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DATA DESCRIPTOR

Genomic analysis of phylogroup D *Escherichia coli* strains using novel *de-novo* reference-based guided assembly

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Escherichia coli are highly diverse bacteria with different pathogenic types, serotypes and phylogenetic types/phylotypes. In recent years, infections with *E. coli* have increased worldwide and so has the emergence of antibiotic resistant strains. In the present study we have assembled, annotated and analysed genome sequences of three strains of the phylogroup D of *E. coli*. These strains were isolated from the river Yamuna, a prominent anthropogenic urban river of northern India. These strains showed varied antibiotic susceptibilities, one was susceptible to all the antibiotics tested except ampicillin while of the other two, one was multi-β-lactam resistant and the other was multi-drug resistant (resistant to multiple β-lactams, fluoroquinolones and kanamycin). The short-sequence reads were assembled into contigs using the *de-novo* approach and further, scaffolding of contigs was performed by using the best reference genome for a particular isolate which resulted in a significant increase in the N_{50} value of each assembly. The bioinformatics assembly approach used in this study could be easily applied to study other bacterial genomes.

Background & Summary

Escherichia coli are highly diverse bacteria with different pathogenic types, serotypes and phylogenetic types/phylotypes^{1,2}. They were earlier believed to be the inhabitants of the lower intestinal tract of human beings and warm-blooded animals which reached the environment through the faecal discharge and waste-water treatment plants³. However, recent studies have shown that besides host, *E. coli* can successfully survive in various ecological niches like soil, water and plantations³⁻⁸. Genomic and phylogenetic studies have identified divergent lineages of *E. coli* which can survive in various ecological niches, well-adapted to a non-host lifestyle⁹. Commensal strains of *E. coli* (gut-associated, non-pathogenic) mostly belong to phylogroups A and B1 while the pathogenic strains belong to phylogroups B2 and D¹⁰.

Investigating the bacterial population inhabiting the local water bodies is important because it reflects the bacterial clones perpetuating in the human population of the adjoining areas. Thus, *E. coli* from water bodies have been extensively investigated by several researchers and concerns over public-health risks associated with such contaminated water have been raised¹¹⁻²². Moreover, water bodies can also act as genetic reactors in a manner similar to the host intestine, facilitating genetic exchange of virulence and antimicrobial resistance genes among different bacteria as these are often associated with mobile genetic elements like plasmids, transposons, insertion sequences etc^{20,23,24}.

As per the latest records (retrieved in October 2022) 226,541 genome sequences of *E. coli* were present in the Enterobase, of which 646 sequences were from strains isolated from India Supplementary Table 1. Deducing the phylogroups of these strains was difficult as the Enterobase records did not specify their phylogroups and most of the original research papers describing these strains did not divulge their phylogroups. Thus, to the best of our knowledge this is the first report describing the genomic features of three *E. coli* phylogroup D strains isolated from India. The strains *E. coli* IP9, *E. coli* KKA and *E. coli* IPE were earlier isolated from the river Yamuna, a major anthropogenic urban river of India^{25,26}. The 22 km stretch of the river that traverses through the National Capital Region of India from which these strains were isolated, receives effluents from industries, hospitals,

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Sample	Strain	Read orientation	Mean Phred Score	Number of reads	% GC	Mean read length (bp)
SAMPLE_A_2_FKDL210232083-1a_H722HDSX2_L2	IPE	R1	36.04	6,482,921	51	150
SAMPLE_A_2_FKDL210232083-1a_H722HDSX2_L2	IPE	R2	35.45	6,482,921	50	150
SAMPLE_B_DKDL210005881-1a_HFTKFDSX2_L3	KKA	R1	35.18	4,834,176	50	150
SAMPLE_B_DKDL210005881-1a_HFTKFDSX2_L3	KKA	R2	35.31	4,834,176	50	150
SAMPLE_C_DKDL210005882-1a_HFTKFDSX2_L3	IP9	R1	36.02	4,518,785	50	150
SAMPLE_C_DKDL210005882-1a_HFTKFDSX2_L3	IP9	R2	34.93	4,518,785	50	150

Table 1. Sequencing raw data statistics of *E. coli* strains.

Genome assembly statistics	<i>E. coli</i> IP9	<i>E. coli</i> KKA	<i>E. coli</i> IPE
# Number of reads after Trimmomatic run	3,682,617	4,255,723	4,762,800
# Number of reads after Flash run	2,182,721 (extended) 1,499,896 (remaining)	2,251,378 (extended) 2,004,345 (remaining)	2,913,564 (extended) 1,849,236 (remaining)
# contigs generated	124	76	137
Total length (bp)	4,910,225	5,101,091	5,225,435
GC (%)	50.84%	50.55%	50.64%
Largest contig (bp)	491,679	476,221	720,451
N ₅₀ (bp)	137,460	283,877	295,668

Table 2. *E. coli* strains genome assembly statistics.

local population etc. The antibiotic susceptibilities/resistance of these strains were determined by the standard disk diffusion assay and confirmed by gene sequencing of the relevant genes, and the results have been published^{25,26}. Among these strains, *E. coli* IP9 was susceptible to all antibiotics tested, except ampicillin, *E. coli* KKA was a multi-β-lactam resistant strain^{25,26} and *E. coli* IPE was a multidrug resistant strain (resistant to multiple β-lactams, fluoroquinolones and kanamycin)^{25,26}.

Despite the presence of a large number of genome sequences in the databases, it is very difficult to select the most appropriate genome as the template for the assembly. Hence, in the present study we have adopted a novel approach to assemble the whole genomes of these strains by combining both *de-novo* and reference-based approaches. Named as *de-novo* reference-based guided assembly, this approach helps the user in selecting the best reference genome from the public databases for a better-read assembly/contig scaffolding. Since these isolates showed varied antibiotic susceptibilities, we have also annotated their genomes to predict/identify genes for antimicrobial resistance and virulence factors. Also, we have provided Gene Ontology (GO) annotations that will be useful in analysing the role of individual genes.

Methods

DNA isolation, library preparation and sequencing. The three *E. coli* strains preserved as glycerol stocks (50% v/v) in a -80 °C deep refrigerator in our laboratory were revived by overnight incubation in LB broth at 37 °C, 200 rpm. Bacteria were grown up to the exponential phase (OD₆₀₀ = 0.8) and harvested by centrifugation at 8000 rpm for 8 minutes at 4 °C. Genomic DNA was extracted using Nucleospin Microbial DNA kit (Macherey Nagel, Germany) and quantified by Qubit 4 fluorometer (Thermo Fisher Scientific, USA). These strains were isolated from the river Yamuna traversing through the National Capital Region of Delhi and identified/characterized by standard microbiological methods described earlier²⁵. The DNA sequencing library was prepared by QIASeq FX DNA Library Kit (Qiagen, USA). Quantitative and qualitative library QC was done by Qubit 4 fluorometer (Thermo Fisher Scientific, USA) and TapeStation 4150 (Agilent technologies, USA), respectively. The libraries were sequenced on NovaSeq 6000 (Illumina, USA) using 2 × 150 bp paired end reads with an insert size of 250–350 bp. The raw data statistics is shown in Table 1.

Pre-processing and *de-novo* assembly: contig generation. Read quality was assessed using FastQC (v0.11.8) (<https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>) and results were summarized using MultiQC (v1.13a) (<https://multiqc.info/>). The reads were trimmed using Trimmomatic²⁷ (v0.39) at default parameters to remove Illumina adaptors, low-quality bases and/or reads less than 36 bp. The trimmed short overlapped paired-end reads obtained after Trimmomatic run were merged using FLASH²⁸ (v1.2.11) at default parameters to create longer reads (single-end) for each isolate Table 2. The merged single-end reads along with the remaining trimmed pair-end reads were used to perform *de-novo* genome assembly using Unicycler²⁹ (v0.4.8; -m 200). A total of 139, 100 and 183 contigs were generated after *de-novo* genome assembly for IP9, KKA and IPE, respectively. The N₅₀ values for *E. coli* strains IP9, KKA and IPE were 129,988 bp, 178,741 bp and 252,171 bp, respectively, and were assessed using QUAST³⁰ (v5.0.2).

Selection of closest reference for scaffolding. The trimmed short paired-end reads obtained after Trimmomatic run were used to calculate the mash value against the 1875 *E. coli* complete genomes, downloaded

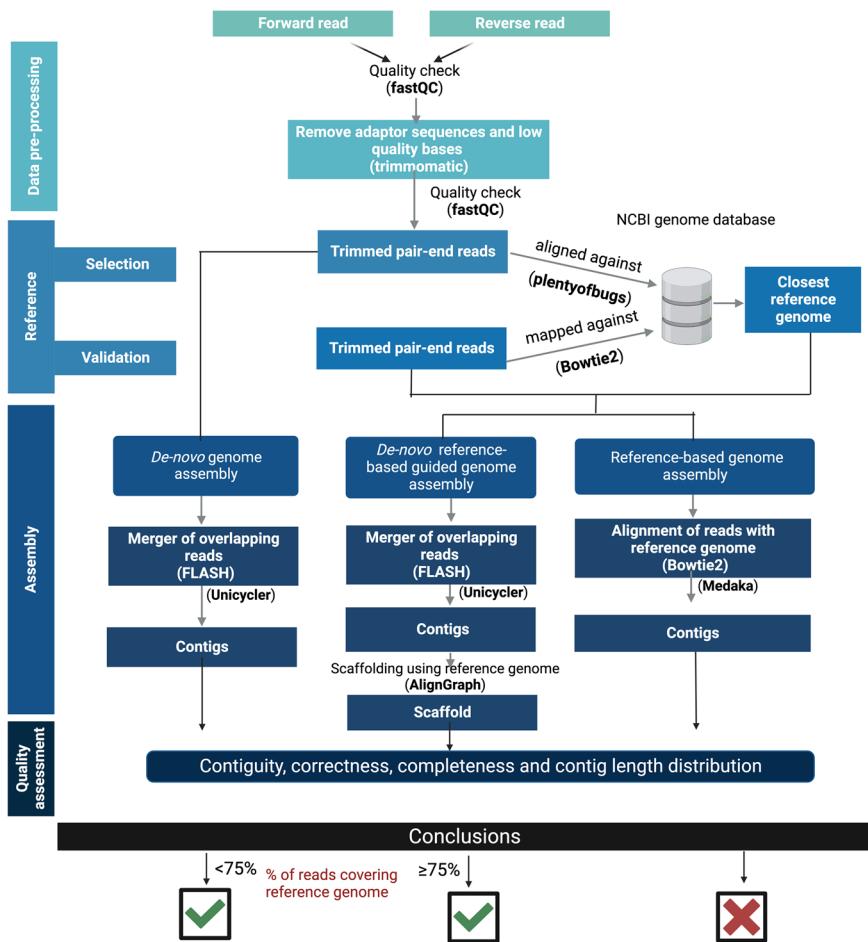


Fig. 1 Schema of *de-novo* reference-based guided genome assembly.

from the NCBI database. Using plentyofbugs (<https://github.com/nickp60/plentyofbugs>) we identified the best reference genome for each strain. Then the trimmed reads of each strain were aligned against these respective best reference genomes using Bowtie 2³¹ and the percentage of alignment was calculated. The best reference genomes selected by the plentyofbugs for the three *E. coli* strains were different. For IP9 it was NZ_CP025859.1 (identity 77.60%), for KKA it was NZ_CP018206.1 (identity 96.34%) and for IPE it was NZ_CP046396.1 (85.39%).

Closest reference-based scaffolding. *De-novo* assembled contigs of each isolate were scaffolded using their respective identified reference genome to fill the gaps between the assembled contigs using the Align-graph³² tool. The number of contigs generated after scaffolding were 124, 75 and 137 for IP9, KKA and IPE, respectively. The N₅₀ values were assessed using QUAST (v5.0.2) which were 137,460 bp, 283,877 bp and 295,668 bp for *E. coli* strains IP9, KKA and IPE, respectively. The complete flow chart of the methodology is shown in Fig. 1. Further, BUSCO³³ analysis revealed that the genomes showed 100% gene completeness Fig. 2.

Genome annotations. The assembled genomes were annotated using the prokaryotic genome annotation pipeline Prokka³⁴ (v1.14.6). Annotations revealed that the draft genomes of *E. coli* strains IP9 and KKA were 4,910,225 bp and 5,101,091 bp, respectively without any circular plasmid sequences. The draft chromosomal genome of *E. coli* strain IPE was 5,225,435 bp long and six complete circular plasmids of 5,165 bp (plasmid 1), 4,234 bp (plasmid 2), 4,072 bp (plasmid 3), 3,174 bp (plasmid 4), 2,101 bp (plasmid 5) and 1,459 bp (plasmid 6) were discerned using Unicycler (v0.4.8) with estimated multiplicities of 14.45x, 16.88x, 24.36x, 12.54x, 23.12x and 41.90x, respectively. Further characterization of these plasmids using the plasmid database PLSDB³⁵ (v. 2021_06_23_v2) showed that Plasmid 1 (5165 bp) was similar to plasmid NZ_LR890613.1 with 99% identity and 47.53% GC content, plasmid 2 (4234 bp) with plasmid NZ_CP043038.1 with 99% sequence identity and 55.38% GC content, plasmid 3 (4072 bp) with plasmid NZ_CP023833.1 with 100% identity and 51.45% GC content, plasmid 4 (3174 bp) with plasmid NZ_CP031658.1 with 100% identity and 46.79% GC content, plasmid 5 (2101 bp) with plasmid CP045788.1 with 100% identity and 41.17% GC content and plasmid 6 (1459 bp) was similar to plasmid NZ_CP061061.1 with 100% identity and 50.93% GC content. In *E. coli* IP9, Prokka identified 124 contigs with 4,545 protein encoding sequences including 938 hypothetical proteins, 12 rRNAs, 82 tRNAs, 1 tmRNA and 24 pseudogenes that were present in 124 contigs. In *E. coli* KKA, it identified 76 contigs containing 4,772 protein encoding sequences including 1154 hypothetical proteins, 11 rRNA, 90 tRNA, 1 tmRNA and 20 pseudogenes. In

BUSCO Assessment Results

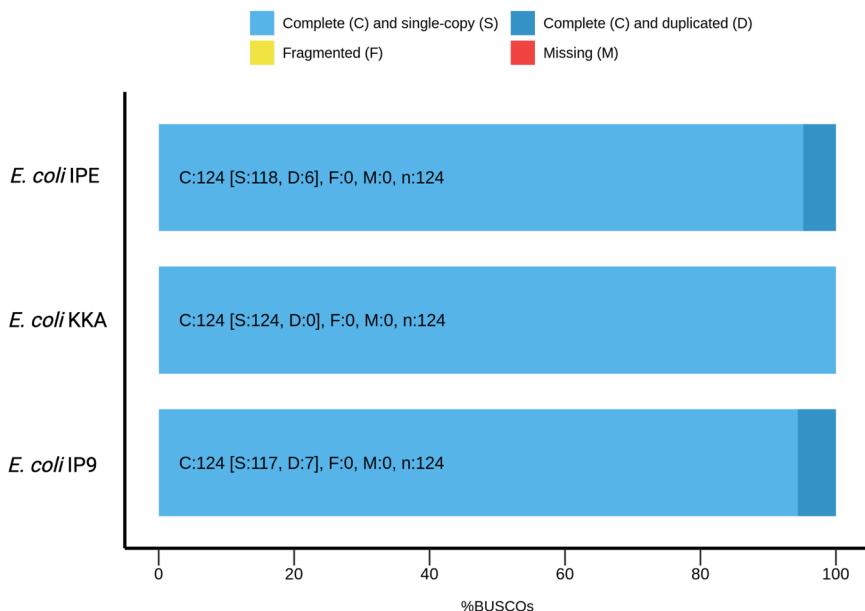


Fig. 2 Quality assessment of the assembled genomes. BUSCO analysis showed 100% gene completeness in genomes of all the three strains, with no fragmented or missing gene orthologs.

E. coli IPE it identified 137 contigs with 4,934 protein encoding sequences including 1250 hypothetical proteins, 15 rRNAs, 86 tRNAs, 1 tmRNA and 20 pseudogenes. The GO annotation of the three *E. coli* strains IP9, KKA and IPE was also performed using the PANNZER2³⁶ web service at default parameters. Of the 4772 proteins of IP9, PANNZER 2 web tool revealed 23,828 Gene Ontology (GO) annotations for 4127 proteins. In KKA, of the total 4545 total proteins, PANNZER 2 provided 22,794 GO annotations for 4193 proteins, and for IPE of the 4934 proteins it provided 23,185 GO annotations for 4381 proteins.

Sequence type (ST), phlyotyping, virulence factors and antimicrobial resistance genes identification. To identify the sequence type (ST), phlyotyping of each strain was performed using EzClermont³⁷ (v 0.7.0) and serotyping was done using ECTyper³⁸. Virulence factors were checked using VFDB³⁹ (Virulence Factors Database) using BLASTn (parameters: identity = 50%, query coverage = 50%, e-value = 1e-6). VFDB revealed the presence of genes encoding for virulence factors like adhesion, effector delivery system, exotoxin, invasion, mobility and nutritional/metabolic factors. Mobile genetic elements were found to be present in all the *E. coli* strains while genes for biofilm formation were found only in multi-β-lactam resistant and multidrug resistant strains. Several antimicrobial resistance genes were present only in multi-β-lactam resistant and multidrug resistant strains (KKA and IPE) but absent in the ampicillin resistant strain (IP9) as discerned using antibiotic resistance gene databases ResFinderdb⁴⁰ at BLASTn parameters, identity = 75%, e-value = 1e-6. The presence of bacterial drug efflux pump genes was checked using BacEffluxPred⁴¹. The results have been summarized in Supplementary Table 2.

Data Records

DNA sequencing data was submitted to NCBI Sequence Read Archive (SRA) database under the IDs: SRR21887619⁴², SRR21887618⁴³ and SRR21887617⁴⁴ and are associated with the NCBI BioProject accession number PRJNA890036. The genome assemblies are available under NCBI GenBank accession number GCA_026183935.1⁴⁵, GCA_026183955.1⁴⁶ and GCA_026183915.1⁴⁷. The genome annotation and gene ontology files are publicly available at Figshare⁴⁸.

Technical Validation

Optimization. Improvement in the N_{50} values of the assemblies after reference-based scaffolding strongly indicated the benefits of our approach. To find the least identity percentage between the sample reads and the genome sequence in the database till which a genome sequence may be used as a template for scaffolding, we determined the N_{50} value of the assembled genomes before and after scaffolding at different identity percentages. For this, we calculated the Mash values between the sample reads and all the *E. coli* genomes available in the NCBI genome database using Mash tool⁴⁹ (v2.3) at a default kmer size of 21. To reduce the time required to scaffold a large number of assembled genomes, the Mash value was normalized in the range of 0–1. Starting from 0, a sliding cut-off of 0.05 was used to select the genomic scaffold. Based on this, 16, 12 and 13 genomes were selected as references for IP9, KKA and IPE, respectively. We also aligned the sample reads with the selected *E. coli* genomes to calculate the % of alignment using Bowtie 2 and SAMtools⁵⁰ (--flagstat). Initially, *de-novo* assembly of all the three sample reads were performed using Unicycler and then scaffolding was done using AlignGraph with all the selected genomes as reference. The N_{50} value before and after scaffolding was calculated using QUAST. Our results

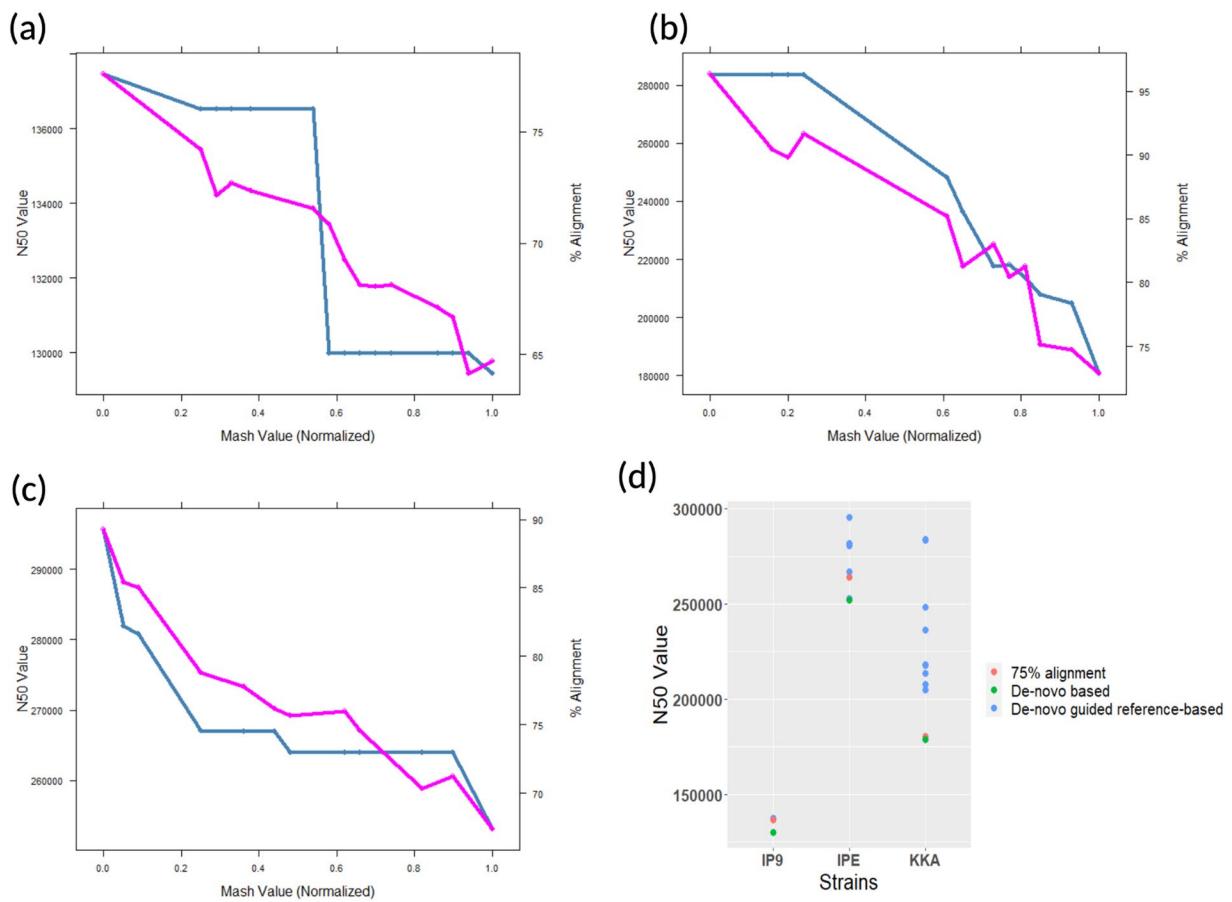


Fig. 3 (a–c) Depiction of N_{50} values (blue colour) and percentage alignment (pink colour) of sequencing reads and reference genomes vis-à-vis Mash values discerned through the *de-novo* reference-based guided approach for *E. coli* strains (a) *E. coli* IP9 (b) *E. coli* KKA (c) *E. coli* IPE; (d) composite depiction of comparative N_{50} values of the three *E. coli* strains using *de-novo* reference-based guided assembly (magenta dots) and *de-novo* assembly (green dots). The orange dot represents the N_{50} value of the assembly when 75% of the sequence reads were aligned with reference genomes.

revealed that as the Mash value (i.e., distance) between the genome investigated and the references increased, the % of alignment and N_{50} both decreased⁵¹ Fig. 3a–c.

We also found that when sample reads were aligned with at least 75% of the reference genome, the N_{50} value after scaffolding was roughly equal to the *de-novo* N_{50} value⁵¹ Fig. 3d. This suggests that selection of the reference for scaffolding should be based on two considerations: (a) at least 75% of the sample reads should be aligned to the reference genome and (b) among all the available genomes in the database, the reference genome should have minimum Mash value.

Benchmarking. To benchmark the performance of our approach vis-à-vis *de-novo* and reference-based assembly, we compared the N_{50} values, contig numbers and contig distribution of the assemblies obtained by all the three methods. Reference-based assembly was performed by aligning trimmed pair-end reads to the reference genome using Bowtie 2. On the basis of aligned reads, a consensus sequence was created using Medaka v1.3.3 (<https://github.com/nanoporetech/medaka>). The consensus sequences were considered as an assembled genome. In all the three genomes, the highest N_{50} values were discerned with the *de-novo* reference-based guided assembly approach *i.e.*, 295,668 bp for IPE, 283,877 bp for KKA and 137,460 bp for IP9. The N_{50} values with the *de-novo* approach were 252,171 bp for IPE; 178,741 bp for KKA and 129,988 bp for IP9. The reference-based assembly gave the lowest N_{50} values *i.e.*, 240,470 bp for IPE; 267,493 bp for KKA and 112,332 bp for IP9.

In context to the contig numbers, no correlation was observed between the number of contigs and the approach used for assembly. The number of contigs generated after *de-novo* reference-based guided assembly approach were 137 for IPE, 75 for KKA were and 124 for IP9. With the *de-novo* approach, the number of contigs were 183 for IPE, 100 for KKA and 139 for IP9. With the reference-based approach, the number of contigs were 85 for IPE, 74 for KKA and 461 for IP9.

Analysis of the contig lengths indicated that the length of the contigs with *de-novo* reference-based guided assembly approach was greater than the other two assembly approaches. Interestingly, with increase in the percentage identity of the investigated genome with the reference genome, lengths of the contigs also increased Fig. 4.

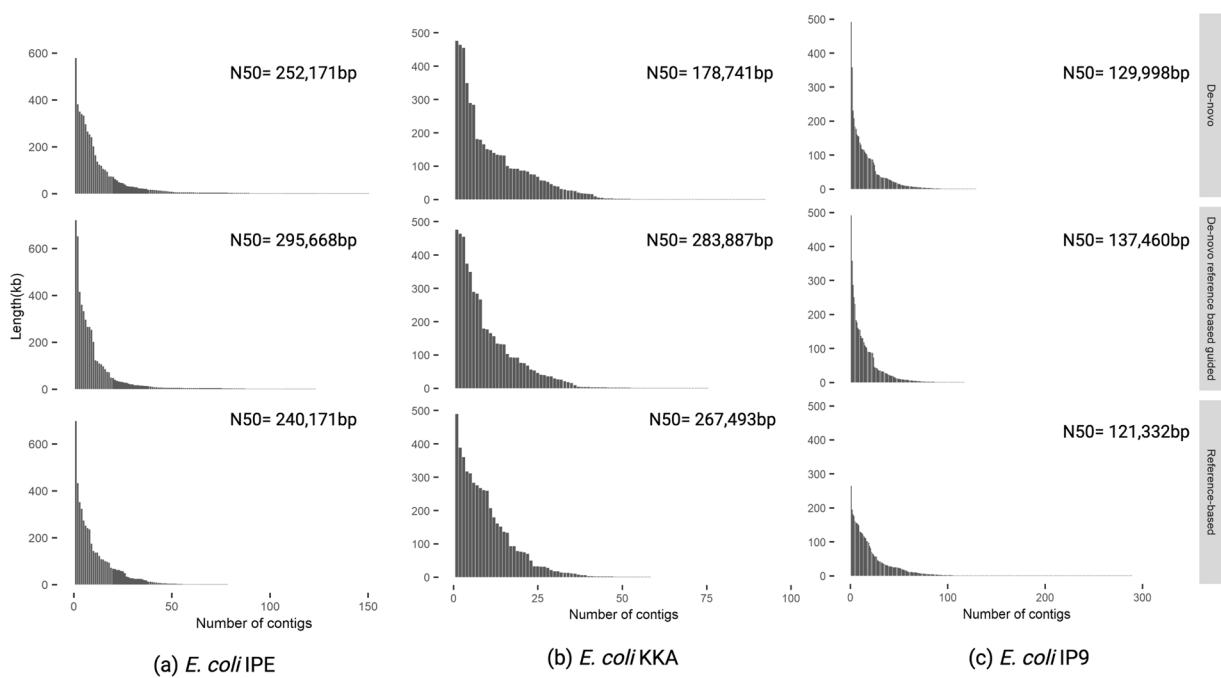


Fig. 4 Contig distribution pattern plot depicts the contig length distribution, contig number and N_{50} value after *de-novo*, reference-based and *de-novo* reference-based guided approach for genome assemblies of (a) *E. coli* IPE (b) *E. coli* KKA (c) *E. coli* IP9.

Overall, results of the benchmarking indicated that *de-novo* reference-based guided assembly gave a higher N_{50} value and contig length.

Quality assessment (3C's) of the genome assemblies. *Contiguity.* Contiguity assessment of the three *E. coli* genome assemblies with our approach in comparison with the *de-novo* and reference-based assembly was done on the basis of the N_{50} values. The N_{50} value of each assembly was calculated using QUAST (QQuality ASsessment Tool). The N_{50} values of the *E. coli* strains IP9, KKA and IPE using the *de-novo* approach were 129,988 bp, 178,741 bp and 252,171 bp, respectively. The N_{50} values of the *E. coli* strains IP9, KKA and IPE using reference-based approach were 112,332 bp, 267,493 bp and 240,470 bp, respectively. While, the N_{50} value of the *E. coli* strains IP9, KKA and IPE using *de-novo* reference-based guided approach were 137,460 bp, 283,877 bp and 295,668 bp, respectively. The maximum increment in N_{50} was recorded with the *de-novo* reference-based guided approach Supplementary Table 3.

Correctness. The correctness of the assembly was assessed by remapping the trimmed pair-end reads on the assembled genomes with all the three approaches using short read aligner Bowtie 2. The percentage (%) of alignment of reads with the *de-novo* assembly approach was 96.65% for IPE, 97.15% for KKA and 93.11% for IP9. The percentage (%) of alignment of the reads with the reference-based assembly approach was 84.43% for IPE, 96.05% for KKA and 77.75% for IP9. The percentage (%) of alignment of reads with the *de-novo* reference-based guided assembly was 96.88% for IPE, 97.47% for KKA and 93.41% for IP9. The correctness of the assembly was found to be maximum with the *de-novo* reference-based guided approach Supplementary Table 3.

Completeness. Assessment of completeness of genome assemblies of the three *E. coli* strains was done by BUSCO (Benchmarking Universal Single-copy Ortholog) using lineage dataset bacteria_odb10 (Creation date: 2020-03-06, number of genomes: 4085, number of BUSCOs: 124) and enterobacterales_odb10 (Creation date: 2021-02-23, number of genomes: 212, number of BUSCOs: 440). The assessment of BUSCO is based on the number of single-copy orthologs that are shared among the newly assembled genome and higher taxonomic groups. A high fraction of complete BUSCOs indicates completeness of assembly while a high proportion of missing and fragmented BUSCOs indicates incompleteness of the assembly. Using bacteria_odb10 124 BUSCOs and with enterobacterales_odb10, 440 BUSCOs were discerned in the three genomes assemblies and none was found to be fragmented or missing with the *de-novo* reference-based guided approach. Similarly, none of the genome assemblies was fragmented or missing using the *de-novo* approach. Though IP9 and KKA genome assemblies were complete, IPE assembly was found to be fragmented with the reference-based approach Supplementary Table 3. This indicated that the *de-novo* reference-based guided and *de-novo* approaches give complete genome assemblies than the reference-based approach. The evaluation of completeness of the 16S rRNA genes of all the strains by the three assembly approaches by BLAST against the 16S rRNA database (NCBI) revealed $\geq 99\%$ alignment in the *E. coli* 16S rRNA sequences present in the database and the assemblies.

The technical checks for assessing the quality of the assembled genomes like, N_{50} value, BUSCO, % of read alignment and reference genome selection using plentyofbugs suggests that genome assembly using the *de-novo* reference-based guided assembly is better than *de-novo* assembly and reference- based assemblies.

The contig distribution pattern based upon the contig number and the length of each contig suggested that the selection of approach for genome assembly should be based upon two considerations: (a) when the identity between the reference and the reads is less than 75%, both *de-novo* and *de-novo* reference-based guided assembly approaches are good, because both give similar N_{50} values. However, the reference-based approach is unsuitable in these cases, as it gives a distorted assembly with a very high contig number and very low N_{50} value. (b) when the identity between the reference and the reads is more than or equal to 75%, *de-novo* reference-based guided assembly is better than *de-novo* and reference-based assemblies because it gives better contiguity (N_{50} values), completeness and correctness of the assembly Fig. 4.

Usage Notes

The assembly method was built using the well-known genome assemblers and tools hence, can be easily integrated in any genome analysis workflow. Further, all the software commands have been compiled under one wrapper code, making it convenient and user-friendly for analysing prokaryotic genomes. We believe that the methods described here would help the scientific community in faster/better assembly using short read sequencing.

Code availability

The output files of technical validation⁵¹ and the codes for *de-novo* reference-based guided assembly⁵² is available on figshare.

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Author contributions

M.A. designed the assembly pipelines and performed bioinformatics analysis of the data. N.S. performed experiments. N.S., M.A. and M.K. prepared the manuscript. M.K. conceived the idea. All authors reviewed the manuscript.

Competing interests

The authors declare no competing interests.

Additional information

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