Complete Genome Sequence of Indian Race 4 of *Xanthomonas oryzae* pv. *oryzae*, the Causal Agent of Bacterial Blight of Rice

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Abstract

Xanthomonas oryzae pv. *oryzae*, the causal bacterium of bacterial blight limits rice production globally. Currently, genome sequences for only a few *X. oryzae* pv. *oryzae* isolates are available from India. Based on the next-generation sequencing and single-molecule sequencing in real-time technologies, we present here the complete genome sequence of *X. oryzae* pv. *oryzae* race 4, a highly virulent member of the Indian *X. oryzae* pv. *oryzae* population that has been extensively used in different research studies. The genome data will contribute to our understanding of *X. oryzae* pv. *oryzae* genomic features and pave the way for research on rice–*X. oryzae* pv. *oryzae* interactions.

Xanthomonas oryzae pv. *oryzae* causes bacterial blight (BB) that constitutes a major biotic threat to rice production worldwide. In India, the disease appears every year and causes substantial loss to rice production (Mondal 2016). More than 40 *Xa* (resistance [*R*]) genes are identified in rice but *X. oryzae* pv. *oryzae* still manages to bypass the rice immune response. The breakdown of rice resistance is mainly due to the emergence of new virulent races of *X. oryzae* pv. *oryzae* at periodic intervals. The diversity in the *X. oryzae* pv. *oryzae* population is well documented by many workers and there are over 30 races reported from several countries. The ever-changing *X. oryzae* pv. *oryzae* races was described by researchers from India as well (Adhikari et al. 1999; Mishra et al. 2013; Mondal et al. 2014; Yugander et al. 2017). From the northwestern and northeastern parts of India, the *X. oryzae* pv. *oryzae* population was pathotyped into six races based on reactions to single as well as combinations of *R* genes in rice (Mondal et al. 2014). Race 4 (strain ITCCBB0002) is a predominant and most virulent member among six races. Race 4 has been extensively used during phenotyping for resistance breeding program (Ellur et al. 2016a,b) as well as for genetic screening of its type 3 secretion system (T3SS) effectors (Mondal et al. 2014). Phytopathogenic *Xanthomonas* spp. utilize T3SS effectors to suppress plant innate immunity (Kumar et al. 2016; Soni and Mondal 2018). T3SS effectors are of two types; namely, transcription activator like (TAL) and non-TAL or *Xanthomonas* outer protein (Xop) effectors (White et al. 2009). *X. oryzae* pv. *oryzae* race 4 possesses 18 TAL and 21 Xop effectors (Mondal et al. 2014). Detailed investigation revealed that XopF and XopR are two crucial effectors of race 4 that contribute to the development of BB in rice (Mondal et al. 2016; Verma et al. 2018, 2019). In order to have detailed insight into the genomic features of race 4, in the present study, we generated a whole-genome sequence using the PacBio (Pacific Biosciences Inc., Menlo

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Keywords

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Table 1. Comparative accounts on genomic features of Indian *Xanthomonas oryzae* pv. *oryzae* race 4 with other Asian strains

Genomic features	Asian <i>X. oryzae</i> pv. <i>oryzae</i> strains			
	Indian race 4	Korean KACC10331	Philippines PXO99A	Japanese MAFF311018
Accession number	CP046148	NC_006834	NC_010717	NC_007705
Length (bp)	4731568	4941439	5238555	4940217
G + C content (%)	63.8	63.7	63.6	63.7
Total genes	4,505	4,939	4,899	4,663
Total protein coding genes (CDS)	4,299	4,734	4,688	4,457
CDS encoding protein with assigned function	3,542	3,721	3,944	3,757
CDS encoding hypothetical protein	757	1,013	744	700
Noncoding RNAs	143	146	151	147
Transfer RNA	57	54	54	53
Ribosomal RNA operons	2	2	2	2
Plasmids	0	0	0	0
Reference	This study	Lee et al. 2005	Salzberg et al. 2008	Ochiai et al. 2005

Park, CA, U.S.A.) sequencing method. This genome information would certainly help researchers to further decipher the *X. oryzae* pv. *oryzae*–rice interaction with reference to virulent race 4 and, thereby, would provide scope in exploring a new management strategy for BB.

Total genomic DNA was extracted and completely sequenced using the PacBio platform. In total, 16,482 polymerase reads were obtained, encompassing of 547.7 Mbp. The de novo assembly was performed using Canu, version 1.5 (Koren et al. 2017) and the total protein coding genes (CDS) were predicted using Glimmer, version 3. The final genome assembly was composed of 4,731,568 bp and had a total of 63.8% GC content. There were 4,505 genes, 4,299 CDS, and 3,542 protein coding genes. Among the total 206 RNA encoding genes, 6 genes encoded for ribosomal RNAs, 57 encoded for transfer RNAs, and 143 were identified as noncoding RNAs. A comparative account on genomic features of Indian *X. oryzae* pv. *oryzae* race 4 with other Asian *X. oryzae* pv. *oryzae* strains, including Korean strain KACC10331, Philippines strain PXO99A, and Japanese strain MAFF311018, was determined (Table 1). This whole-genome shotgun project has been deposited in the GenBank database under accession number CP046148.

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