

COMPARISON OF THE TRADITIONAL AND MODERN APPROACHES TO MODELLING ACID-BASE

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Introduction:

The approaches to modelling acid-base chemistry can be largely divided into two groups, the ‘traditional’ and ‘modern’ approaches. The traditional approach is based mainly on the work of Siggaard- Andersen and co workers [1, 2] and divides acid–base disturbances into respiratory (changes of pCO₂) and metabolic (changes of BE). It has originally been represented in a form of acid base nomogram and more recently by a so called Van Slyke Equation. The modern approach is credited to the work of Stewart and Figge and Fencil, and Constable [3, 4, 5]. It divides acid base disturbances into respiratory (changes of pCO₂), metabolic (changes of Strong Ion Difference—SID) and changes in plasma protein (main non-bicarbonate buffer) concentrations (A_{tot}) (Figure 1).

Both approaches include parameters for the quantification of unmeasured anions. These are known as strong ion gap in the case of the modern approach and anion gap or corrected anion gap in the case of traditional approach. Recently, many studies have compared the clinical utility of parameters of either approach [6, 7]. However, when performing such comparisons it is important to compare like with like, an understanding which only comes via appreciation of the mathematics included in the approaches.

Methods:

This presentation will explain systematically the similarities and differences of the approaches. To do so, plasma is used as an example and the mathematical formulation of the two approaches explained in simple terms. A patient example will be used to illustrate the application of the two approaches, evaluating whether both approaches give same picture of the patient.

Results:

It can be shown mathematically that very little difference exists between the approaches and that the mathematics of either approach can be easily derived from the other with a few simple assumptions. For example, the van Slyke equation can be derived from Stewart’s equations describing non-bicarbonate buffers using only the

Reaction equations	Mathematical representation	
	Modern approach	Traditional approach
$H^+ + HCO_3^- \leftrightarrow H_2O + CO_2$	$[H^+][HCO_3^-] = K_c \cdot pCO_2$	$pH = pK_c + \log \frac{[HCO_3^-]}{\alpha \cdot pCO_2}$
$H^+ + A^- \leftrightarrow HA$	$[H^+][A^-] = K_A \cdot [HA]$	$BE = (24.4 - [HCO_3^-]) + \beta(pH - 7.4)$
	$[HA] + [A^-] = A_{tot}$	
	$SID - [HCO_3^-] - [A^-] = 0$	

Fig. 1. Buffering reactions in plasma and their mathematical representation. All non-bicarbonate buffers (albumin, globulins and phosphate) are lumped under the symbols HA/A⁻. The two equations of the traditional approach are known as Henderson-Hasselbalch equation for the bicarbonate buffer and van Slyke equation for calculation of base excess (BE). K_c—dissociation constants; pK_c = -log₁₀K_c; SID—strong ion difference; α—solubility of carbon dioxide; β—buffer capacity of non-bicarbonate buffers (of the whole blood or just plasma).

assumption of constant buffer capacity. A patient example can illustrate that there is not only a theoretical equivalence, but also a numerical equivalence between certain parameters of the two approaches (e.g. corrected anion gap and strong ion gap).

Conclusion:

In conclusion, it can be shown that the approaches are largely equivalent and that quantitative links between acid-base and electrolyte status can be made with either approach, provided plasma albumin levels are measured.

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