Comparative Extra- and Intracellular Proteomics Analysis during Rice and *Xanthomonas oryzae* pv. *Oryzae* interaction

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*Xanthomonas oryzae* pv. *oryzae* (Xoo) is one of the most important diseases of bacterial blight of rice. Here, we demonstrated a proteomics investigation of extra- and intracellular proteome isolated from culture medium (*in vitro*) and rice leaves infected with Xoo compatible (K3) race (*in vivo*). Two-dimensional gel electrophoresis (2-DGE) coupled with MALDI-TOF-MS and/or liquid chromatography mass spectrometry (nLC–ESI–MS/MS) was employed for the proteome investigation. The 2-DGE analyses revealed that 156 and 249 proteins from extra- and intracellular proteome, respectively, were differentially up- or down-regulated from *in vivo* and *in vitro* cultured Xoo. A total of 141 spots from extracellular proteome were identified by MS techniques including 60 unique proteins. Among the identified proteins, VirK protein (spot 17) and outer membrane protein (spot 143) were confirmed by RT–PCR analysis, revealing that a parallel transcript level of genes corresponding to them was in consistent with expression pattern in 2-DGE in both *in vitro* and *in vivo*. Interestingly, we found that 3 genes (spot 8, 23, 91) fused with RFP as a reporter were co-expressed in PBZ pro:: GFP transgenic plant using particle bombardment, demonstrating that 3 proteins might be regarded as putative effectors. Thus, our findings suggest that *in vivo* extra or intracellular proteome should provide more in-depth insights to understand rice and bacterial blight interaction.

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