Answer to the comment by Dumas, Bergdoll and Masson

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The Sh*ble* protein gene has been cloned from tallysomycin-producing *Streptoalloteichus hindustanus*, which belongs to the family Pseudonocardiaceae, systematically further distinct from Streptomycetaceae. Our conclusion "Mutation of the N-terminal protein 9 of BLMA from *Streptomyces verticillus* abolishes the binding affinity for bleomycin" was reached using BLMA, not the Sh*ble* protein. We all accept that proline appears to play a key role in the beta-strand of the hinge peptide. We showed that a monoclonal antibody, generated against BLMA, did not cross react with the Sh*ble* protein [Sugiyama et al. (1995) FEBS Lett. 362, 80–84]. Therefore, we independently determined the 1.5 Å crystal structure of BLMA from *S. verticillus*. Although Dumas and his group determined the crystal structure of the Sh*ble* protein at 2.3 Å resolution, the atomic coordinates were not deposited in the Protein Data Bank until 17 October 1998. We showed the BLMA structure in 1996 [Kawano et al. (1996) Photon Factory Activity Report 96-G218, 138]. We have submitted the details elsewhere. In this case, the structure was determined by the single isomorphous replacement method including the anomalous scattering effect method at 2.0 Å resolution and refined at a 1.5 Å high resolution. In the revised manuscript, submitted elsewhere on 13 July 1999, we cited the work of Dumas' group to compare the three-dimensional structures of BLMA and the Sh*ble* protein. Although their conclusions [Dumas et al. (1994) EMBO J. 13, 2483–2492] were the same as ours, there were also several significant differences between our findings and those of Dumas, e.g. the loss of the resistance property of Pro-9/Gly mutant BLMA. There could also be a significant difference in the protein folding property, since ours is cytoplasmic and that of Dumas is periplasmic. BLMA and the Sh*ble* protein are immunologically quite distinct which also makes our work unique compared to that of Dumas.

Admittedly, we had not read the paper by Bergdoll et al. (Structure 5, 391–401, 1997) when preparing our paper for FEBS Letters.

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