Clinical pathology selected abstracts

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Use of a bicentric study to compare umbilical cord and neonatal blood samples for chemistry tests at birth

April 2024—Neonatal anemia is a common comorbidity of premature infants and may result from certain obstetric conditions or diseases, or, in the case of iatrogenic anemia, from multiple phlebotomies in the first days of life. Once infants enter the neonatal intensive care unit (NICU), they undergo a series of laboratory tests at baseline and then as needed for treatment or monitoring. These tests commonly include blood cultures, CBCs, coagulation profiles, metabolic screens, blood gases, blood glucose, and chemistry profiles. Phlebotomy-associated blood loss is more clinically relevant in lower birth-weight neonates since they have lower total circulating blood volumes. When blood is drawn from an indwelling umbilical catheter, even more blood is removed due to the need to flush residual intravenous fluid from the line. The use of umbilical cord blood has been proposed as an alternative to neonatal phlebotomies for initial NICU laboratory testing. Umbilical cord blood cultures have been shown to have a higher sensitivity for the diagnosis of neonatal early-onset sepsis than peripheral blood cultures. CBCs and coagulation tests were also studied to determine the difference between neonatal peripheral blood and umbilical cord blood, and the results were comparable. The authors conducted a study to compare umbilical cord blood to infant peripheral blood for high-sensitivity C-reactive protein (hs-CRP), y-glutamyl transpeptidase (GGT), procalcitonin (PCT), sodium, potassium, chloride, calcium, phosphorus, magnesium, total proteins, albumin, alanine aminotransferase (ALT), and aspartate aminotransferase (AST) levels. Seventy-one newborns with a planned admission to the NICU were enrolled in the bicentric cohort study. The authors collected paired samples of umbilical cord blood and neonatal blood. The umbilical cord blood was collected from the portion of the cord attached to the infant or near the placenta. An intraclass correlation coefficient (ICC) was calculated for a repeatability analysis, followed by a Bland-Altman analysis to compare the two sampling methods. The

multivariable coefficient of determination (R^2) was also reported to quantify the degree of correlation between the methods. The results showed that the degree of agreement between the two sampling methods was fair to good for hs-CRP (ICC=0.79), phosphorus (ICC=0.83), and albumin (ICC=0.76). It was good to excellent for GGT (ICC=0.95) and procalcitonin (ICC=0.90). The authors concluded that umbilical cord blood may be a viable alternative to neonatal blood sampling for certain chemistry tests at birth. It may reduce iatrogenic blood loss, thereby preventing early-onset anemia and the need for packed RBC transfusions. However, additional studies are necessary to assess the ability of this strategy to improve neonatal outcomes.

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A fully interpretable machine-learning model to increase effectiveness of urine screening

A principal activity of any microbiology laboratory is to diagnose urinary tract infections using urine culture. This can be a manual process that requires seeding a culture plate with urine, incubating the sample overnight, and visually inspecting the sample for signs of bacterial growth. A culture plate may be read as no significant growth, contaminated sample, or positive growth. A urine culture with positive growth needs additional processing to identify the type of bacteria and determine antibiotic sensitivity. This testing process typically takes 24 to 48 hours. Most urine cultures are negative, so it is desirable to reduce the workload and reporting time for negative specimens. Therefore, a critical need exists for a rapid, reliable, and cost-effective decision-support tool to determine which specimens should undergo urine culture. The authors conducted a study to identify a new set of

logic rules, using parameters from an automated analyzer and clinical data, to better detect negative urine samples that do not need to undergo further analysis. They chose a fully transparent decision tree model with the intent of optimizing it using new strategies. Because decision trees are logical and relatively easy to understand compared with other models, it is easy to convert them into a set of rules for automated analyzers. The authors analyzed 15,312 samples from 10,534 patients with specific clinical features using the Sysmex UF-1000i automated analyzer. They collected data from May 2021 to May 2022. The screening rule used by the laboratory defined a urine sample as negative if BACT \leq 100 \land WBC \leq 75 \land YST \leq 30. Using this rule, 6,995 samples were labeled negative, which allowed a workload reduction of 45.6 percent. The remaining samples were labeled positive and then cultured. The results were recorded as no significant growth, positive, or contaminated (when two types of bacteria were detected by visual inspection with no predominant type). The authors grouped the no significant growth and contaminated patients into two classes: positives, or patients with positive urine culture results, and negatives, or patients with negative urine culture or contaminated results. They then modified the decision tree models, incorporating more features. They created a decision tree for each feature group to evaluate how each group impacts performance. They then created a decision tree containing all features to evaluate whether or not the combination of different features is beneficial. Finally, the authors took the best set of features and created a decision tree with a lookahead of one to determine whether this procedure was more beneficial than a classic decision tree. The results showed that the best model achieved a sensitivity of 94.5 percent and classified negative samples based on age, bacteria, mucus, and two scattering parameters. The model reduced the workload by an additional 16 percent compared with current laboratory procedures. This would lead to an estimated total savings of about 40,000 euros (approximately \$43,000 USD) per year based on the laboratory processing about 15,000 samples per year. The authors noted that these rules are consistent with guidelines and scientific rationale in the literature. They concluded that laboratory medicine needs to consider creating environments that are enabled by middleware or other architectures that will allow machine-learning models to be more readily used clinically. This study demonstrated an effective and interpretable screening method for urine culture in microbiology laboratories using the Sysmex UF-1000i analyzer. The authors claim that unlike other machinelearning models, their rules for urine cultures are transparent and interpretable, making it easier to implement them and to update and validate the models.

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