A draft genome sequence and functional screen reveals the repertoire of type III secreted proteins of \textit{Pseudomonas syringae} pathovar \textit{tabaci} 11528

David J Studholme*1, Selena Gimenez Ibanez1, Daniel MacLean1, Jeffery L Dangl2, Jeff H Chang3,4 and John P Rathjen1

Address: 1The Sainsbury Laboratory, Norwich, NR4 7LH, UK, 2Department of Biology, CB# 3280, Coker Hall, The University of North Carolina at Chapel Hill, Chapel Hill, North Carolina 27599-3280, USA, 3Department of Botany and Plant Pathology, Oregon State University, 2082 Cordley Hall, Corvallis, OR 97331, USA and 4Center for Genome Research and Biocomputing, Oregon State University, 2082 Cordley Hall, Corvallis, OR 97331, USA

Email: David J Studholme* - david.studholme@tsl.ac.uk; Selena Gimenez Ibanez - selena.gimenez-ibanez@tsl.ac.uk; Daniel MacLean - dan.maclean@tsl.ac.uk; Jeffery L Dangl - dangl@email.unc.edu; Jeff H Chang - changj@cgrb.oregonstate.edu; John P Rathjen - john.rathjen@tsl.ac.uk

* Corresponding author

Correction

After the publication of this work [1], we became aware of several errors in our descriptions of proteins associated with the type III secretion system (T3SS) of \textit{P. syringae} pathovar \textit{tabaci} (\textit{Pta}) strain 11528.

As mentioned in the text of the article [1], \textit{Pta} 11528 encodes a full-length homologue of HopAB2. Therefore, in Figure 1, HopAB2 should not have been marked with asterisks. A corrected summary of the Hop protein repertoire in \textit{Pta} 11528 is shown in Figure 1 of this Correction. We confirmed the presence of a full-length hopAB2 using capillary sequencing. Unfortunately, in the draft assembly of Illumina sequence data presented in the paper [1], there was a mis-assembly error that resulted in deletion of 271 nucleotides from the 5' end of the hopAB2 gene. This type of error is, unfortunately, not uncommon in assemblies of short sequence reads, though recent versions of the Velvet assembly software seem to be less prone to such errors. We are currently generating 454 GS-FLX sequence data from \textit{Pta} 11528 genomic DNA and hope to make public an improved genome assembly and annotation in due course.

Contrary to the original manuscript [1], HopR1 is degenerate in \textit{Pta} 11528. In the \textit{Pta} 11528 draft assembly, the hopR1 gene was split into at least two open reading frames (RefSeq: ZP_05639788.1, ZP_05639787.1; locus tags C1E_3889, C1E_3890) suggesting that is a degenerate pseudogene. We confirmed the presence of an internal stop codon in hopR1 using capillary sequencing. This degeneracy should have been indicated by marking hopR1 with a double asterisk (***) in Figure 1. This has been remedied in Figure 1 of this Correction.

\textit{Pta} 11528 encodes a full-length homologue of T3SS helper protein HrpA2 (Locus tag C1E_5326 in our annotation; RefSeq: ZP_05641290.1). Therefore hrpA2 should have been shown in boldface and underlined in Figure 1 of the manuscript [1]. This has been remedied in Figure 1 of this Correction.

\textit{Pta} 11528 encodes a full-length HopM1 homologue (RefSeq: ZP_05641297.1; locus tag C1E_5336; GenBank: ACR46722.1). The fact that HopM1 is intact and not degenerate should have been indicated in Figure 1 (by highlighting hopM1 in boldface and underlined) in the
original manuscript [1]. This has been remedied in Figure 1 of this Correction.

We regret any inconvenience caused by these errors and are grateful to Dr Magdalen Lindeberg for bringing them to our attention.

**References**

1. Studholme DJ, Ibanez SG, MacLean D, Dangl JL, Chang JH, Rathjen JP: A draft genome sequence and functional screen reveals the repertoire of type III secreted proteins of *Pseudomonas syringae* pathovar *tobaci* 11528. *BMC Genomics* 2009, 10:395.