

# Correction for Bartoli et al., Whole-Genome Sequencing of 10 *Pseudomonas syringae* Strains Representing Different Host Range Spectra

Claudia Bartoli,<sup>a,b,c,d</sup> Sébastien Carrere,<sup>c,d</sup> Jay Ram Lamichhane,<sup>a,b,e</sup> Leonardo Varvaro,<sup>a</sup>  Cindy E. Morris<sup>b</sup>

Department of Science and Technology for Agriculture, Forestry, Nature and Energy (DAFNE), Tuscia University, Viterbo, Italy<sup>a</sup>; INRA, UR0407, Pathologie Végétale, Montfavet, France<sup>b</sup>; INRA, Laboratoire des Interactions Plantes-Microorganismes (LIPM), UMR441, Castanet-Tolosan, France<sup>c</sup>; CNRS, Laboratoire des Interactions Plantes-Microorganismes (LIPM), UMR2594, Castanet-Tolosan, France<sup>d</sup>; INRA, UAR 1240 Eco-Innov, BP 01, Thiverval-Grignon, France<sup>e</sup>

Volume 3, no. 2, e00379-15, 2015. Page 1: [Table 1](#) should appear as shown below.

TABLE 1 Genome characteristics

Strain name	Phylogroup	Accession no.	Genome size (bp)	Insert size (bp)	No. of contigs	$N_{50}$ (bp)	No. of protein-coding genes	G+C content (%)
CFBP 1657	1	<a href="#">JYHH00000000</a>	6,058,456	374	138	122,411	5,286	58.43
CFBP 1702	1	<a href="#">JYHK00000000</a>	6,492,303	397	265	98,077	5,912	58.60
PaVt10	1	<a href="#">JYHC00000000</a>	5,901,785	392	455	30,814	5,192	58.82
41a	2	<a href="#">JYHJ00000000</a>	5,983,849	372	24	665,729	5,131	59.11
CFBP 1754	2	<a href="#">JYHI00000000</a>	6,112,417	394	182	132,813	5,599	58.97
CFBP 3205	3	<a href="#">JYHB00000000</a>	5,719,264	404	343	35,334	5,220	58.29
CFBP 3225	3	<a href="#">JYHE00000000</a>	5,143,641	390	360	34,681	4,692	58.40
CFBP 3226	3	<a href="#">JYHG00000000</a>	5,739,983	370	247	73,921	5,235	58.11
CFBP 4219	3	<a href="#">JYHD00000000</a>	6,049,239	403	377	47,492	5,561	58.12
PseNe107	3	<a href="#">JYHF00000000</a>	6,071,865	396	247	109,046	5,605	58.02

Published 4 June 2015

Copyright © 2015 Bartoli et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](#).