

# Complete genome dynamics of a dominant-lineage strain of *Xanthomonas oryzae* pv. *oryzae* harbouring a novel plasmid encoding a type IV secretion system

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## Abstract

*Xanthomonas oryzae* pv. *oryzae* (*Xoo*) is a serious pathogen causing bacterial blight disease in rice. Population genomic studies have revealed that rampant inter-strain rather than inter-lineage differences are contributing to the evolutionary success of this pathogen. Here, we report the complete genome sequence of BXO1, a strain of *Xoo* belonging to a dominant lineage from India. A complete genome-based investigation revealed the presence of two plasmids, pBXO1-1 (66.7 kb) and pBXO1-2 (25.6 kb). The pBXO1-1 plasmid encodes 71 genes, 38 of which encode hypothetical proteins of unknown function. However, these hypothetical genes possess atypical GC content, pointing towards their acquisition and movement through horizontal gene transfer. Interestingly, pBXO1-2 encodes a type IV secretion system (T4SS), which is known to play an important role in the conjugative transfer of genetic material, and also provides fitness to pathogenic bacteria for their enhanced survival. Neither plasmid has been reported previously in any other complete *Xoo* genome published to date. Our analysis also revealed that the pBXO1-2 plasmid is present in *Xanthomonas albilineans* str. GPE PC73, which is known to cause leaf scald, a lethal disease in sugarcane. Our complete genome sequence analysis of BXO1 has provided us with detailed insights into the two novel strain-specific plasmids, in addition to decoding their functional capabilities, which were not assessable when using the draft genome sequence of the strain. Overall, our study has revealed the mobility of a novel T4SS in two pathogenic species of *Xanthomonas* that infect the vascular tissues of two economically important monocot plants, i.e. rice and sugarcane.

## INTRODUCTION

*Xanthomonas* is a yellow-pigmented, Gram-negative bacteria that causes serious diseases in a wide range of economically important plants, such as rice, sugarcane, banana, citrus, pepper, cabbage, etc. Among *Xanthomonas* species, *Xanthomonas oryzae* pv. *oryzae* (*Xoo*), which causes bacterial blight disease in rice, is a major threat to rice cultivation. *Xoo* strains display tremendous variation in their pathogenicity towards different resistance genes that are deployed for the development of resistant rice cultivars [1]. This is also reflected in the large-scale inter-strain variation found at a locus encoding lipopolysaccharide biosynthetic gene clusters in the genome of *Xoo* isolates [2]. Population genomic studies of more than 100 isolates revealed that inter-strain variation is more conspicuous than inter-lineage variation in

*Xoo* species [3]. Hence, it is important to carry out systematic and genomic characterizations of *Xoo* strains to comprehend the mechanisms underlying the rapid evolution and success of this important pathogen infecting a major staple crop.

Third-generation long-read sequencers such as PACBIO and ONT generate longer reads for assembling the complete genomes of many species, allowing us to understand the dynamic variations at inter-strain levels, which occur through plasmids, repetitive elements such as transcriptional activator-like effectors (TALE), integrons, conjugative and IS elements, etc. [4]. The presence of plasmids can provide ecological fitness to the pathogen to survive in every environment or to withstand adverse conditions [5]. Plasmids are also known to carry virulence genes or toxins contributing to the pathogenicity of a bacterium [6, 7]. Unfortunately,

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**Abbreviations:** MGEs, mobile genetic elements; *parA*, chromosome partitioning protein; ptw, plant tissue water soaking; *repA*, replication initiator protein A; TALE, transcriptional activator-like effector; T4SS, type IV secretion system; *Xoo*, *Xanthomonas oryzae* pv. *oryzae*.

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the vast majority of available genomic sequences are drafts, making it difficult to study inter-strain variations mediated by plasmids in a systematic manner. However, with the advent of cost-effective long-read technologies, it is possible to obtain gap-free genome sequences that provide insights into the plasmid content of an isolate and facilitate comparative genomic analyses [8].

In the present study, we carried out a genome-based investigation of *Xoo* strain BXO1, which belongs to a dominant lineage of this pathogen in India [3]. We also report here that this strain harbours two novel plasmids, pBXO1-1 and pBXO1-2, which have not been reported in the complete genome of any *Xoo* strain published to date. In a recent study, another strain from the dominant Indian *Xoo* lineage was found to harbour a novel plasmid with a size of 43 Kb [9], but this plasmid is not related to the plasmids of the BXO1 strain. While pBXO1-1 encodes a cluster of hypothetical genes with atypical GC content, pBXO1-2 encodes a T4SS cluster that has not yet been reported in *Xoo* on either chromosomes or plasmids. Further, its presence in another species of *Xanthomonas* i.e. *Xanthomonas albilineans*, which infects sugarcane (monocot), suggests that it provides an adaptive advantage to *Xanthomonas* spp. infecting different monocot plants. Our study has provided novel insights into plasmid-mediated variation in *Xoo* strains and emphasizes the importance of complete genome studies to address inter-strain variations in the *Xoo* population.

## RESULTS

### Complete genome sequencing of *Xoo* strain BXO1

Complete genome sequencing of the BXO1 strain was performed using the Oxford Nanopore MinION platform. The assembled sequence of BXO1 contains a circular chromosome of 4 991 257 bp with two plasmids (pBXO1-1 and pBXO1-2) with a size of 66 752 and 25 634 bp, respectively. The basic features of BXO1's complete genome are given in Table 1. The genome coverage obtained was 127x with average G+C content of 63.7%. A total of 4 857 coding sequences (CDSs), 53 tRNAs and 2 copies of the *rrn* operon (5 s, 16 s, 23 s) were found on the genome. The average G+C content of pBXO1-1 and pBXO1-2 was 61 and 57.3%, with 71 and 29 CDSs, respectively. Further, completeness and contamination was found to be 100 and 0.36%, respectively. We also looked for TAL effectors in the complete genome and found 19 TAL

**Table 1.** General features of *Xanthomonas oryzae* pv. *oryzae* BXO1 strain

	Chromosome	Plasmid 1 (pBXO1-1)	Plasmid 2 (pBXO1-2)
Size (bp)	4 991 257	66752	25634
GC content (%)	63.7	61	57.3
CDS	4857	71	29
tRNA	53	0	0
Ribosomal RNA operon	2	0	0
IS elements (complete)	301	0	0
TAL effector genes	19	0	0

genes on the chromosomal DNA, whereas both plasmids lack TALE genes. A schematic representation of BXO1's genome is shown in Fig. 1.

### Complete genome-based investigation reveals novel plasmids in *Xoo*

We identified two plasmids in the BXO1 strain, pBXO1-1 and pBXO1-2, with sizes of 66.7 and 25.6kb, respectively. The pBXO1-1 plasmid encodes 71 genes, out of which 38 genes were found to be hypothetical. Hypothetical genes were further checked for homology via a BLASTP search of the National Center for Biotechnology Information (NCBI) database. However, these hypothetical genes possess atypical GC content, pointing towards their acquisition through horizontal gene transfer. Although both plasmids lack type III effector genes, annotation of the plasmid pBXO1-1 revealed the presence of different conjugative transfer genes and toxins/antitoxins (*relE/parE* family toxin, *phd* antitoxin) (Fig. 2). The different conjugative transfer genes present on pBXO1-1 are *traY*, *traW*, *traU*, *traQ*, *traO*, *traN*, *traM*, *traH*, *traI*, *traJ*, *traK*, *trwB* and *trbA*, *trbB*, *trbN* and *mobD*, which enable self-transfer of plasmids. In addition to the conjugative transfer genes, the other core genes present on pBXO1-1 include *repA* (replication initiator protein A), *parA* (chromosome partitioning protein) and genes that encode DNA topoisomerase, restriction endonuclease and XRE family transcriptional regulator. Further, pBXO1-1 showed 93.61% homology to *Paraburkholderia* strain DSM 17164 plasmid pEMT1 (CP026110.1) and 93.64% homology to *Paraburkholderia aromaticivorans* strain BN5 plasmid pBN4 (CP022994.1).

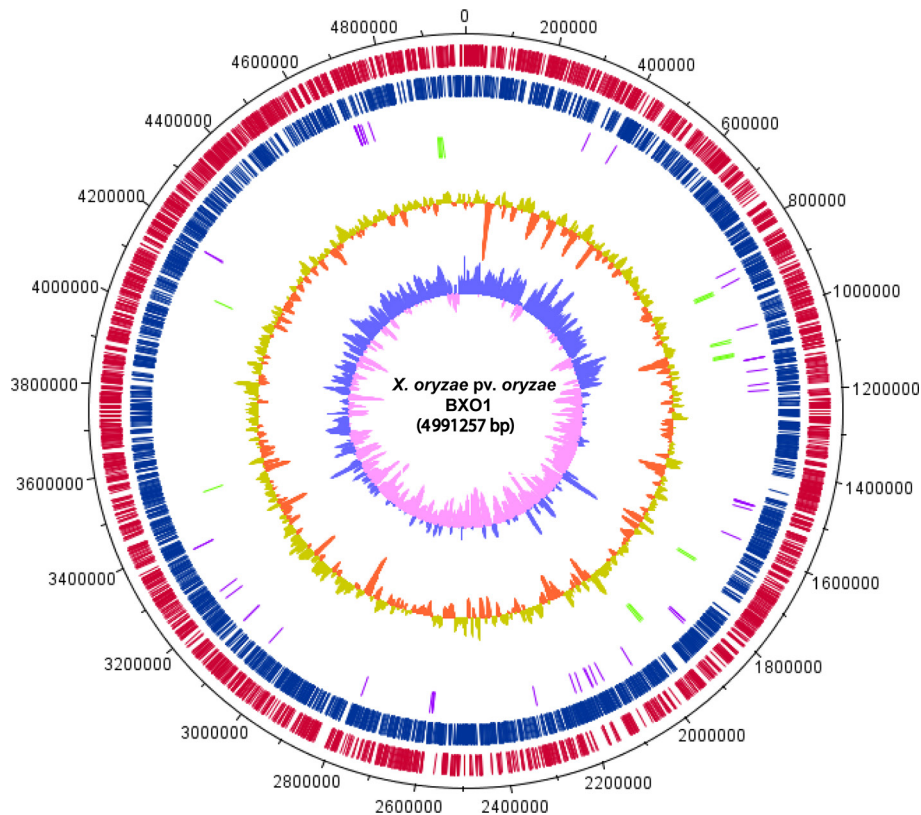
pBXO1-2 encodes 29 genes, out of which 10 genes encode the T4SS cluster (*Vir* components) (Fig. 2). pBXO1-2-encoded *vir* genes, including *virD2*, *virD4*, *virB2*, *virB3*, *virB4*, *virB5*, *virB6*, *virB8*, *virB9*, *virB10* and *virB11*. The other genes present on pBXO1-2 include *parA* and *parB*, *trfA*, *trfB*, *sprT* and *kfrA*, which are involved in core functions, i.e. maintaining plasmid replication, partitioning etc.

### Inter-species movement of a novel plasmid in *Xanthomonas* pathogens infecting monocots

pBXO1-2 plasmid showed 96% similarity to the *X. albilineans* str. GPE PC73 plasmid (FP340277.1), suggesting its movement at the inter-species level. A comparison between the pBXO1-2 and GPE PC73 plasmids is shown in Fig. 3. *X. albilineans* is another member of the genus *Xanthomonas*, which is a xylem-invading pathogen causing leaf scald disease in sugarcane. *X. albilineans* is considered to be an evolutionary intermediate between several *Xanthomonas* species that has undergone reductive genome evolution [10].

## DISCUSSION

Bacterial populations display astonishing inter-strain variations mediated by horizontal gene transfer involving the movement of mobile genetic elements (MGEs) such as plasmids, integrative conjugative and IS elements, etc.



**Fig. 1.** Circular representation of the BXO1 genome. The rings represent (from outside to inside): (i) protein-coding genes on the forward strand (red), (ii) protein-coding genes on the reverse strand (blue), (iii) tRNA genes (purple), (iv) transcriptional activator-like effectors (TALs) (green), (v) GC content and (vi) GC skew (distribution of guanine and cytosine nucleotides in the genome).

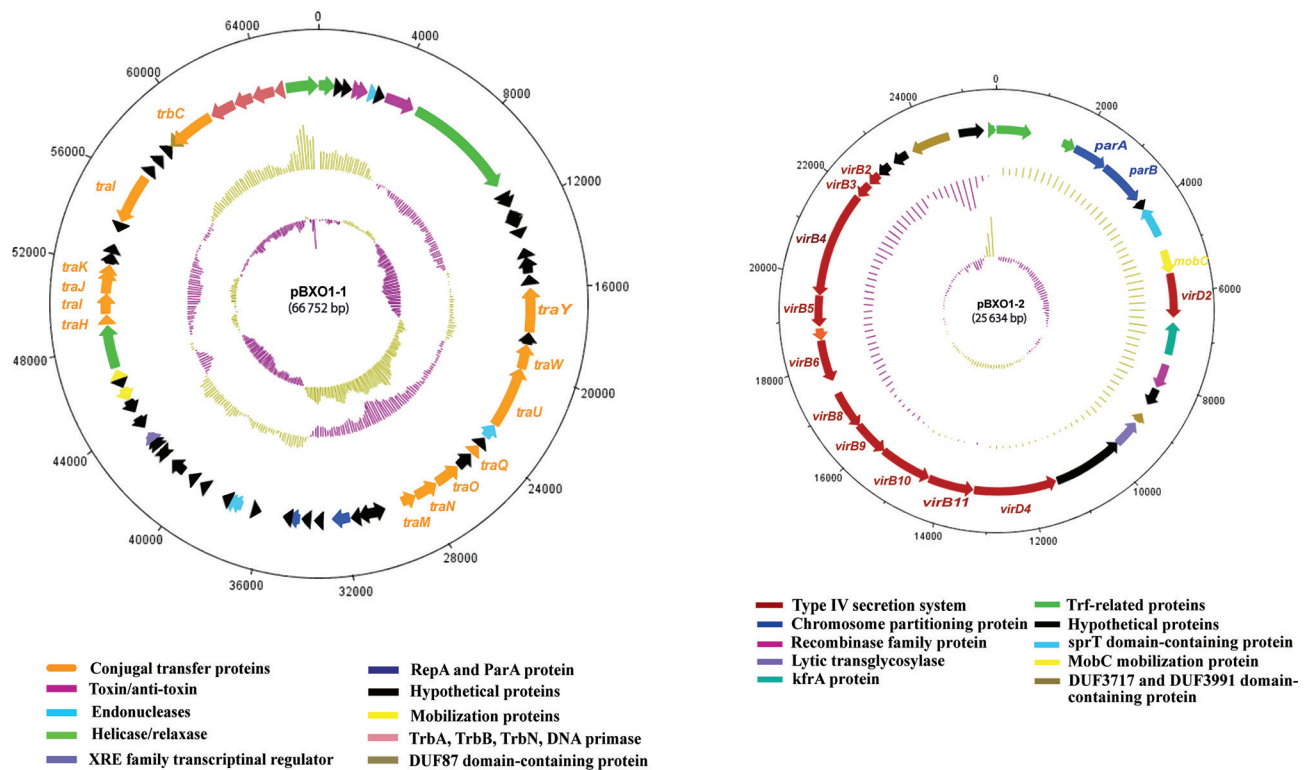
[11]. Hence, a systematic study of the genome dynamics of a successful strain is important, particularly in pathogenic bacteria. Presently, the vast majority of genome sequences are drafts, making it difficult to undertake a detailed and systematic study of mobile DNA. Our complete genome study allowed us to identify two novel plasmids in a *Xoo* strain, indicating that plasmid-mediated variation(s) may be playing an important role in the evolution of this rice pathogen. The fact that the plasmid is present in another *Xanthomonas* species (*X. albilineans*) suggests that plasmids may be actively moving between different species in this genus, thereby contributing to inter-strain and interspecies dynamics. However, the possibility that *Xoo* strain BXO1 and *X. albilineans* str. GPE PC73 might have independently obtained this plasmid from a non-*Xanthomonas* source cannot be ruled out. Interestingly, both *Xoo* and *X. albilineans* infect the vascular tissues of monocot plants, suggesting that this plasmid may have adaptive value for growth within this tissue.

*Xanthomonas* T4SS seems to be a highly diverse and versatile system [12]. It has been shown that *Xanthomonas citri* deploys the T4SS to secrete toxins that contain conserved C-terminal domains to kill other bacterial species in a contact-dependent manner [13]. Similarly, *Burkholderia cenocepacia* contains a 92 kb plasmid that encodes T4SS, which is responsible for providing the plant tissue water-soaking (PTW) phenotype

on onion tissue [14]. Intriguingly, pBXO1-2-encoded T4SS did not show any similarity with *Xanthomonas axonopodis* pv. *citri* and *Xanthomonas campestris* pv. *vesicatoria* (strain 85-10) T4SS, pointing towards functional diversification of T4SS among *Xanthomonas* [15]. Thus, further studies are required to prove its role in fitness, virulence or pathogenicity in the hosts. However, the distribution of the plasmid with T4SS indicates that the plasmid is playing a role in the ecology and evolution of *Xanthomonas* species.

Short-read sequencing technology platforms have enabled researchers to generate draft genomes of more than 100 strains in a population-based study [3]. This has allowed an understanding of relationship and population structure to a level of detail that was not possible using a few housekeeping genes [16–18]. However, a complete genome sequence is required to systematically understand inter-strain variation originating from repetitive and mobile elements. The advent of long-read technologies such as Oxford Nanopore is allowing us to obtain complete genomes of bacteria rapidly and in a cost-effective manner. We were successful in using both short-read sequence data from Illumina and long-read data from Oxford Nanopore to carry out assembly. This enabled us to sequence the complete genome and detect two plasmids in this strain. The *Xoo* genome is particularly rich in repetitive elements such as TAL genes and IS elements.





**Fig. 2.** Circular diagrams showing pBXO1-1 and pBXO1-2 plasmids from the BXO1 strain of *Xanthomonas oryzae* pv. *oryzae*. The presence of type IV secretion system components and conjugal transfer genes is indicated by red and orange. The two innermost rings represent GC content and GC skew, respectively.

To the best of our knowledge, the present study is the first report on the use of Oxford Nanopore Technology (MinION) in successfully obtaining the complete genome of a *Xoo* strain.

Our study has unravelled an important facet of inter-strain variation mediated by novel plasmids harbouring novel gene clusters of importance in host-microbe interactions, including the T4SS. The presence of two novel plasmids in one strain highlights the importance of strain-specific genome dynamics mediated by such elements. In one of the plasmids, a large number of clustered hypothetical genes are present and this suggests the importance of plasmids in providing *Xoo* strains with novel functions. The use of such cost-effective long-read sequencing platforms can enable researchers to provide comprehensive insights into inter-strain and inter-lineage genome dynamics.

## METHODS

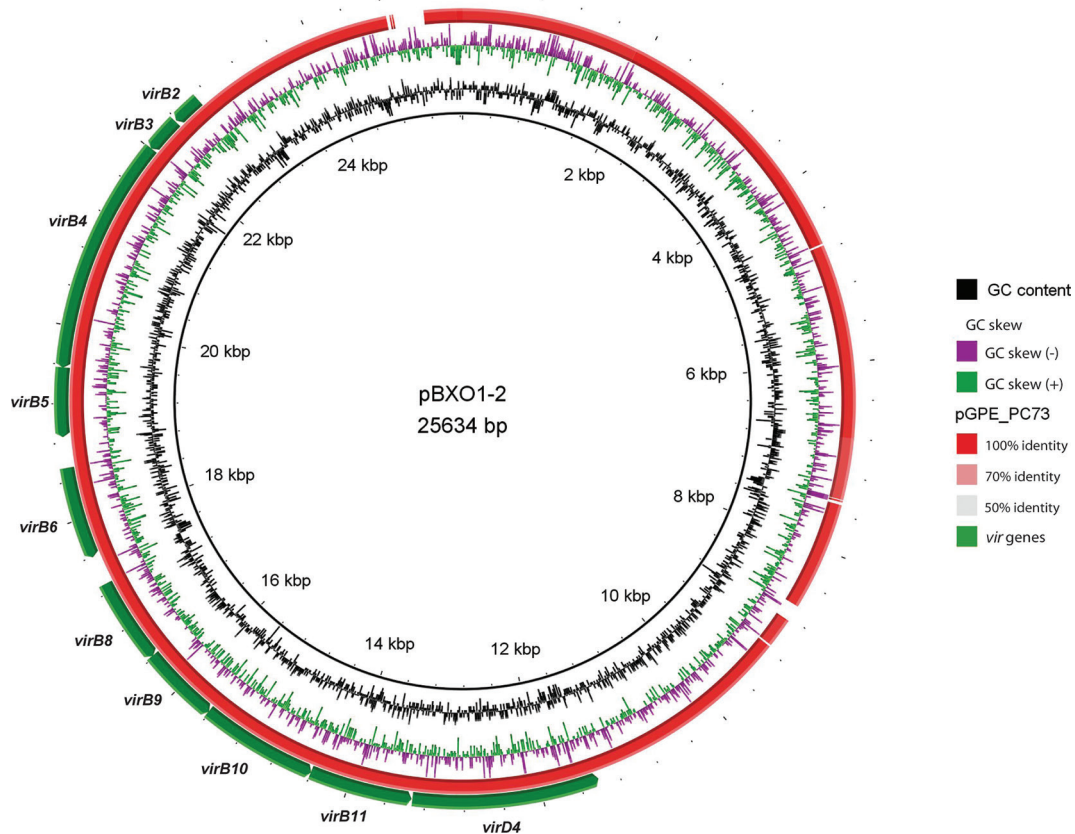
### DNA extraction and nanopore sequencing

BXO1 culture was grown in peptone sucrose (PS) broth media at 28°C for 48 h. The cells were harvested and genomic DNA was isolated using the DNeasy Blood and Tissue Kit (Qiagen). The quantity and quality of DNA was assessed using Nanodrop and the Qubit 2.0 Fluorometer. Library preparation was performed using the Ligation Sequencing Kit 1D (SQK-LSK108). Initially, 4 µg of genomic DNA was sheared using Covaris g-TUBE

(Covaris, Brighton, UK). Then, the DNA end prep step was performed using NEBNext Ultra II End-repair/dA-Tailing modules. All bead washing steps were performed using AMPure beads (Beckman Coulter). Further, native barcoding and adaptor ligation steps were performed as per the protocols given by Oxford Nanopore Technologies. Finally, 12 µl of prepared library DNA was used and sequenced using the MinION (FLO-MIN-106 vR9.4) flow cell with MinKNOW software (v1.13.1) (<http://community.nanoporetech.com>; Oxford Nanopore Technologies) for 48 h. Nanopore raw FAST5 reads were base-called and converted to the FASTQ format using Albacore v2.3.1 software (<http://community.nanoporetech.com>).

### Genome assembly and annotation

The reads obtained after demultiplexing were assembled using Unicycler v0.4.4 [19] with the conservative mode. The assembled genomes were then error-corrected for multiple rounds with short reads generated by Illumina using Pilon v1.22 [20]. The assembled genome was then checked for completeness and the presence of contamination using CheckM v1.0.11 [21]. Genome coverage was checked using the BBMap v38.20 tool [22]. The genome was submitted to the NCBI Whole Genome Shotgun (WGS) portal with the accession numbers CP033201, CP033202 and CP033203 and annotated using the NCBI's Prokaryotic Genome Annotation Pipeline (PGAP; [https://www.ncbi.nlm.nih.gov/genome/annotation\\_prok/](https://www.ncbi.nlm.nih.gov/genome/annotation_prok/)).



**Fig. 3.** Comparative analysis of pBXO1-2 with the *X. albilineans* str. GPE PC73 plasmid. The circles represent (from inner to outermost): (i) pBXO1-2 (taken as reference genome), (ii) GC content, (iii) GC skew, (iv) the GPE PC73 plasmid and (v) *vir* gene cluster.

### Identification of mobile elements

The genes were represented in circular form and the GC content of the genes in chromosome and plasmids was visualized using DNA Plotter [23]. Hypothetical genes were further validated using BLASTP [24]. IS elements were identified using ISSaga [25]. In order to look for TAL effectors, TAL DNA sequences were retrieved from <http://www.xanthomonas.org/experts.html> and a BLASTN search was performed against the sequenced genome. We also validated our TAL gene sequences using AnnoTALE software [26]. Comparison of pBXO1-2 and GPE PC73 plasmids was generated using blast ring image generator.

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### Author contributions

A. K., K. B. and S. K. carried out the complete genome sequencing and NCBI submission. A. K. performed downstream analysis with the help of S. K. A. K. and K. B. drafted the manuscript with input from R. V. S. and P. B. P. P. B. P. participated in its design and the interpretation of data

with all the authors and applied for funding. All authors have read and approved the manuscript.

### Conflicts of interest

The authors declare that there are no conflicts of interest.

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