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Genomic and metabolic comparison with *Dickeya dadantii* 3937 reveals the emerging *Dickeya solani* potato pathogen to display distinctive metabolic activities and T5SS/T6SS-related toxin repertoire

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<i>D. solani</i> 3337 gene (ID)		Identity (%) ¹	Cter motif identity (%) ²
<i>hecA2</i> (0501)	<i>D. dadantii</i> 3937	77	29
	<i>D. chrysanthemi</i> 1591	66	29
	<i>D. paradisiaca</i> 703	59	
	<i>D. zeae</i> 586	64	
<i>cdi</i> (0409)	<i>D. dadantii</i> 3937	73	33
	<i>D. chrysanthemi</i> 1591	67	32
	<i>D. paradisiaca</i> 703	49	
	<i>D. zeae</i> 586	62	
<i>hcpA</i> (3404)	<i>D. dadantii</i> 3937	99	
	<i>D. chrysanthemi</i> 1591	98	
	<i>D. paradisiaca</i> 703	none	
	<i>D. zeae</i> 586	97	
<i>vgrGA</i> (3403)	<i>D. dadantii</i> 3937	98	
	<i>D. chrysanthemi</i> 1591	97	
	<i>D. paradisiaca</i> 703	none	
	<i>D. zeae</i> 586	97	
<i>rhsA</i> (3401)	<i>D. dadantii</i> 3937	91	100
	<i>D. chrysanthemi</i> 1591	93	13
	<i>D. paradisiaca</i> 703	none	
	<i>D. zeae</i> 586	90	16
<i>rhsIA</i> (3400)	<i>D. dadantii</i> 3937	100	
	<i>D. chrysanthemi</i> 1591	none	
	<i>D. paradisiaca</i> 703	none	
	<i>D. zeae</i> 586	none	
<i>hcpB</i> (4345)	<i>D. dadantii</i> 3937	99	
	<i>D. chrysanthemi</i> 1591	98	
	<i>D. paradisiaca</i> 703	none	
	<i>D. zeae</i> 586	98	
<i>vgrGB</i> (4346)	<i>D. dadantii</i> 3937	88	
	<i>D. chrysanthemi</i> 1591	88	
	<i>D. paradisiaca</i> 703	none	
	<i>D. zeae</i> 586	89	
<i>rhsB</i> (4348)	<i>D. dadantii</i> 3937	none*	
	<i>D. chrysanthemi</i> 1591	none*	
	<i>D. paradisiaca</i> 703	none	
	<i>D. zeae</i> 586	none*	
<i>rhsIB</i> (4349)	<i>D. dadantii</i> 3937	none*	
	<i>D. chrysanthemi</i> 1591	none*	
	<i>D. paradisiaca</i> 703	none	
	<i>D. zeae</i> 586	none*	
<i>hcpC</i> (3992)	<i>D. dadantii</i> 3937	99	
	<i>D. chrysanthemi</i> 1591	98	
	<i>D. paradisiaca</i> 703	none	
	<i>D. zeae</i> 586	98	
<i>vgrGC</i> (3993)	<i>D. dadantii</i> 3937	91	
	<i>D. chrysanthemi</i> 1591	94	
	<i>D. paradisiaca</i> 703	none	
	<i>D. zeae</i> 586	93	
<i>rhsC</i> (4000)	<i>D. dadantii</i> 3937	90	24
	<i>D. chrysanthemi</i> 1591	none*	

	<i>D. paradisiaca</i> 703	none	
	<i>D. zea</i> 586	85	97
<i>rhsIC</i> (4001)	<i>D. dadantii</i> 3937	none*	
	<i>D. chrysanthemi</i> 1591	none*	
	<i>D. paradisiaca</i> 703	none	
	<i>D. zea</i> 586	95	

¹ none: no homologous gene (threshold blastp evalue : 10^{-5}). *: gene present but not homologous.

² for toxin encoding genes (*hecA2*, *cdi*, *rhsABC*). # / #: when variation is restricted to the Cter motif (Ct toxin domain), number of conserved amino acid in the Cter motif. When no value is indicated, the variation is not restricted to the Cter.