

Correction

Open Access

Genome sequence and rapid evolution of the rice pathogen *Xanthomonas oryzae* pv. *oryzae* PXO99A

Steven L Salzberg*¹, Daniel D Sommer¹, Michael C Schatz¹, Adam M Phillippy¹, Pablo D Rabinowicz^{2,3}, Seiji Tsuge⁴, Ayako Furutani^{4,5}, Hirokazu Ochiai⁵, Arthur L Delcher¹, David Kelley¹, Ramana Madupu^{2,6}, Daniela Puiu¹, Diana Radune^{2,6}, Martin Shumway^{2,7}, Cole Trapnell¹, Gudlur Aparna⁸, Gopaljee Jha⁹, Alok Pandey⁸, Prabhu B Patil⁸, Hiromichi Ishihara¹⁰, Damien F Meyer¹¹, Boris Szurek¹², Valerie Verdier¹², Ralf Koebnik¹², J Maxwell Dow¹³, Robert P Ryan¹³, Hisae Hirata¹⁴, Shinji Tsuyumu¹³, Sang Won Lee¹⁵, Young-Su Seo¹⁵, Malinee Sriariyanum¹⁵, Pamela C Ronald¹⁵, Ramesh V Sonti⁸, Marie-Anne Van Sluys^{9,16}, Jan E Leach⁹, Frank F White¹⁷ and Adam J Bogdanove¹¹

Address: ¹Center for Bioinformatics and Computational Biology, University of Maryland, College Park, MD 20742, USA, ²The Institute for Genomic Research, Rockville, MD 20850, USA, ³Institute for Genome Sciences, University of Maryland, Baltimore, MD 21201, USA, ⁴Laboratory of Plant Pathology, Kyoto Prefectural University, Sakyo, Kyoto 606-8522, Japan, ⁵Department of Genetic Resources, National Institute of Agrobiological Sciences, Kannondai, Tsukuba 305-8602, Japan, ⁶Current address: J. Craig Venter Institute, Rockville, MD 20850, USA, ⁷Current address: National Center for Biotechnology Information, National Institutes of Health, Bethesda, MD 20894, USA, ⁸Centre for Cellular and Molecular Biology, Council of Scientific and Industrial Research, Hyderabad, India, ⁹Institute of Himalayan Bioresource Technology, Council of Scientific and Industrial Research, Palampur, India, ¹⁰Department of Bioagricultural Sciences and Pest Management, Colorado State University, Fort Collins, CO, USA, ¹¹Department of Plant Pathology, Iowa State University, Ames, IA, USA, ¹²Institut de la Recherche pour le Developpement, 911 Av. Agropolis, Montpellier, 34090, France, ¹³BIOMERIT Research Centre, BioSciences Institute, University College Cork, Cork, Ireland, ¹⁴Graduate School of Natural Science & Technology, Shizuoka University, 836 Ohya, Suruga-ku, Shizuoka, 422-8017, Japan, ¹⁵Department of Plant Pathology, UC Davis, Davis, CA 95616, USA, ¹⁶Departamento de Botânica, IB-USP, São Paulo, SP, Brazil and ¹⁷Department of Plant Pathology, Kansas State University, Manhattan, KS, USA

Email: Steven L Salzberg* - salzberg@umiacs.umd.edu; Daniel D Sommer - dsommer@umiacs.umd.edu; Michael C Schatz - mschatz@umiacs.umd.edu; Adam M Phillippy - amp@umiacs.umd.edu; Pablo D Rabinowicz - prabinowicz@som.umaryland.edu; Seiji Tsuge - s_tsuge@kpu.ac.jp; Ayako Furutani - a9920614@kpu.ac.jp; Hirokazu Ochiai - ochiai@nias.affrc.go.jp; Arthur L Delcher - adelcher@umiacs.umd.edu; David Kelley - dakelley@umiacs.umd.edu; Ramana Madupu - rmadupu@jcvi.org; Daniela Puiu - dpuiu@umiacs.umd.edu; Diana Radune - dbushman@jcvi.org; Martin Shumway - shumwaym@ncbi.nlm.nih.gov; Cole Trapnell - cole@cs.umd.edu; Gudlur Aparna - aparna@ccmb.res.in; Gopaljee Jha - jmsgopal@yahoo.co.in; Alok Pandey - alok@ccmb.res.in; Prabhu B Patil - prabhupatil@gmail.com; Hiromichi Ishihara - hiromichi.ishihara@colostate.edu; Damien F Meyer - dfmeyer@iastate.edu; Boris Szurek - boris.szurek@mpl.ird.fr; Valerie Verdier - valerie.verdier@mpl.ird.fr; Ralf Koebnik - koebnik@mpl.ird.fr; J Maxwell Dow - m.dow@ucc.ie; Robert P Ryan - r.ryan@ucc.ie; Hisae Hirata - hisaeh@agr.shizuoka.ac.jp; Shinji Tsuyumu - tsuyumu@agr.shizuoka.ac.jp; Sang Won Lee - drlee@ucdavis.edu; Young-Su Seo - yseo@ucdavis.edu; Malinee Sriariyanum - msriar@ucdavis.edu; Pamela C Ronald - pronald@ucdavis.edu; Ramesh V Sonti - sonti@ccmb.res.in; Marie-Anne Van Sluys - mavsluys2004@yahoo.com; Jan E Leach - jan.leach@colostate.edu; Frank F White - fwhite@ksu.edu; Adam J Bogdanove - ajbog@iastate.edu

* Corresponding author

Published: 11 November 2008

Received: 29 October 2008

BMC Genomics 2008, 9:534 doi:10.1186/1471-2164-9-534

Accepted: 11 November 2008

This article is available from: <http://www.biomedcentral.com/1471-2164/9/534>

© 2008 Salzberg et al; licensee BioMed Central Ltd.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/2.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Correction

Following the publication of the article 'Genome sequence and rapid evolution of the rice pathogen *Xanthomonas oryzae* pv. *oryzae* PXO99^A. BMC Genomics 2008, 9:204' [1], the submitting author became aware that two co-authors had been omitted. Therefore, this article, which states the contributions that these authors made to the original article, has been submitted as a correction. We apologize for any inconvenience this oversight may have caused.

Corrected author list

Steven L Salzberg, Daniel D Sommer, Michael C Schatz, Adam M Phillippy, Pablo D Rabinowicz, Seiji Tsuge, Ayako Furutani, Hirokazu Ochiai, Arthur L Delcher, David Kelley, Ramana Madupu, Daniela Puiu, Diana Radune, Martin Shumway, Cole Trapnell, Gudlur Aparna, Gopaljee Jha, Alok Pandey, Prabhu B Patil, Hiromichi Ishihara, Damien F Meyer, Boris Szurek, Valerie Verdier, Ralf Koebnik, J Maxwell Dow, Robert P Ryan, Hisae Hirata, Shinji Tsuyumu, Sang Won Lee, Young-Su Seo, Malinee Sriariyanum, Pamela C Ronald, Ramesh V Sonti, Marie-Anne Van Sluys, Jan E Leach, Frank F White and Adam J Bogdanove.

Corrected authors' contributions

SLS, JEL, FFW, and AJB conceived the project. SLS, PDR, and AJB coordinated and oversaw the project. SLS and PDR managed all genomic sequencing. DP and MCS did the initial assembly of the genome. DR directed the sequence finishing and gap closure activities. MCS, AMP, and ALD created the final assembly. RM was in charge of the initial, semi-automated genome annotation. MCS, CT, and SLS carried out the overall structural analysis of the genome. PBP and RVS performed the whole genome alignments for phylogenetic analysis. DK, CT, DDS, and SLS compared the gene content of PXO99^A and MAFF. CT and MVS analyzed IS elements. GA and RVS analyzed the adhesin locus. MCS, ALD, and SLS discovered and characterized the 212 kb duplication. FFW carried out the TAL effector analysis, assisted by RK and AJB. CT documented rearrangements in the PXO99^A genome relative to MAFF. DDS, SLS and RK investigated the CRISPRs. SeT, AF, and HO validated the MAFF assembly. SLS identified regions of possible lateral gene transfer. DK optimized annotation of hypothetical protein genes. SeT, AF, GA, GJ, AP, PBP, RVS, HI, DFM, BS, VV, JMD, RPR, HH, ShT, SWL, YS, MS, PCR, RVS, MVS, JEL, FFW, and AJB contributed to the manual annotation. SLS and AJB drafted the manuscript, assisted by PDR, SeT, GA, PBP, RVS, RK, MVS, JEL, and FFW. All authors approved the final manuscript.

References

1. Salzberg SL, Sommer DD, Schatz MC, Phillippy AM, Rabinowicz PD, Tsuge S, Furutani A, Ochiai H, Delcher AL, Kelley D, et al.: **Genome sequence and rapid evolution of the rice pathogen *Xanthomonas oryzae* pv. *oryzae* PXO99^A.** *BMC Genomics* 2008, 9:204.

Publish with **BioMed Central** and every scientist can read your work free of charge

"BioMed Central will be the most significant development for disseminating the results of biomedical research in our lifetime."

Sir Paul Nurse, Cancer Research UK

Your research papers will be:

- available free of charge to the entire biomedical community
- peer reviewed and published immediately upon acceptance
- cited in PubMed and archived on PubMed Central
- yours — you keep the copyright

Submit your manuscript here:
http://www.biomedcentral.com/info/publishing_adv.asp

