

Chromosome translocation and its consequence in the genome of *Burkholderia cenocepacia* AU 1054

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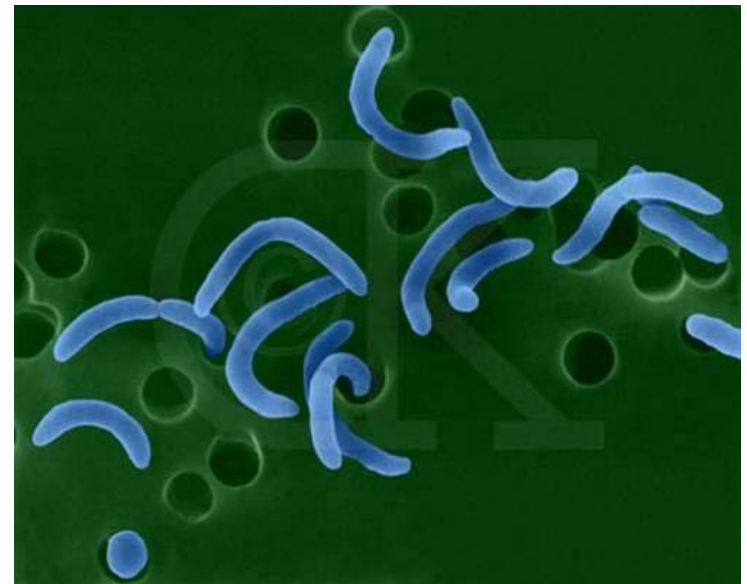
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Number of bacterial chromosomes

Most prokaryotic genomes consist of a single chromosome. However, there are also some multipartite prokaryotic genomes comprised of more than one chromosome.



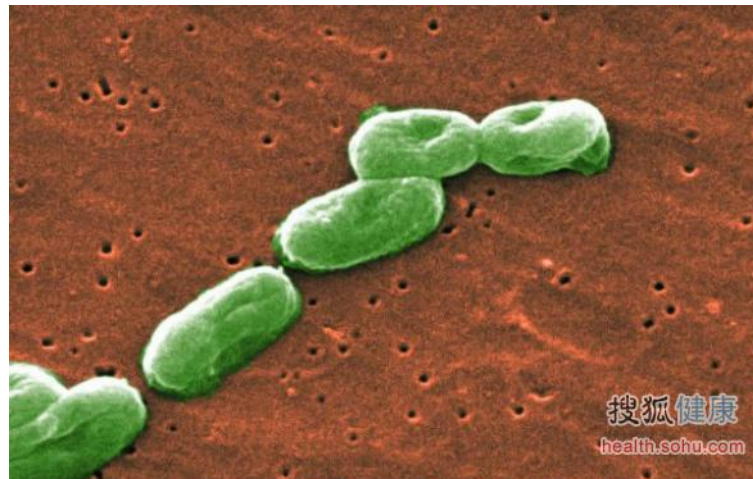
Escherichia coli
One chromosome



Vibrio cholerae
Two chromosomes

Burkholderia

Among thousands of sequenced prokaryotes, only 11 have three chromosomes. These 11 genomes belong to 6 species of the same genus, *Burkholderia*.



Burkholderia

The genus *Burkholderia* is a group of Gram-negative, nonspore forming β -proteobacteria. It comprises more than 40 species, which range from plant symbionts to commercially important rice pathogens and from opportunistic pathogens of humans to the deadly and potential bio-warfare agent *B. pseudomallei*.

BCCs

Within the *Burkholderia* genus, the *Burkholderia cepacia* complex (Bcc) is a collection of at least nine genetically distinct but phenotypically correlated species. Bccs are important and virulent pathogens found in cystic fibrosis (CF) patients.

B. cenocepacia

Among Bcc isolates from CF patients in different regions of Europe, nearly 80% belongs to the species *B. cenocepacia*.

Reference: McDowell et al. 2004, J Med Microbiol

Research aim

Due to its importance to human health and its unusual genome structure, researches related to the distribution of genes among multiple replicons of the pathogen are of special importance and necessity. In this paper, predicted essential genes on the three chromosomes of *B. cenocepacia* AU 1054 are compared.

Database



[Genome](#) > [Bacteria](#) > *Burkholderia cenocepacia* AU 1054 chromosome 1, complete sequence

Lineage: [Bacteria](#); [Proteobacteria](#); [Betaproteobacteria](#); [Burkholderiales](#); [Burkholderiaceae](#); [Burkholderia](#); [Burkholderia cepacia complex](#); [Burkholderia cenocepacia](#); [Burkholderia cenocepacia AU 1054](#)

Chromosomes: [1](#), [2](#), [3](#)

Genome Info:	Features:	BLAST homologs:	Links:	Review Info:
Refseq: NC_008060	Genes: 3054	COG	Genome Project	Publications: None
GenBank: CP000378	Protein coding: 2965	TaxMap	Refseq FTP	Refseq Status: Provisional
Length: 3,294,563 nt	Structural RNAs: 70	TaxPlot	GenBank FTP	Seq. Status: Completed
GC Content: 66%	Pseudo genes: 19	GenePlot	BLAST	Sequencing center: DOE Joint Genome Institute
% Coding: 87%	Others: None	gMap	TraceAssembly	Completed: 2006/06/05
Topology: circular	Contigs: None		CDD	Organism Group

Essential gene prediction

To predict essential genes in these genomes, a method and program named DEG_match is employed. DEG_match is developed by our group and has not been published previously.

The program can be used to determine the essentiality of function-known genes in any annotated bacterial genomes. The current version of DEG_match is 1.0 and it is freely available at <http://cobi.uestc.edu.cn/resource/AU1054/>.



Online Supplementary Material

[Chromosome translocation and its consequence in the genome of *Burkholderia cenocepacia* AU-1054](#)

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1. [Deg_Match](#)

A program to identify essential genes based on the standard gene names.

2. [Essential genes](#)

Main finding

Chromosome II: 45 essential genes, 2.8M bp;

Chromosome III: 65 essential genes, 1.2 M bp.

It is interesting that the number of essential genes on the medium chromosome II is significantly less than that on the shortest chromosome III given that the former is 2.5 times as long as the latter in the strain AU 1054.

Essential genes having no functional counterparts on chromosome I

Chromosome II: $23/45 = 51.1\%$;

Chromosome III: $54/65 = 83.1$.

That is to say, the bias between the two shorter chromosomes is more significant when only essential genes that have no functional counterparts on the largest chromosome are taken into account.

Compared with the other ten strains

All the 10 other genomes have more essential genes on chromosome II than on chromosome III.

That is to say, the unusual distribution of essential genes appears only in the strain *B. cenocepacia* AU 1054.

Biased distribution of the other genes

Ribosomal protein-coding genes: one versus six;

tRNA genes: five versus sixteen;

Comparatively, both the number of ribosomal protein-coding genes and that of tRNA genes are higher on chromosome II than on chromosome III for all of the other 10 *Burkholderia* strains with three chromosomes

Strains	Chr.	Chr. Length (bp)	Protein coding genes	TRNA genes	Ribosomal proteins	Essential Genes (ratio)	Essential genes with no counterparts	Specific Essential genes
<i>B. cenocepacia</i> AU 1054	I	3294563	2965	46	51	265 (8.9%)	XX	XX
	II	2788459	2472	5	1	45 (1.8%)	23	21
	III	1196094	1040	16	6	65 (6.3%)	54	52
<i>B. cenocepacia</i> HI2424	I	3483902	3159	60	56	308 (9.7%)	XX	XX
	II	2998664	2686	5	1	47 (1.7%)	23	21
	III	1055417	918	2	1	16 (1.7%)	6	4
<i>B. cenocepacia</i> J2315	I	3870082	3464	66	56	307 (8.9%)	XX	XX
	II	3217062	2807	6	1	43 (1.5%)	26	26
	III	875977	752	2	1	8 (1.1%)	2	2
<i>B. cenocepacia</i> MC0-3	I	3532883	3160	60	56	309 (9.8%)	XX	XX
	II	3213911	2795	5	1	43 (1.5%)	22	19
	III	1224595	1053	2	1	15 (1.4%)	7	4
<i>B. multivorans</i> ATCC 17616	I	3448421	3084	59	55	316 (10.2%)	XX	XX
	II	2473162	2130	5	1	46 (2.2%)	19	16
	III	919805	767	2	1	19 (2.5%)	8	5

<i>B. multivorans</i> ATCC 17616 doe	I	3448466	3146	59	56	306 (9.7%)	XX	XX
	II	2472928	2151	4	1	36 (1.7%)	21	17
	III	919806	823	2	1	19 (2.3%)	11	7
<i>B. ambifaria</i> MC40-6	I	3443583	3074	60	56	310 (10%)	XX	XX
	II	2769414	2382	6	1	43 (1.8%)	20	19
	III	1127947	967	2	1	18 (1.9%)	5	4
<i>B. ambifaria</i> AMMD	I	3556545	3206	61	57	314 (9.7%)	XX	XX
	II	2646969	2346	6	2	42 (1.8%)	16	16
	III	1281472	1013	2	1	20 (2.0%)	5	5
<i>B. vietnamiensis</i> G4	I	3652814	3274	61	57	310(9.5%)	XX	XX
	II	2411759	2096	4	1	43 (2.1%)	25	22
	III	1241007	1114	2	0	24 (2.2%)	11	8
<i>Burkholderia</i> sp. 383	I	3694126	3334	60	57	319 (9.6%)	XX	XX
	II	3587082	3174	5	1	49 (1.5%)	23	22
	III	1395069	1209	2	0	15 (1.2%)	6	5
<i>B. xenovorans</i> LB400	I	4895836	4430	57	56	315 (7.1%)	XX	XX
	II	3363523	2960	8	2	58 (2.0%)	31	28
	III	1471779	1312	0	0	17 (1.3%)	5	2

Peculiar character of AU 1054

Overall, there are unusual biases of tRNA genes and essential genes, particularly ribosomal protein-coding genes, between the two shorter chromosomes of *B. cenocepacia* AU 1054.

After further analyses, this unusual distribution is not found in any other sequenced bacterial genomes with three chromosomes, including the other strains of the species *B. cenocepacia*.

Therefore, the unusual distribution of essential genes is a peculiar character of *B. cenocepacia* AU 1054 genome.

The possible reason for the unusual distribution of essential genes

To reveal the possible reason for this interesting phenomenon, we performed a genome-wide blast search for all of the three chromosomes of the strain AU 1054.

Blast analysis

The results show that most parts of the chromosomes of AU 1054 and HI2424 match well each other. However, a small part of chromosome I of AU 1054 is found to be homologous with chromosome III of HI2424. Correspondingly, half of chromosome III of AU 1054 is found to be homologous with chromosome I of HI2424.

This suggests that a chromosomal translocation has happened between the two chromosomes. The unusual distribution of essential genes and tRNA genes on chromosome III of AU 1054 should be a consequence of the translocation.

Synteny analysis

To show the translocation in more detail, we perform a synteny analysis with the web server Cinteny

http://cinteny.cchmc.org.



Create New Project

Project name ([Check availability](#))
Email

Select Files to upload

Marker data

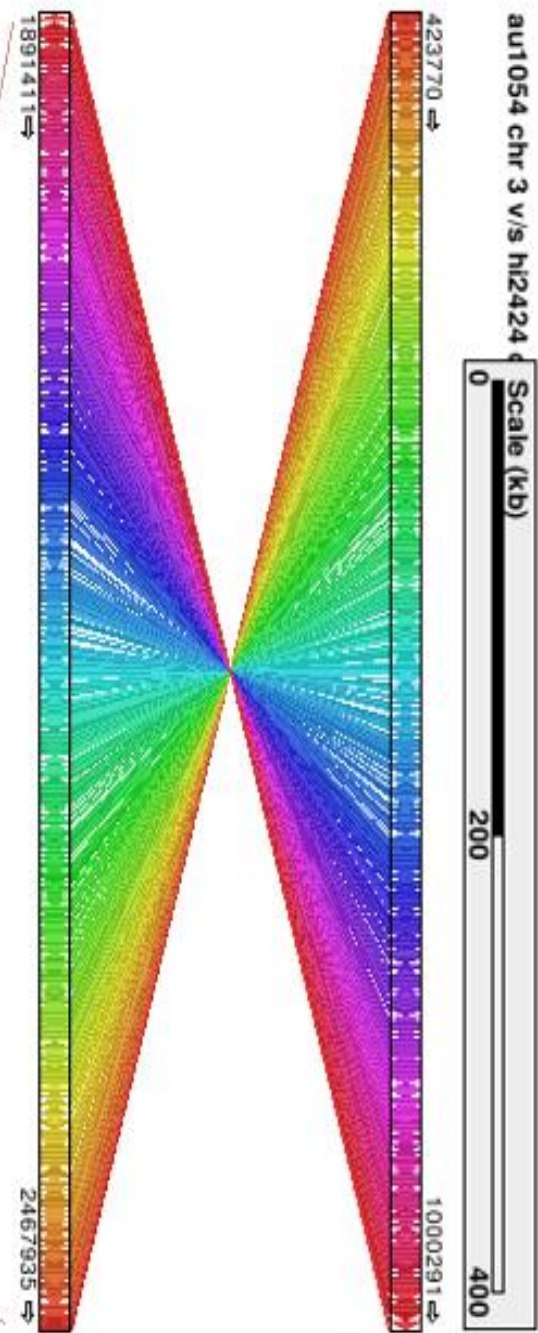
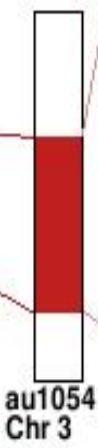
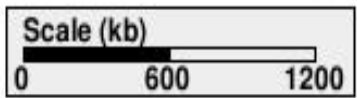
Homology data

Common Names (Optional)

Note: The data should be formatted as described in the [Data format page](#). Feel free to [Contact us](#) if you need assistance.

After comparatively analyzing chromosomes of the two strains, it is found that most parts of chromosomes I and II of the two strains show conserved gene order.

That is to say, genes on them vary collinearly. However, half part of chromosome III of AU1054 are reversely syntenic to the corresponding part of chromosome I of HI2424.



Similar extra-chromosome translocation is not found in any other strains of the genus *Burkholderia*.

During the translocation, chromosome I of AU 1054 lost some essential genes and chromosome III gained some essential genes.

Transcriptome analysis

Area	CF conditions	SE conditions
Chromosome I	136	74
Chromosome II	13	106
Chromosome III	12	34
Exchanged part of Chr. I	1	11
Exchanged part of Chr. III	12	15

Original transcriptome data for generating this table are extracted from by Yoder-Himes et al 2009, PNAS.

When merely considering the translocated parts of chromosomes I and III, it is found that the number of induced genes on the latter is significantly greater than that on the former under the two mimicking environments, particularly under CF condition.

Therefore, the translocated parts of chromosomes I and III in the strain *B. cenocepacia* AU1054 are unequally important when viewed from the aspects of both essentiality and expressivity.

Consequently, the translocation altered gene distribution on the three chromosomes and hence made chromosome III of the strain AU1054 more important than before.

Summary

Chromosome III of the *B. cenocepacia* AU 1054 genome is found to contain much more essential genes than those of the other *Burkholderia* strains with three chromosomes.

Through blast search and synteny analysis, it is proposed that non-homologous chromosomal translocation between chromosomes I and III in the species *B. cenocepacia* is responsible for the unusual distribution of essential genes.

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Thank you for
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