Correction



Correction: Code-Assisted Discovery of TAL Effector Targets in Bacterial Leaf Streak of Rice Reveals Contrast with Bacterial Blight and a Novel Susceptibility Gene

The PLOS Pathogens Staff

There are data and labeling errors in Figure 3. In the original Figure 3, the gel image for Os07g06970 is incorrect. It is a duplicate of the image for Os01g40290. The new Figure 3 contains the correct image. Also, the original Figure 3 was generated using Locus IDs from Release 5.0 of the Rice Genome Annotation Project. Relative to Release 7.0, used for all other reporting in the article, one of these Locus IDs, Os10g38495, is obsolete. It has been updated in the new Figure 3 to the corresponding Release 7.0 Locus ID, Os10g38489. The remaining Locus IDs are the same in Release 5.0 and Release 7.0 and unchanged in the new Figure 3.

Please see the corrected Figure 3 here. The legend remains unchanged.

Citation: The *PLOS Pathogens* Staff (2014) Correction: Code-Assisted Discovery of TAL Effector Targets in Bacterial Leaf Streak of Rice Reveals Contrast with Bacterial Blight and a Novel Susceptibility Gene. PLoS Pathog 10(4): e1004126. doi:10.1371/ journal.ppat.1004126

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Figure 3. Type III secretion system dependence of the most significant rice gene expression changes. RT-PCR results reflecting transcript abundance are shown for rice genes identified by GeneChip expression analysis as the ten (or fewer) most significantly differentially expressed in response to (A) *X. oryzae* pv. oryzicola BLS256 (Xoc), (B) *X. oryzae* pv. oryzae strain PXO99^A (Xoo), (C) Xoc and Xoo similarly, or (D) Xoc and Xoo to different extents. Leaf samples were harvested at 36 hours after inoculation with wild-type strains or with the type III secretion (T3S⁻) deficient derivatives. RT-PCR results for previously reported Xoo-induced genes, *OSSWEET11* and *TFIIA*₂1 [9], [10], are omitted. An actin gene (*Os04g57210*) that is not differentially expressed was used as a reference for relative transcript abundance across samples. The experiment was repeated twice and yielded the same results.

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There is an error in Figure 2, Table S1, Table S6, and Table S9. Release 7.0 Locus ID Os10g38489 correctly corresponds to Os10g38495 from Release 5.0, *i.e.* to probeset Os.2612.1.S1_at. However, the Release 7.0 Locus ID recorded for data associated with this probeset in Figure 2, Table S1, Table S6, and Table S9 is the paralog Os10g38640 and is incorrect. Os.2612.1.S1_at does not represent Os10g38640. Os10g38640 should be replaced with Os10g38489 in Figure 2, Table S1, Table S6, and Table S9, in each of which it occurs exactly once. The primers listed for Os10g38640 in Table S9 correspond uniquely to Os10g38489. They were designed for the Release 5.0 gene model at that coordinate, Os10g38495, and should be left unchanged.

There is an additional error in Figure 2 and Table S1, that is also in Table S4. In Figure 2, Table S1, and Table S4, the Release 7.0 Locus ID recorded for data associated with probeset Os.46631.1.S1_x_at is Os07g29750 and is incorrect. Os.46631.1.S1_x_at does not represent Os07g29750. The correct Locus ID for Os.46631.1.S1_x_at is the paralog Os10g39840. Os10g39840 is unchanged from Release 5.0 to Release 7.0 and appears correctly in Figure 3. Os07g29750 should be replaced with Os10g39840 in Figure 2, Table S1, and Table S4, in each of which it occurs exactly once.

There is additional information to add to Table S9. Primers used to amplify *Os10g39840* (to generate the corresponding data in Figure 3) are (5' to 3') forward primer CCGATCAGGAGGTAC-GAGAAGAAGG and reverse primer GCACGCCTCAACTAC-CAAATTGC.

There are two errors in Table 1 and Table S7. Os10g38489, unlike Os10g38640, is a predicted target, displaying a candidate EBE for Tal1b of Xoc. Os10g38489 with associated data is added to the corrected Table 1 and corrected Table S7. Os07g29750 is incorrectly included in Table 1 and Table S7 as a predicted target of Xoc Tal4c. Based on the probeset that correctly maps to Os07g29750, OsAffx16482.1.S1_x_at, Os07g29750 is not differentially expressed in any pairwise comparison, and therefore would not be considered a predicted target, despite its candidate EBE for Tal4c. Os07g29750 is removed from the new Table 1 and Table S7. It is not be replaced in these tables with Os10g39840 because Os10g39840 displays no candidate EBE for any Xoc TAL effector. There is therefore no net change in the total number of predicted targets.

The corrected Table 1 can be seen here.

Table 1. Predicted X. oryzae pv. oryzicola BL256 TAL effector targets in rice (cv. Nipponbare) induced during infection and results of verification experiments.^a

| TAL effector | Target Locus ID ^b | Probe set ID(s) | Fold change 2-96h Xoc ^c | Fold change Mock-Xoc 96h ^d | <i>q</i> (Mock- Xoc) ^e | EBE Score ^f | EBE rel. score ^g | EBE rank ^h | EBE to TLS ⁱ | EBE to TXS ^j | EBE to TATA box ^k | EBE to Y patch ^l | Indu | uced by Xag expressing the <i>tal</i> gene ^m | Description |
|-----------------|---------------------------------|--|--|--|---|---------------------------|-----------------------------------|--------------------------|----------------------------|----------------------------|------------------------------------|--------------------------------|--|---|--|
| | | | | | | | | | | | | | <i>tal</i> gene knockout strain of Xoc ⁱ | Xag expressing the <i>tal</i> gene ^m | |
| Tal4a | 01g27210 | Os.7911.1.S1_at | 1.63 | 1.66 | 1.8E-01 | 29.22 | 2.85 | 341 | 253 | 143 | -50 | none | + | - | Glutathione S- transferase, putative, expressed |
| Tal6 | 01g31220 | Os.6438.1.S1_a_at Os.6438.2.S1_x_at | 1.48 1.48 | 1.53 1.52 | 8.0E-02 1.1E-02 | 18.75 | 2.38 | 685 | 157 | 152 | none | 33 | - | + | Expressed protein |
| Tal2d | 01g51040 | Os.53457.1.S1_at | 2.30 | 2.23 | 1.9E-01 | 14.32 | 2.19 | 324 | 527 | none | -328 | 0 | + | - | Transmembrane protein 16K, putative, expressed |
| Tal9b | 01g51040 | Os.53457.1.S1_at | 2.30 | 2.23 | 1.9E-01 | 14.07 | 2.81 | 275 | 18 | 0 | -299 | none | - | + | Transmembrane protein 16K, putative, expressed |
| Tal2g | 01g52130 | Os.41841.1.S1_at | 13.00 | 9.59 | 1.3E-06 | 13.94 | 1.97 | 77 | 427 | 58 | 28 | none | - | + | Sulfate transporter, putative, expressed |
| Tal3b | 01g53220 | Os.35681.1.S1_at | 3.50 | 4.12 | 2.2E-06 | 17.72 | 2.92 | 611 | 146 | -5 | -137 | none | nd | nd | HSF-type DNA-binding domain containing protein, expressed |
| Tal6 | 02g14770 | Os.2450.1.S1_a_at Os.2450.3.S1_x_at | 1.88 1.85 | 1.77 1.55 | 1.3E-02 6.8E-02 | 18.48 | 2.35 | 569 | 92 | 48 | -70 | -37 | + | - | Phosphoenolpyruvate carboxylase, putative, expressed |
| Tal11a | 02g15290 | Os.56119.1.S1_at | 1.72 | 4.93 | 4.1E-07 | 20.15 | 3.18 | 582 | 422 | none | -288 | none | + | - | VQ domain containing protein, putative, expressed |
| Tal5a | 02g15290 | Os.56119.1.S1_at | 1.72 | 4.93 | 4.1E-07 | 23.32 | 1.88 | 107 | 148 | 30 | -3 | -180 | - | + | VQ domain containing protein, putative, expressed |
| Tal7 | 02g15710 | OsAffx.2629.1.S1_at | 5.70 | 5.52 | 8.4E-02 | 15.75 | 1.94 | 265 | 951 | none | 150 | 434 | nd | nd | Plastocyanin-like domain containing protein, putative, expressed |
| Tal3b | 02g34970 | Os.47735.1.S1_at | 9.07 | 5.31 | 4.0E-07 | 15.33 | 2.53 | 75 | 110 | 29 | -282 | none | - | + | No apical meristem protein, putative, expressed |
| Tal2a | 02g43760 | Os.1349.1.S1_at OsAffx.2950.1.S1_s_at | 1.25 1.23 | 1.45 1.32 | 1.7E-03 5.3E-03 | 15.87 | 1.75 | 21 | 521 | none | -334 | -5 | nd | + | Ubiquitin carboxyl- terminal hydrolase, family 1, putative, expressed |
| Tal7 | 02g43760 | Os.1349.1.S1_at OsAffx.2950.1.S1_s_at | 1.25 1.23 | 1.45 1.32 | 1.7E-03 5.3E-03 | 16.45 | 2.03 | 547 | 628 | 341 | 17 | 117 | + | - | Ubiquitin carboxyl- terminal hydrolase, family 1, putative, expressed |

Table 1. Cont.

| TAL effector | Target Locus ID ^b | Probe set ID(s) | Fold change 2-96h Xoc ^c | Fold change Mock-Xoc 96h ^d | <i>q</i> (Mock- Xoc) ^e | EBE Score ^f | EBE rel. score ^g | EBE rank ^h | EBE to TLS ⁱ | EBE to TXS ^j | EBE to TATA box ^k | to TA EBE to K ^k Y patch ¹ tal g knoc strai Xo | Induc | ced by | Description |
|-----------------|---------------------------------|--|--|--|---|---------------------------|-----------------------------------|--------------------------|----------------------------|----------------------------|------------------------------------|--|--|--|---|
| | | | | | | | | | | | | | <i>tal</i> gene knockout strain of Xoc ^l | Xag expressing the <i>tal</i> gene ^m | |
| Tal3c | 02g47660 | Os.7751.1.S1_at | 2.25 | 2.24 | 1.9E-03 | 10.93 | 1.92 | 53 | 140 | -63 | -98 | none | - | + | Basic helix-loop-helix, putative, expressed |
| Tal4c | 02g47660 | Os.7751.1.S1_at | 2.25 | 2.24 | 1.9E-03 | 24.73 | 3.01 | 434 | 367 | 310 | -25 | none | + | - | Basic helix-loop-helix, putative, expressed |
| Tal2c | 03g03034 | Os.10510.1.S1_at Os.53217.1.S1_x_at | 1.49 1.26 | 3.11 2.83 | 1.1E-02 6.8E-02 | 19.55 | 1.83 | 0 | 142 | 114 | -779 | 6 | - | + | Flavonol synthase/ flavanone 3- hydroxylase, putative expressed |
| Tal3b | 03g03034 | Os.10510.1.S1_at Os.53217.1.S1_x_at | 1.49 1.26 | 3.11 2.83 | 1.1E-02 6.8E-02 | 16.73 | 2.76 | 258 | 759 | 567 | none | none | + | - | Flavonol synthase/ flavanone 3- hydroxylase, putative expressed |
| Tal11a | 03g05370 | OsAffx.24978.1.S1_at | 10.98 | 13.02 | 5.2E-04 | 17.39 | 2.74 | 307 | 798 | 331 | 526 | none | + | - | Expressed protein |
| Tal3c | 03g07540 | OsAffx.3165.1.S1_at | 6.33 | 3.84 | 3.6E-02 | 12.33 | 2.17 | 350 | 248 | 99 | -625 | none | - | + | bHLH family protein, putative, expressed |
| Tal7 | 03g25490 | Os.34992.2.S1_at | 2.10 | 2.02 | 3.8E-05 | 16.32 | 2.01 | 494 | 199 | 30 | -363 | 9 | + | - | Cytochrome P450 72A1, putative, expressed |
| Tal4a | 03g37840 | Os.20541.1.S1_at | 2.24 | 1.96 | 2.2E-04 | 15.58 | 1.52 | 0 | 362 | 151 | -3 | none | - | + | Potassium transporte putative, expressed |
| Tal2d | 04g49194 | Os.17316.1.S1_at | 22.42 | 10.49 | 3.9E-07 | 8.22 | 1.26 | 0 | 101 | 26 | -715 | none | - | + | Naringenin,2- oxoglutarate 3- dioxygenase, putative expressed |
| Tal3a | 05g12450 | OsAffx.26856.1.S1_at | 1.81 | 1.34 | 2.3E-01 | 16.07 | 2.01 | 294 | 446 | 315 | none | none | + | - | Hydroquinone glucosyltransferase, putative, expressed |
| Tal3b | 05g27590 | Os.57186.1.S1_at | 2.40 | 4.42 | 3.4E-08 | 11.40 | 1.88 | 2 | 103 | 33 | -1 | none | - | + | Wound-induced protein WI12, putative expressed |
| Tal11b | 06g14750 | OsAffx.15432.1.S1_at | 1.29 | 1.30 | 2.0E-01 | 12.44 | 2.77 | 129 | 313 | 195 | 160 | -15 | + | - | Phosphatidylinositol- 4-phosphate 5-Kinase family protein, putative, expressed |
| Tal1c | 06g14750 | OsAffx.15432.1.S1_at | 1.29 | 1.30 | 2.0E-01 | 12.00 | 2.44 | 256 | 178 | 47 | none | none | + | - | Phosphatidylinositol- 4-phosphate 5-Kinase family protein, putative, expressed |

Table 1. Cont.

| TAL effector | Target Locus ID ^b | Probe set ID(s) | Fold change 2-96h Xoc ^c | Fold change Mock-Xoc 96h ^d | <i>q</i> (Mock- Xoc) ^e | EBE Score ^f | EBE rel. score ^g | EBE rank ^h | EBE to TLS ⁱ | EBE to TXS ^j | EBE to TATA box ^k | EBE to Y patch ⁱ | EBE to Y patch ^I Induced b <i>tal</i> gene | ced by | Description |
|-----------------|---------------------------------|--|--|--|---|---------------------------|-----------------------------------|--------------------------|----------------------------|----------------------------|------------------------------------|--------------------------------|--|--|--|
| | | | | | | | | | | | | | <i>tal</i> gene knockout strain of Xoc ^l | Xag expressing the <i>tal</i> gene ^m | |
| Tal2a | 06g14750 | OsAffx.15432.1.S1_at | 1.29 | 1.30 | 2.0E-01 | 17.59 | 1.94 | 88 | 79 | -22 | -618 | -33 | nd | - | Phosphatidylinositol- 4-phosphate 5-Kinas family protein, putative, expressed |
| Tal4c | 06g37080 | Os.16282.1.A1_at OsAffx.15788.1.S1_at | 5.54 11.84 | 7.15 9.94 | 2.7E-10 6.3E- 09 | 14.64 | 1.78 | 0 | 150 | 39 | -1 | none | - | + | L-ascorbate oxidase precursor, putative, expressed |
| Tal8 | 06g37080 | Os.16282.1.A1_at OsAffx.15788.1.S1_at | 5.54 11.84 | 7.15 9.94 | 2.7E-10 6.3E- 09 | 19.92 | 2.32 | 605 | 661 | 560 | -36 | 548 | + | - | L-ascorbate oxidase precursor, putative, expressed |
| Tal2g | 06g46500 | Os.49496.1.S1_at | 6.40 | 6.88 | 4.3E-08 | 14.27 | 2.01 | 117 | 89 | 59 | -489 | -47 | - | + | Monocopper oxidase putative, expressed |
| Tal11a | 06g47950 | OsAffx.15977.1. S1_s_at | 1.78 | 1.67 | 2.8E-02 | 16.20 | 2.55 | 19 | 527 | none | -328 | 0 | nd | nd | Tetratricopeptide-like helical, putative, expressed |
| Tal1c | 07g06970 | Os.49794.1.S1_at | 2.95 | 2.27 | 1.3E-02 | 5.97 | 1.22 | 0 | 216 | 24 | none | none | - | + | HEN1, putative, expressed |
| Tal3a | 07g06970 | Os.49794.1.S1_at | 2.95 | 2.27 | 1.3E-02 | 16.21 | 2.03 | 354 | 930 | 815 | 444 | none | + | - | HEN1, putative, expressed |
| Tal4b | 07g34510 | Os.51294.1.S1_at | 0.95 | 1.00 | 2.8E-01 | 8.88 | 1.63 | 33 | 302 | 151 | -425 | none | nd | nd | Retrotransposon protein, putative, unclassified, expresse |
| Tal3b | 07g36430 | Os.31021.1.S1_at | 2.53 | 2.40 | 2.6E-02 | 15.78 | 2.6 | 108 | 117 | 31 | -4 | none | - | + | Expressed protein |
| Tal6 | 07g47790 | Os.8920.1.S1_at | 4.16 | 8.41 | 3.6E-02 | 13.38 | 1.7 | 8 | 798 | 610 | -192 | 694 | + | - | AP2 domain containing protein, expressed |
| Tal4a | 09g20220 | Os.4759.1.S1_at | 2.17 | 2.38 | 4.9E-02 | 28.93 | 2.83 | 280 | 170 | 139 | -751 | 34 | + | - | Glutathione S- transferase, putative, expressed |
| Tal2d | 09g23560 | Os.5983.1.S1_at | 2.19 | 5.02 | 2.8E-01 | 14.19 | 2.17 | 288 | 525 | none | none | 93 | nd | nd | Dehydrogenase, putative, expressed |
| Tal6 | 09g29100 | Os.18607.1.S1_at | 1.64 | 1.97 | 3.6E-02 | 17.00 | 2.13 | 167 | 0 | 0 | 0 | 0 | - | + | Cyclin, putative, expressed |
| Tal4b | 09g32100 | Os.16365.1.S1_at | 3.34 | 2.45 | 8.0E-03 | 8.15 | 1.5 | 16 | 270 | 84 | 21 | none | - | + | Expressed protein |
| Tal1b | 10g38489 | Os.2612.1.S1_at | 4.75 | 4.14 | 4.00E-07 | 8.75 | 4.13 | 325 | 64 | 20 | none | none | nt | nt | glutathione S- transferase GSTU6, putative, expressed |

| TAL effector | Target Locus ID ^b | Probe set ID(s) | Fold change 2-96h Xoc ^c | Fold change Mock-Xoc 96h ^d | <i>q</i> : (Mock- Xoc) ^e | EBE Score ^f | EBE rel. score ^g | EBE rank ^h | EBE to TLS ⁱ | EBE to TXS ^j | EBE to TATA box ^k | EBE to Y patch ¹ | Induced by | | Description |
|-----------------|---------------------------------|--|--|--|---|---------------------------|-----------------------------------|--------------------------|----------------------------|----------------------------|------------------------------------|--------------------------------|--|--|---|
| | | | | | | | | | | | | | <i>tal</i> gene knockout strain of Xoc ^l | Xag expressing the <i>tal</i> gene ^m | |
| Tal9a | 11g01480 | Os.18448.1.S1_s_at OsAffx.30765.1.S1_at | 5.42 5.74 | 3.94 4.10 | 8.2E-06 5.4E- 06 | 19.71 | 2.56 | 206 | 776 | 621 | 365 | none | + | - | MYB family transcription factor, putative, expressed |
| Tal9a | 12g01490 | Os.18448.1.51_at | 5.21 | 3.92 | 2.6E-05 | 19.71 | 2.56 | 205 | 302 | 191 | 151 | none | + | - | MYB family transcription factor, putative, expressed |
| Tal6 | 12g42970 | Os.11382.1.51_at | 2.31 | 1.65 | 2.2E-04 | 16.84 | 2.14 | 139 | 132 | 30 | -565 | 12 | - | + | GATA zinc finger domain containing protein, expressed |
| Tal6 | 12g42970 | Os.11382.1.S1_at | 2.31 | 1.65 | 2.2E-04 | 18.27 | 2.32 | 411 | 107 | 5 | -590 | -13 | - | + | GATA zinc finger domain containing protein, expressed |

^aExpression values are from the GeneChip expression experiment; see Materials and Methods.

^bPrefix "LOC_Os" is omitted.

^cFold change in transcript abundance in leaves at 96h relative to 2h after inoculation with X. oryzae pv. oryzicola BLS256 (Xoc).

^dFold change in transcript abundance at 96h in Xoc-inoculated leaves relative to mock-inoculated leaves.

^eCalculated for the comparison of transcript abundance in Xoc vs. mock inoculated leaves across all time points.

^fScore is according to Doyle et al. [32] except that new RVDs 'SN' and 'YG', present in Tal2g, were assigned nucleotide association frequencies of 'NN' and 'NG', respectively (see text).

⁹EBE relative score, ratio of the observed EBE score to the best possible score for the TAL effector [32].

^hEBE rank among the single best scoring sites for the TAL effector in each rice promoter [32].

Distance in bases from the 5' end of the EBE to the translational start site (TLS) of the target locus; a positive value indicates a location downstream of the EBE.

^jDistance in bases from the 5' end of the EBE to the transcriptional start site (TXS) based on cDNA evidence in the Rice Genome Annotation Project Release 7 (http://rice.plantbiology.msu.edu/); a positive value indicates a location downstream of the EBE; none, cDNA evidence of TXS missing.

*Distance in bases from the 5' end of the EBE to the nearest identified putative TATA box; a positive value indicates a location downstream of the EBE; none, putative TATA box not present.

Distance in bases from the 5' end of the EBE to the nearest identified putative Y patch; a positive value indicates a location downstream of the EBE; none, putative Y patch not present.

^mResults of RT-PCR 48h after inoculation, relative to a negative control inoculation (see Supplemental Figure S1); Xoc, X. oryzae pv. oryzicola BLS256; Xag, X. axonopodis pv glycines EB08; +, induced; -, not induced; nd, transcript not detected by RT-PCR (in each case, amplification by standard PCR from genomic DNA as template was confirmed); nt, not tested.

doi:10.1371/journal.ppat.1003972.t001

The corrected Table S7 can be downloaded here. The legend remains unchanged.

Supporting Information

Table S7. All computationally predicted targets in rice (cv. Nipponbare) of TAL effectors of *Xanthomonas oryzae* pv. oryzicola BLS256 (Xoc) and TAL effectors of *Xanthomonas* oryzae pv. oryzae PXO99^A (Xoo). (XLSX)

Reference

 Cernadas RA, Doyle EL, Niño-Liu DO, Wilkins KE, Bancroft T, et al. (2014) Code-Assisted Discovery of TAL Effector Targets in Bacterial Leaf Streak of Rice Reveals Contrast with Bacterial Blight and a Novel Susceptibility Gene. PLoS Pathog 10(2): e1003972. doi:10.1371/journal.ppat.1003972