RETRACTION

An Unusual Mechanism of Isopeptide Bond Formation Attaches the Collagenlike Glycoprotein BclA to the Exosporium of *Bacillus anthracis*

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Volume 2, no. 3, doi:10.1128/mBio.00084-11, 2011. In this article, authors Li Tan, Mei Li, and Charles L. Turnbough, Jr., claimed that the *Bacillus anthracis* exosporium proteins BclA and BxpB were cross-linked via isopeptide bonds between the amino-terminal residue of BclA and the side chain of any one of several acidic residues in BxpB. Direct evidence for these isopeptide bonds was provided by the identification of cross-linked peptides derived from proteolytically digested physiological complexes of BclA (or a BclA fusion protein) and BxpB. In these experiments, peptide sequences and positions of cross-links were determined by liquid chromatography-tandem mass spectrometry (LC-MS/MS) analysis. The authors recently reexamined the mass spectra used in these analyses and discovered that they were incorrectly interpreted and do not provide evidence for cross-linked peptides or isopeptide bond formation. The misinterpreted data are included in Figure 1 and Tables 1 to 3, and a model based on these data is shown in Figure 5. Furthermore, the analysis of the data in Figure 3 reported to show covalent complexes formed between BclA and variants of BxpB is possibly wrong. This analysis depends on control experiments in which LC-MS/MS was used to identify proteolytic peptides of mutant BxpB proteins. Again, the mass spectra used to identify these peptides were interpreted incorrectly, making a reliable analysis of the data impossible. Due to the misinterpreted data described above, the authors request that the *mBio* paper be retracted and offer sincere apologies to others in the field for any confusion caused by publication of this paper.

The authors also request correction of the statement in Acknowledgments in which personnel in the UAB Mass Spectrometry Core Facility are acknowledged for performing LC-MS/MS analyses. When Charles L. Turnbough, Jr., the corresponding author, wrote this acknowledgment, it was his understanding (and that of Mei Li) that experts in the core facility had actively participated in the interpretation of mass spectra and had concurred with all peptide identifications. However, this collaboration did not occur. Instead, the involvement of the core facility was effectively limited to data acquisition, and Li Tan analyzed the mass spectra without assistance. When this situation was discovered, unfortunately well after the paper was published, all relevant mass spectra were reanalyzed with expert assistance.

Finally, some of the data in the paper are correct and important and can continue to be referenced. These data include the results shown in Figures 2 and 4. Figure 2 shows the formation of extremely stable complexes between BxpB and a BclA N-terminal domain-enhanced green fluorescent protein (NTD::eGFP) fusion, with from one to three copies of the fusion protein attached to a single molecule of BxpB. Figure 4 shows the in vitro formation of stable complexes between purified recombinant BclA and BxpB, an experiment that has been repeated many times. The nature of the stable BclA-BxpB interaction remains to be determined.

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