infections. The authors concluded that, in accordance with their findings, strategies to further reduce infections should focus on the prevention of *C. difficile* and pneumonia.

Magill SS, O'Leary E, Janelle SJ, et al. Changes in prevalence of health care-associated infections in U.S. hospitals. *N Engl J Med.* 2018;379(18):1732–1744.

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