

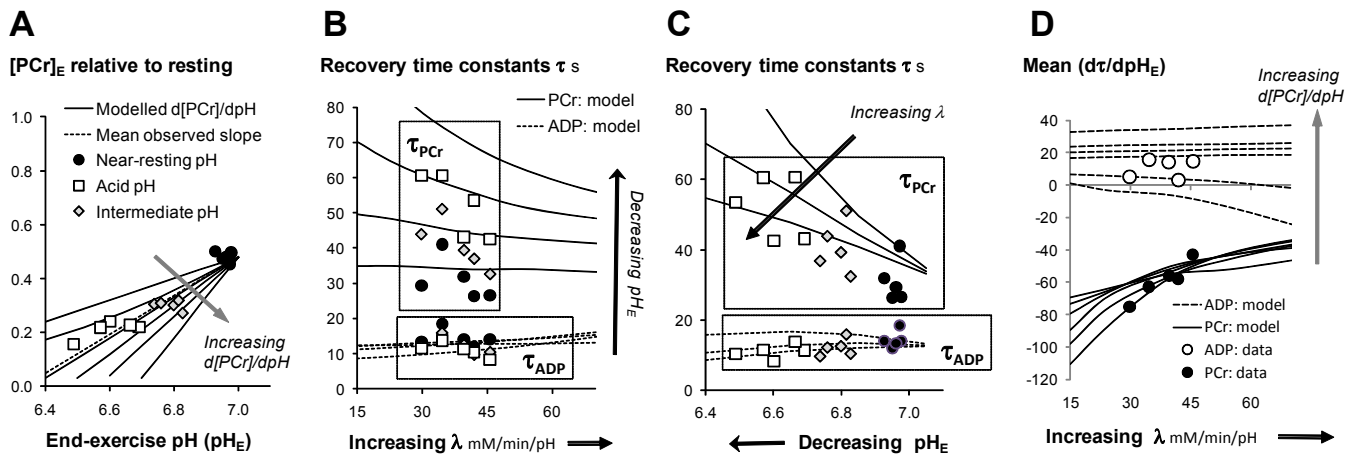
# The pH-dependence of post-exercise PCr and ADP recovery: a simple modelling approach reproduces important features of 31P MRS data from skeletal muscle

G. Kemp<sup>1</sup>, N. van den Broek<sup>2</sup>, K. Nicolay<sup>2</sup>, and J. Prompers<sup>2</sup>

<sup>1</sup>Magnetic Resonance and Image Analysis Research Centre, University of Liverpool, Liverpool, Merseyside, United Kingdom, <sup>2</sup>Biomedical NMR, Department of Biomedical Engineering, Eindhoven University of Technology, Eindhoven, Netherlands

**Introduction.** Noninvasive <sup>31</sup>P MRS measurements of the post-exercise recovery kinetics of pH<sub>E</sub>, [PCr]<sub>E</sub> and [ADP]<sub>E</sub> contain much information about muscle mitochondrial function and cellular acid-base balance *in vivo*, but quantitative interpretation depends on understanding the physiology (1-4). Both analytical and simulation approaches may be useful, particularly given the interactions between these variables imposed by the creatine kinase equilibrium. The dependence of the phosphocreatine recovery time constant ( $\tau_{PCr}$ ) on end-exercise pH (pH<sub>E</sub>) is important in inferences about mitochondrial function, and the pH<sub>E</sub>-dependence of the end-exercise/initial-recovery rate of acid efflux ( $E_E$ , which can be estimated from pH and PCr recovery data (5)) likely reflects a fundamental cellular physiological setting (e.g. higher in glycolytic fibres). It has recently been noted (1) that the slopes of these two relationships,  $\lambda = -(dE_E/dpH_E)_{mean}$  and  $(d\tau_{PCr}/dpH_E)_{mean}$ , correlate across individuals, suggesting that intersubject differences in the pH-dependence of  $\tau_{PCr}$  are related to differences in cellular pH control (1). It was noted (1) that a simple model reproduces the pH<sub>E</sub>-dependence of  $\tau_{PCr}$  (2). Here we show that, further, it directly predicts the  $\lambda$ -dependence of  $(d\tau_{PCr}/dpH_E)_{mean}$  as well as individual values of  $\tau_{PCr}$  and  $\tau_{ADP}$ , but that these depend also on the relationship between pH<sub>E</sub> and [PCr]<sub>E</sub>, which is not under direct experimental control.

**Methods.** Experimental data and methods are as previously published (1). The basis of the model is that under the feedback influence (3) of [ADP]<sub>E</sub> (which is in creatine kinase equilibrium with pH and [PCr]<sub>E</sub>), oxidative ATP synthesis drives PCr recovery, this being accompanied by net H<sup>+</sup> generation (4) which is opposed by linearly pH-dependent H<sup>+</sup> efflux (1, 5). Values of mitochondrial capacity  $Q_{MAX}$  and  $\lambda$  are obtained from each subject's data, and assumptions about mitochondrial control and cellular buffering are described elsewhere (4-8).



**Results and Discussion.** Figure A shows relationships between [PCr]<sub>E</sub> and pH<sub>E</sub> in the present simulations (solid lines: [PCr]<sub>E</sub> is varied incrementally and pH<sub>E</sub> is obtained for various values of d[PCr]<sub>E</sub>/dpH<sub>E</sub>, increasing as the arrow indicates) and in the data points from each of the 5 subjects (1), sorted for clarity into means for each individual of studies where pH<sub>E</sub> was 'near-resting', 'intermediate', and 'acid' (a mean data d[PCr]<sub>E</sub>/dpH<sub>E</sub> line is also shown: see legend for key). The more steeply [PCr]<sub>E</sub> decreases with pH<sub>E</sub>, the more steeply [ADP]<sub>E</sub> increases (not shown).

Figure B shows simulated  $\tau_{PCr}$  (solid lines) and  $\tau_{ADP}$  (dashed lines) as a function of  $\lambda$  for various values of pH<sub>E</sub>, which here is varied holding [ADP]<sub>E</sub> constant:  $\tau_{PCr}$  decreases markedly with increasing  $\lambda$  while  $\tau_{ADP}$  changes little. Figure C shows the same thing (with the same key) in a different way, the lines showing  $\tau_{PCr}$  and  $\tau_{ADP}$  as a function of pH<sub>E</sub> for various values of  $\lambda$ : the increase in  $\tau_{PCr}$  with decreasing pH<sub>E</sub> is more marked at high efflux settings (high  $\lambda$ ). The data points in Figures B & C (key as in Figure A) show that the experimental results (1) exhibit the same behaviour as the theoretical lines. The increase in  $\tau_{PCr}/\tau_{ADP}$  as pH<sub>E</sub> decreases (Figure C) was recently reported in a patient group (9).

In Figures B & C d[PCr]<sub>E</sub>/dpH<sub>E</sub> was chosen to keep [ADP]<sub>E</sub> constant as pH<sub>E</sub> is varied, but different assumptions are possible, and better match the experimental initial conditions in Figure A, where [ADP]<sub>E</sub> (not shown) rises modestly with decreasing pH<sub>E</sub>. In the summary Figure D (which has a similar format to Fig 4B in the experimental paper (1)) each pair of lines (solid =  $\tau_{PCr}$ , dashed =  $\tau_{ADP}$ ) makes a different assumption about d[PCr]<sub>E</sub>/dpH<sub>E</sub> (as in Figure A). Figure D shows that the pH<sub>E</sub>-dependence of  $\tau_{PCr}$  decreases with increasing  $\lambda$ , while  $\tau_{ADP}$  is insensitive to  $\lambda$  except in the extreme case where d[PCr]<sub>E</sub>/dpH<sub>E</sub> is so shallow that [ADP]<sub>E</sub> falls with decreasing pH<sub>E</sub>.

Thus a simple model of mitochondrial control and acid efflux explains much of post-exercise PCr and ADP recovery in relation to pH<sub>E</sub>. More generally, simple modelling can avoid some ambiguities of purely verbal argument about an multiply-interacting physiological system, and provide a bridge to more detailed mechanistic treatments of mitochondrial control (8) and acid handling by the myocyte.

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