Disparate Hemoglobin Results
Casey E. Gooden,* Anne M. Winkler, and Corinne R. Fantz

CASE DESCRIPTION

A 60-year-old woman, a Jehovah’s Witness, presented with an abdominal wall hematoma at the injection site of low molecular weight heparin. The hematoma was accompanied by a decrease in the hemoglobin concentration from 11.1 g/dL (6.9 mmol/L) [reference interval, 11.4–14.4 g/dL (7.1–9.2 mmol/L)] on the previous day to 7.8 g/dL (4.8 mmol/L). The patient rapidly destabilized and refused any human-derived blood products because of her religious beliefs.

The clinicians noticed disparate hemoglobin results from the point-of-care blood gas analyzer [6.0–7.2 g/dL (3.7–4.5 mmol/L)] and the core laboratory hematology instrument [4.1–4.5 g/dL (2.5–2.8 mmol/L)] over the next day. A sample of the patient’s plasma is shown in Fig. 1.

QUESTIONS
1. What can cause reddish brown plasma?
2. What products are acceptable to Jehovah’s Witnesses to treat blood loss?
3. How do you explain the disparate hemoglobin results?

The answers are below.

ANSWERS

The color is from a blood substitute not approved by the US Food and Drug Administration (FDA). This product was obtained from the manufacturer through the FDA for Department of Pathology and Laboratory Medicine, Emory University School of Medicine, Atlanta, GA.

* Address correspondence to this author at: Department of Pathology and

Laboratory Medicine, Emory University School of Medicine, 1364 Clifton Rd., H183, Atlanta, GA 30322. Fax 404-727-2519; e-mail cegoode@emory.edu.
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Compassionate use. Hemoglobin substitutes are cross-linked, polymerized, or conjugated human or bovine hemoglobin (1), and they impart a reddish brown color. Jehovah’s Witnesses will not accept blood fractions (red blood cells, plasma, platelets, granulocytes). Acceptable treatments include crystalloids, vasopressors, and hemostatic products (2). Unlike the point-of-care measurement, the core laboratory included a correction for hemolysis. Because this correction subtracted free hemoglobin (or blood substitute), we considered the point-of-care result correct.

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References

News & Views

A Standardized Open-Source Mass Spectrometry Toolkit: Potential for Facilitating Proteomics Research

Ross J. Molinaro*

In October 2012, Nature Biotechnology published an article by Chambers and colleagues describing the ProteoWizard Toolkit (1). Despite the successes of mass spectrometry–based proteomics, the interpretation of massive data sets remains a challenge. The open-source Toolkit provides a set of software libraries and interfaced applications robust enough to potentially bridge all of the common data formats of mass spectrometry vendors, a recognized hindrance to the development of proteomic software tools for facilitating proteomics data analysis. Although the development of previously described “open” formats has suffered from several limitations, Chambers and colleagues mitigate these challenges through open-source, permissively licensed, cross-platform software that is robust enough to be used in both academic and commercial projects. This repository, where proteomics software developers can share their work, uses a modular framework of many independent libraries grouped in dependency levels. The Data, Utility, and Analysis layers within the modular structure of the Toolkit are responsible for interfacing with mass spectrometry data, performing computations, and providing common proteomics-centric analysis modules, respectively. In addition to describing handling computations for chemical formulas, peptide calculations, and isotope envelopes, this article also highlights examples of the Toolkit in action. ProteoWizard boasts data library access and browsing and printing capabilities through a common language infrastructure for peptide- and protein-identification data, performance of in silico digests of a protein read, and data-access capabilities that can enable mass spectrometry–based problem solving beyond proteomics investigations. Additional available analysis classes are described.

Work is ongoing to collaboratively create a modular-analysis infrastructure in which experts will be able to...