The Analysis of Multiple Genome Comparisons in Genus Escherichia and Its Application to the Discovery of Uncharacterised Metabolic Genes in Uropathogenic Escherichia coli CFT073

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A survey of a complete gene synteny comparison has been carried out between twenty fully sequenced strains from the genus Escherichia with the aim of finding yet uncharacterised genes implicated in the metabolism of uropathogenic strains of E. coli (UPEC). Several sets of adjacent colinear genes have been identified which are present in all four UPEC included in this study (CFT073, F11, UTI89, and 536), annotated with putative metabolic functions, but are not found in any other strains considered. An operon closely homologous to that encoding the L-sorbose degradation pathway in Klebsiella pneumoniae has been identified in E. coli CFT073; this operon is present in all of the UPEC considered, but only in 7 of the other 16 strains. The operon's function has been confirmed by cloning the genes into E. coli DH5a and testing for growth on L-sorbose. The functional genomic approach combining in silico and in vitro work presented here can be used as a basis for the discovery of other uncharacterised genes contributing to bacterial survival in specific environments.

1. Introduction

Uropathogenic E. coli (UPEC) are the causal agents of 80% of all community-acquired urinary tract infections (UTIs) [1]. The ability of UPEC to colonise the urinary tract has been studied in depth in terms of virulence factors such as pili and hemolysins [2]; however, the ability to utilise the metabolites available in this environment has not been fully investigated to date. While studies of growth rates in urine have been conducted (for instance by Gordon and Riley [3]), it has never been established exactly what is used as the primary carbon source (or if there is a single one) for growth of UPEC, and which genes enable the utilisation of this carbon source. There has been discussion of metabolic genes contributing to uropathogenicity, considering two UPEC: CFT073 and 536 [4]. D-serine has been postulated as a potential carbon and nitrogen source due to the presence of D-serine catabolic genes in these 2 UPEC, though the requirement for these genes or their involvement in the course of a UTI has yet to be investigated.

The use of multiple genome analysis in research has been reviewed elsewhere [5], and several tools for genome comparisons are available, as well as software applications for their analysis. The most prominent tool is BLAST [6] for whole genome analyses. The set of genus Escherichia genome sequences has already been used to compare regulatory networks [7] and to investigate the genetic basis of pathogenesis in enterotoxigenic E. coli [8]. Sequencing projects (such as [4, 9]) have used up to three complete genome sequences for genomic comparisons, though this is only a small subset of the Escherichia genome sequences currently available. Recently Rasko et al. [10] have used a BLAST score ratio (BSR) technique to compare the gene contents of 17 E. coli genome sequences which has identified fewer pathovar-specific genes than might be expected.
Table 1: Strains of genus *Escherichia* used in this study, all with completely sequenced genomes or whole genome shotgun sequences freely available from GenBank. Unless otherwise indicated, they are *Escherichia coli*.

| Strain     | Type                  | Sorbose operon | Source/Accession number |
|------------|-----------------------|----------------|-------------------------|
| CFT073     | UPEC (uropathogenic)  | +              | AE014075                |
| F11        | UPEC                  | +              | AAJU00000000            |
| 536        | UPEC                  | +              | CP000247                |
| UT189      | UPEC                  | +              | CP000243                |
| 042        | EAEC (enteroaggregative) |               |                        |
| B7A        | ETEC (enterotoxigenic) | −              | Sanger Center           |
| E24377A    | ETEC                  | −              | CP000800                |
| B171       | EPEC                  | −              | AAJT00000000            |
| E22        | EPEC                  | −              | AAJV00000000            |
| E2348      | EPEC                  | −              | Sanger Center           |
| E110019    | EPEC                  | −              | AAJX00000000            |
| 53638      | EIEC (enteroinvasive) | −              | AAKB00000000            |
| MG1655     | Commensal (Gastrointestinal tract) | − | U00096 |
| HS         | Commensal (Gastrointestinal tract) | − | CP000802 |
| SMS-3-5    | Environmental         | +              | CP000970                |
| O157:H7 str. Sakai | EHEC (enterohaemorrhagic) | + | BA000007 |
| O157:H7 EDL933 | EHEC               | +              | AE005174                |
| *Shigella sonnet* 53G | Bacillary Dysentery     | +              | Sanger Center           |
| *Shigella flexneri* 2a str. 301 | Bacillary Dysentery | + | AE005674 |
| *Shigella dysenteriae* Sd197 | Bacillary Dysentery | + | CP000034 |

The potential for taking advantage of the large number of already available and imminent genome sequences in the genus *Escherichia* is great, when combined with well-targeted experimentation. While there is no certainty from purely computational approaches that a gene is necessary or helpful in a particular environment, its presence in bacteria which thrive in that environment and its absence in bacteria which do not represent evidence for pressure to retain the gene, therefore, its function aids the persistence of the bacteria in that niche. In this study the genome sequence of *E. coli* CFT073 has been compared to 19 other complete genome sequences of bacteria of the genus *Escherichia* using a synteny approach to infer which genes are present in or absent from the other strains. Table 1 shows a list of these strains which includes four UPEC and three *Shigella* strains.

Genes in CFT073 which according to their GenBank entries [11] are metabolic genes, but which do not have a specific functional assignment (e.g., gene c4985 is annotated as “Putative sorbose PTS component”), or genes of unknown function which form sets of adjacent colinear genes with those partially characterised metabolic genes, have been investigated to determine their relative occurrences in UPEC and the other strains. Some of those sets of genes more often found in UPEC than the other strains used in this study have been investigated to further elucidate their function.

One putative operon has been experimentally verified as an L-sorbose utilisation operon, after having been identified as being present more frequently in UPEC than in the other strains considered. Lehmacher and Bockemühl [12] showed in a study of 266 strains from the collection of the Institut für Hygiene und Umwelt that L-sorbose utilisation varies widely over differing pathotypes of *E. coli* and *Shigella*, from 14 of the 15 *E. coli* isolates associated with neonatal meningitis to a complete lack of utilisation by *Shigella* (of the 26 tested in the study). Although no UPEC were included, 67% of the EPEC and EAEC strains tested utilised L-sorbose.

2. Materials and Methods

2.1. Multiple Genome Comparisons. The CFT073 genome [9] was compared gene-by-gene with the genomes of the nineteen other strains listed in Table 1 using TBLASTN [6], and a synteny result was obtained by manual inspection of each individual gene-nucleotide comparison. Homology as a percentage identity from TBLASTN was combined with the position and homology of nearest neighbours and overall position in the genome to infer synteny conservation. The use of BLAST scores to determine gene conservation is well established (such as the BSR technique [10]), and this process was refined by adding a neighbour-dependent analysis to determine gene synteny. For sets of two or more genes in a similar position on two genomes, retention of function of each gene was inferred by identity with a cut-off of 90% over the whole length of each gene. Single genes in similar positions on the two genomes were inferred as conserved only if their mutual identity was above 95% over their whole length.

MG1655 does not grow in urine, whereas CFT073 does [13]. Some metabolic genes in CFT073 that are not present in MG1655 may confer a fitness advantage in the urinary tract due to better ability to use available substrates for growth. Genes present in CFT073 but not in MG1655 were therefore
studied to look for such metabolic genes. This produced an initial list of candidate genes that could be implicated in the metabolism of CFT073 in the urinary tract, but have not yet been characterised. This set of genes was inspected manually for those genes which appeared to have a metabolic function from their GenBank annotation [11], but without a definite, specific biological function, henceforth referred to as putatively metabolic genes (PMGs).

Where there was a PMG surrounded by uncharacterised genes, this region of the genome sequence was viewed using the NCBI’s Sequence Viewer 2.1 and all adjacent genes transcribed in the same direction as the PMG and less than 100 base pairs separated were labelled as part of a Set of Adjacent Cologinear genes (SAC) and included in the analysis. The algorithm for inferring whether a SAC was present in each of the *Escherichia* genomes considered was as follows: where the SAC was greater than 3 genes in length it was considered present if at most one of the genes was absent according to the synteny comparison; where there were 3 or fewer genes, all genes had to be present to conclude that the set of genes was present.

BLASTp was then used on each gene in the SACs against the full nonredundant database of Genbank [14] to try to find homologies to already annotated genes. Where homologs could not be found, protein domain similarities were sought using Pfam [15] and SEED (http://theseed.uchicago.edu/FIG/index.cgi) in an endeavour to elucidate their function. Further, the NCBI’s Conserved Domain Database was searched for conserved domains. The results of the Conserved Domain Database searches can be seen in Supplementary Table 2 in supplementary material available online at doi:10.1155/2009/782924.

A phylogenetic comparison between the putative L-sorbose operons from those sequenced bacteria of the genus *Escherichia*, using *Klebsiella pneumoniae* (GI: 150953431) and *Klebsiella oxytoca* (see acknowledgments for reference) as an outgroup, was conducted using ClustalX [16]. BLAST was used to extract the putative L-sorbose operons for most of the bacteria, but Artemis [17] was required to extract the relevant parts of both the *Klebsiella* strains and F11, which do not yet have complete single contig genome sequences.

### 2.2. Experimental Verification of Putative Functions of Genes c4981 to c4987 from Escherichia coli CFT073.

*Escherichia coli* strain DH5α was used as the test host for L-sorbose growth as it is not ampicillin resistant and selection is not required. A phylogenetic comparison between the putative L-sorbose operons identified in CFT073 was excised using the forward and reverse primers 5′-GC-CAGCGACATGCAGAGTTAAGTAGCCGGA-3 and 5′-AA-ATCTCTCTGTAAACGCCGAATATACC-3, respectively. The consequent 7.5 kb fragment was amplified using these primers with Phusion DNA polymerase (Finnzyme) and cloned into the pSC-B plasmid (Stratagene). The consequent construct was transformed into DH5α and bacteria with a correctly inserted plasmid were selected by blue/white screening on 100 µg ml⁻¹ ampicillin, 40 µg ml⁻¹ X-Gal, 20 µg ml⁻¹ IPTG plates and were picked off and spread onto a Nutrient Broth 2 (Oxoid) plate with 100 µg ml⁻¹ ampicillin to produce single colonies. The insertion and orientation were confirmed by sequencing from the M13 primers to be as shown in Figure 1 and the plasmid was named pQR793.

One colony was then picked from the Nutrient Broth 2 plate and grown in 5 ml of a modified liquid M6 medium (5-20 gl⁻¹ (NH₄)₂SO₄, 3.86 gl⁻¹ NaH₂PO₄·H₂O, 4.03 gl⁻¹ KCl, 4.16 gl⁻¹ Citric Acid, 1.04 gl⁻¹ MgSO₄·7H₂O, 0.25 gl⁻¹ CaCl₂·2H₂O, 20.6 ml⁻¹ ZnSO₄·7H₂O, 27.2 ml⁻¹ MnSO₄·H₂O, 8.1 ml⁻¹ CuSO₄·5H₂O, 4.2 ml⁻¹ CoSO₄·7H₂O, 100.6 ml⁻¹ FeCl₃·6H₂O, 0.3 ml⁻¹ H₃BO₃, 0.2 ml⁻¹ Na₂MoO₄·2H₂O adjusted to pH 7.3 by NaOH) with 1% glucose, 0.001% thiamine (a requirement for DH5α to grow) and 100 µg ml⁻¹ ampicillin; shaken at 150 rpm, 37°C overnight, then inoculated into two 100 ml shake flasks, one containing the same medium composition as the starter culture and the other containing 1% L-sorbose instead of glucose. Simultaneously DH5α with an empty pUC19 plasmid and CFT073 were grown in the same manner as negative and positive controls, respectively, (no ampicillin was used in the growth of CFT073 as it is not ampicillin resistant and selection is not required).

These flasks were shaken at 150 rpm at 37°C for 145 hours and samples were taken at intervals to measure optical density of the samples at wavelength 600 nm. Each culture was repeated twice to confirm the result growth or lack thereof.

### 3. Results and Discussion

#### 3.1. Multiple Genome Comparison.

The set of genome sequences used in this study will be referred to as the EGSS (*Escherichia* genome sequence set); the results of the complete synteny comparison of the genome of CFT073 against the rest of the EGSS can be seen in Supplementary Table 1.

Overall 133 PMGs were inferred; they can be seen in Supplementary Table 2, along with the results of the NCBI Conserved Domain Search, and are summarised in Table 2. All of the individual genes marked with putative metabolic functions in the CFT073 genome sequence were positioned adjacent to genes transcribed in the same sense, so the sets of adjacent colinear genes were included in the investigation, a summary of which can be seen in Table 2, and positions of which in the CFT073 genome can be seen in Figure 2. It should be emphasised that the criterion for consideration of these genes was only that the genes marked with putative functions be absent from *E. coli* K-12 MG1655, without any further consideration of whether they would specifically be useful in the lifecycle of CFT073. 9 of these genes are present in all of and only in the UPEC and 49 genes are among those identified by Lloyd et al. [18], which compared the gene content of 7 additional UPEC and 2 different faecal strains of *E. coli* by comparative genomic hybridisation against CFT073 to find those genes unique to uropathogens.

The synteny comparison shows several characteristics indicating a higher prevalence of the genes from CFT073 in the other UPEC than in the other strains. It is worth noting...
that the sets of adjacent colinear genes identified in this study are not in general parts of the large pathogenicity islands identified in CFT073 by others [9, 18], with the exception of those marked with an asterisk in Table 2.

SAC No. 6 (as labelled in Table 2) is within a large pathogenicity island, PAI-CFT073-metV (according to the nomenclature set out by Lloyd et al. [18]), in which the SAC is restricted to the area c3405 to c3410. These genes are retained in all the UPEC, in *E. coli* E2348, and in *E. coli* SMS-3-5, but not in any other strain. Retention of the SorCDFBAME genes (SAC No. 15) in some of the EAEC and EPEC and all of the *Shigella* is consistent with the findings of Lehmacher and Bockemühl [12] who despite the negative phenotype showed that they retain the DNA for many of these genes.

It was found that 121 of the 133 PMGs identified are present in the same position in all four UPEC; these include the putative genes for L-sorbose degradation. The only SAC not present in any of the UPEC other than CFT073 is No. 1. Those found in the same place in all UPEC, but in none of the other strains, are 8, 12, and 19. The SACs identified here have a tendency to be present or absent as a whole, rather than on a gene-by-gene basis.

An investigation of each of the PMGs was conducted using BLAST, the SEED tool, Pfam, and the NCBI Conserved Domain Database, in an attempt to identify putative functions for all the genes. SAC No. 8 (genes c4013 to c4018) has several genes annotated putatively already, c4015 to c4017 as part of a ribose ABC transporter, and c4018 as a tagatose 1,6-diphosphate aldolase. The hypothetical genes bear similarities to other sugar metabolism encoding genes: c4013 to a dehydrogenase and c4015 to c4017 as part of a ribose ABC transporter, and c4018 as a tagatose 1,6-diphosphate aldolase. The hypothetical genes could encode enzymes for the uptake and catabolism of a 5- or 6-carbon sugar or sugar derivative.

Since there is a limited number of carbon sources present in urine—predominantly urea, uric acid, and creatinine (and L-sorbose in small amounts)—it might seem plausible that the sets of genes identified here may encode proteins for the utilisation of these chemicals. However, an analysis of the genes investigated here has so far failed to find any good matches to known metabolic pathways for these three carbon containing compounds. UPEC are not confined to
Table 2: Synteny conservation of sets of adjacent colinear genes in 18 sequenced strains of genus *Escherichia*; all these sets of genes are present in *E. coli* CFT073. Those genes which are part of genomic islands, as identified in [18], are marked with an asterisk.

| SAC no. | Gene c numbers | No. of genes | Putative function | E. coli F11 | E. coli 536 | E. coli UT189 | E. coli E2348 | E. coli O42 | E. coli B71 | E. coli E22 | E. coli E24377A | E. coli E22 | E. coli B7A | E. coli E410019 | E. coli 53689 | E. coli sonntag53G | E. coli HS | E. coli K12 MG1655 | E. coli O157:H7 | E. coli SMS-3 | S. flexneri 2a str. 201 | S. dysenteriae Sd197 |
|---------|----------------|--------------|-------------------|------------|------------|--------------|--------------|------------|------------|------------|----------------|------------|------------|----------------|--------------|----------------|------------|----------------|----------------|----------------|----------------|----------------|
| 1       | c0317 c0323    | 7            | Polysaccharide biosynthesis* | −         | −         | −         | −             | −         | −         | −         | −             | −         | −         | −             | −             | −             | −         | −             | −             | −             | −             | −             |
| 2       | c0330 c0333    | 4            | Fucose metabolism      | +         | +         | +         | −             | −         | −         | −         | −             | −         | −         | −             | −             | −             | −         | −             | −             | −             | −             | −             |
| 3       | c0409 c0415    | 7            | 2,5-diketo-D-gluconic acid metabolism | +         | +         | +         | +             | −         | −         | −         | −             | −         | −         | −             | −             | −             | −         | −             | −             | −             | −             | −             |
| 4       | c0757 c0765    | 9            | Chorismate biosynthesis | +         | +         | +         | −             | −         | −         | −         | −             | −         | −         | −             | −             | −             | −         | −             | −             | −             | −             | −             |
| 5       | c1955 c1960    | 6            | PTS system, cellbiose specific | −         | −         | −         | +             | +         | +         | −         | −             | −         | −         | −             | −             | −             | −         | −             | −             | −             | −             | −             |
| 6       | c3405 c3410    | 6            | PTS system, maltose/glucose specific* | +         | +         | +         | −             | −         | −         | −         | −             | −         | −         | −             | −             | −             | −         | −             | −             | −             | −             | −             |
| 7       | c3750 c3756    | 7            | 5- or 6-carbon sugar metabolism | +         | +         | +         | −             | −         | −         | −         | −             | −         | −         | −             | −             | −             | −         | −             | −             | −             | −             | −             |
| 8       | c4013 c4018    | 6            | Carbohydrate metabolism      | +         | +         | −         | −             | −         | −         | −         | −             | −         | −         | −             | −             | −             | −         | −             | −             | −             | −             | −             |
| 9       | c4276 c4280    | 5            | PTS system, galactitol specific | −         | −         | −         | +             | −         | −         | −         | −             | −         | −         | −             | −             | −             | −         | −             | −             | −             | −             | −             |
| 10      | c4481 c4488    | 8            | PTS system, fructose specific | +         | +         | +         | −             | −         | −         | −         | −             | −         | −         | −             | −             | −             | −         | −             | −             | −             | −             | −             |
| 11      | c4756 c4759    | 4            | PTS system, glucose specific | +         | +         | +         | −             | −         | −         | −         | −             | −         | −         | −             | −             | −             | −         | −             | −             | −             | −             | −             |
| 12      | c4760 c4780    | 21           | Entner-Doudoroff pathway      | +         | +         | +         | −             | −         | −         | −         | −             | −         | −         | −             | −             | −             | −         | −             | −             | −             | −             | −             |
| 13      | c4828 c4830    | 3            | Shikimate metabolism      | +         | +         | +         | −             | −         | −         | −         | −             | −         | −         | −             | −             | −             | −         | −             | −             | −             | −             | −             |
| 14      | c4924 c4926    | 3            | Citrate metabolism      | +         | +         | +         | −             | −         | −         | −         | −             | −         | −         | −             | −             | −             | −         | −             | −             | −             | −             | −             |
| 15      | c4981 c4987    | 7            | L-sorbose metabolism      | +         | +         | +         | −             | −         | −         | −         | −             | −         | −         | −             | −             | −             | −         | −             | −             | −             | −             | −             |
| 16      | c5020 c5025    | 6            | 3-ketoacid metabolism      | −         | −         | −         | −             | −         | −         | −         | −             | −         | −         | −             | −             | −             | −         | −             | −             | −             | −             | −             |
| 17      | c5030 c5041    | 12           | 2-oxoglutarate metabolism      | +         | +         | +         | −             | −         | −         | −         | −             | −         | −         | −             | −             | −             | −         | −             | −             | −             | −             | −             |
| 18      | c5298 c5303    | 6            | 3-ketoacid metabolism      | +         | +         | +         | −             | −         | −         | −         | −             | −         | −         | −             | −             | −             | −         | −             | −             | −             | −             | −             |
| 19      | c5346 c5351    | 5            | Arginine metabolism      | +         | +         | +         | −             | −         | −         | −         | −             | −         | −         | −             | −             | −             | −         | −             | −             | −             | −             | −             |
Table 3: Comparison of SAC No. 15 in CFT073 to the *Klebsiella pneumoniae* L-sorbose degradation operon.

| CFT073 gene ID | CFT073 name                                      | *Klebsiella* Locus | Protein Similarity (%) |
|----------------|--------------------------------------------------|--------------------|------------------------|
| c4981          | Putative oxidoreductase                          | SorE               | 91                     |
| c4982          | PTS system, mannose-specific IID component       | SorM               | 97                     |
| c4983          | PTS system, mannose-specific IIC component       | SorA               | 95                     |
| c4984          | Putative sorbose PTS component                   | EIII-B Sor PTS     | 92                     |
| c4985          | Putative sorbose PTS component                   | EIII-F Sor PTS     | 82                     |
| c4986          | sorbitol-6-phosphate 2-dehydrogenase             | D-glucitol-6-P-Dehydrogenase | 92              |
| c4987          | Putative transcriptional regulator of sorbose uptake and utilization genes | Sor regulator | 92                     |

using the small molecule carbon sources in urine; they adhere primarily to the epithelial cells in the urinary tract so potentially the mucus produced by these cells could be used to fulfill the metabolic needs of UPEC.

The benefit of D-serine utilisation genes for UPEC has been suggested [4]; so these genes were investigated in the UPEC included in this study to assess their relative prevalence. It was noted that according to the initial synteny comparison (Supplementary Table 1), these genes are not present in *E. coli* F11 or 536. However, there are D-serine utilisation genes in both F11 and 536 at an alternative position in the genome identified by Brzuszkiewicz et al. [4]. Moreover, UTI89 also has D-serine utilisation genes in this alternative position on its genome as well as those found in this study. None of the non-UPEC in the EGSS have this alternative operon, which is characterised by a particularly large intergenic region (~1 kb) adjacent to it, conserved between F11, 536 and UTI89. This D-serine utilisation operon is therefore unique within the strains considered here to the UPEC.

3.2. *L*-sorbose In Silico Analysis. *L*-sorbose [19] can be present in urine (and in the gastrointestinal tract). It can be seen from Table 2 that it is predominantly the UPEC and *Shigella* strains which contain the operon enabling use of *L*-sorbose as a carbon source.

The putative *L*-sorbose operon in CFT073 was compared to that of *Klebsiella pneumoniae* using BLASTp. Both of these strains are in the family *Enterobacteriaceae* and the function of *Klebsiella*’s operon has been experimentally verified [20]. The results of this comparison are shown in Table 3, which shows identity above 90% for all but one of the genes.

The ClustalX comparison of the putative sorbose operons of 13 strains of bacteria produced the phylogenetic tree shown in Figure 3. These bacteria are all of genus *Escherichia* (except the *Klebsiella* strains) and include several *Shigella* strains, *Shigella boydii* Sb227 (Accession Number: CP000036.1) and *Shigella sonnei* Ss046 (Accession Number: CP000038.1), not used in the full genome analysis because their genomes are not completely sequenced. The operons were located in the genome sequence thus far generated for them and extracted to compare to the others in the EGSS. Also included is the inferred *L*-sorbose operon from Avian Pathogenic *Escherichia coli* O1:K1:H7 (APEC 01) [21] (Accession Number: CP000468.1), which clusters with the UPEC, separate from the enterohaemorrhagic *E. coli* (EHEC) and *Shigella* strains. This is also true of the environmental *E. coli* SMS-3-5. The EHEC and *Shigella* L-sorbose operons are grouped together.

3.3. Experimental Verification of Function of Genes c4981 to c4987 from *Escherichia coli* CFT073. The genes c4981 to c4987 were successfully cloned into the pSC-B plasmid and confirmed by sequencing as being oriented as shown in...
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Figure 4: Growth curves for DH5α containing plasmid pQR793, compared to CFT073 and DH5α with an empty pUC-19 plasmid. DH5α with pQR793 is represented by □ and •, DH5α with pUC19 by △ and ◆, and CFT073 by ▲ and ■ where empty symbols represent growth on glucose and filled symbols represent growth on L-sorbose. Where duplicate samples were taken, readings varied by less than 0.01 OD₆₀₀ units using a CO8000 Cell Density Meter (WPA).

4. Conclusions

Multiple genome sequence analysis has been used to identify several sets of adjacent colinear genes in E. coli CFT073 that are not present in E. coli MG1655 and might be implicated in metabolism in the human urinary tract. Specifically a previously incompletely annotated operon encoding proteins involved in L-sorbose catabolism have been identified and experimentally confirmed encompassing genes c4981 to c4987 of the genome of uropathogenic Escherichia coli strain CFT073. The sets of genes from CFT073 found solely in UPEC include an arginine metabolic operon, which has previously been implicated in UPEC fitness in the urinary tract. The use of such sets of genomic data will become increasingly important as the rate of sequencing increases while experimental verification of gene function lags considerably behind. Although elucidation of novel gene function cannot be done purely through comparative genomics, it can aid searches for important genes, not necessarily previously characterised in other species or strains.

Abbreviations

APEC: Avian pathogenic Escherichia coli
EGSS: Escherichia genome sequence set
HGT: Horizontal gene transfer
PMG: Putatively metabolic gene
PTS: Phosphotransferase transport system
UPEC: Uropathogenic Escherichia coli
UTI: Urinary tract infection.

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