

CORRECTION

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Correction: Comparative genomic profiling of Dutch clinical *Bordetella pertussis* isolates using DNA microarrays: identification of genes absent from epidemic strains

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Correction

After the publication of this work [1] we found out that Table 1 was not filled in correctly in the original article. The total number of strains analyzed in the *ptxP1* or the *ptxP3* lineage was not shown between the brackets, leading to incompleteness of the data. The revised Table 1 is shown below.

We regret any inconvenience that the incompleteness of Table 1 in the original article might have caused.

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Received: 19 March 2010 Accepted: 24 March 2010

Published: 24 March 2010

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1. King AJ, van Gorkom T, Pennings JL, van der Heide HG, He Q, Diavatopoulos D, et al: Comparative genomic profiling of Dutch clinical *Bordetella pertussis* isolates using DNA microarrays: identification of genes absent from epidemic strains. *BMC Genomics* 2008, **9**:311.

doi:10.1186/1471-2164-11-196

Cite this article as: King et al.: Correction: Comparative genomic profiling of Dutch clinical *Bordetella pertussis* isolates using DNA microarrays: identification of genes absent from epidemic strains. *BMC Genomics* 2010 **11**:196.

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Table 1 Presence of regions of difference in Dutch clinical isolates from 1993 to 2004

Region of difference	BP-number	No. of genes	Size	<i>ptxP1</i> lineage	<i>ptxP3</i> lineage
Locus:			(kb)		
<i>RD-3</i>	BP0910A-BP0937	23	24.9	0% (17)	0% (26)
<i>RD-5</i>	BP1135-BP1141	7	8.6	0% (17)	0% (26)
<i>RD-6</i>	BP1158-BP1176	19	18.7	94% (17)	100% (26)
<i>RD-27</i>	BP1553	1	0.8	82% (17)	100% (26)
<i>RD-10</i>	BP1948-BP1966	18	22.7	100% (27)	0% (53)
<i>RD-28</i>	BP2122-BP2123	2	1.7	94% (17)	100% (26)
<i>RD-29</i>	BP2822-BP2839	17	16.9	94% (17)	100% (26)
<i>RD-18</i>	BP3314-BP3322	9	9.4	94% (17)	92% (26)
<i>RD-1*</i>	BP0515-BP0516	2	1	0% (17)	13% (32)

Regions of difference (RDs) are numbered according to Brinig et al [23]. RD-1* is part of RD-1 as was found by Brinig et al [23]. The percentage of strains harbouring the region and the number of strains analyzed are indicated. Size, refers to the size of the deletion.