

CORRIGENDUM

Increased glycolytic flux as an outcome of whole-genome duplication in yeast

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Correction to: *Molecular Systems Biology* 3:129. doi:10.1038/msb4100170; published online 31 July 2007

The authors of the above paper have detected an error in their published paper.

In Figure 2C, we incorrectly used a value of V_{\max} for the PDH reaction that was expressed in terms of flux per minute rather than per second. This updated version of the figure uses the correct value of V_{\max} from Rizzi *et al* (1997) cited in the supplemental information of our original manuscript. The change reinforces our conclusion that increasing flux through glycolysis tends to decrease the relative flux through respiration as compared to fermentation. The authors would like to thank Lukas Endler for discovering their error.

Please see the corrected figure below.

The authors apologize for any inconvenience caused.

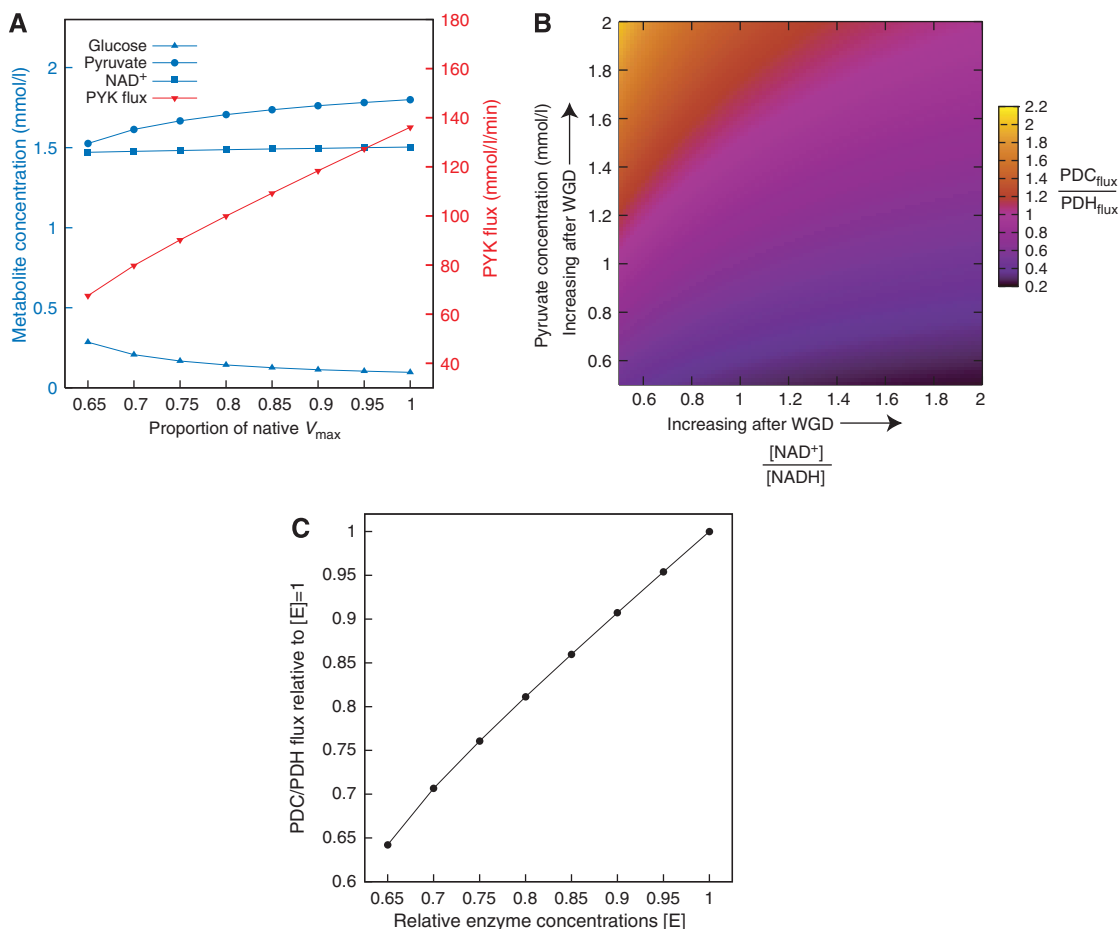


Figure 2 (A) Changes in the concentration of key metabolites in response to overall decreases in the V_{\max} values for the reactions of glycolysis (blue, left axis scale), as well as the change in PYK flux over the same range (red, right axis scale). (B) Ratio of the flux through pyruvate decarboxylase (PDC, fermentative pathways) to the flux through pyruvate dehydrogenase (PDH, respiratory pathway) as a function of pyruvate concentration and the ratio of NAD⁺ to NADH concentration (because NAD⁺ and NADH are two oxidation states of the same molecule, their concentrations vary inversely and hence are constrained to sum to 8.01 in B; Theobald *et al*, 1997). (C) Effect of compartmentalization on the relative fluxes of the first reaction in respiration (PDH) and in fermentation (PDC). On the x-axis is the relative enzyme concentration modeling a change from a rough pre-duplication state of 0.65 to a post-duplicate value of 1.0 (see A). On the y-axis is given the ratio of the fluxes between the two reactions relative to the flux when [E] on the x-axis is equal to 1.0.