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Erratum for: Gauger AK, Axe D (2011) The evolutionary accessibility of new enzyme functions: A case study from the biotin pathway. BIO-Complexity 2011(1):1-17. doi:10.5048/BIO-C.2011.1

Using genes from *E. coli*, we previously found one instance where a single amino acid replacement in BioF that increases sequence identity with Kbl appeared to eliminate the $BioF_2$ function in vivo. We reported this substitution to be H152N. In the course of further study, we discovered that our original plasmid that fails to confer $BioF_2$ function actually has a second mutation in the *bioF* gene, this one encoding the substitution S265G. By making new plasmid constructs carrying the H152N mutation alone and the S265G mutation alone, we determined that neither of these mutations eliminates $BioF_2$ function on its own. Function is lost only when the two are combined.

This correction reduces our previous estimate of the minimum number of nucleotide substitutions required for conversion from seven to six, with corresponding revisions needed in our Results and Discussion sections. In particular, most of the first three paragraphs under the subheading **Stage 2: Testing short-listed candidates by BioF →Kbl mutation** are now irrelevant, as they discuss the essential role of an amino-acid residue now known not to be essential. Also, the following sentence in our discussion (page 12) should be revised:

> In fact, even the unrealistically favorable assumption that *kbl* duplicates carry no fitness cost leaves the conversion just beyond the limits of feasibility.

The corrected sentence should read:

> Only under the unrealistically favorable assumption that *kbl* duplicates carry no fitness cost does the Kbl→BioF conversion fall just within the limits of feasibility.

The main point of the paper is unchanged.

Further details, including a brief discussion of the functional significance of H152 and S265, may be found in a forthcoming paper (in press): Reeves MA, Gauger AK, Axe DD (2014) Enzyme families—Shared evolutionary history or shared design? A study of the GABA-aminotransferase family. BIO-Complexity 2014 (4). doi:10.5048/BIO-C.2014.4.