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Draft genome sequences of constitutive rdar biofilm forming *Escherichia coli* isolates

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Background: *Escherichia coli* is a well-studied model organism with respect to various aspects of bacterial physiology and behavior. Biofilm formation is defined as multicellular microbial communities surrounded by a self-produced matrix of extracellular polymeric and non-polymeric substances adherent to each other, to interfaces and to biotic or abiotic surfaces [1]. Strains of *E. coli* exhibit diverse biofilm phenotypes. A well-studied biofilm type under the control of the orphan biofilm regulator CsgD characterized by the formation of an extracellular matrix consisting mainly of amyloid curli fimbriae and the exopolysaccharide cellulose is the red, dry, and rough (rdar) colony morphotype. Whereas *E. coli* K-12 model strains express at most a rudimentary rdar morphotype at temperature below 30°C only [2, 3], clinical isolates have been shown to frequently form the rdar morphotype semi-constitutively at 30°C and body temperature [3-6].

Material/methods: The genomes of eight semi-constitutive rdar biofilm forming *E. coli* strains were sequenced with Illumina Miseq or PacBio sequencing and annotated with the NCBI prokaryotic genome annotation pipeline. Minimally passaged strains include strains isolated from human feces (three strains) [5] and human uropathogenic/urosepsis strains (four strains), ([6]; this study). Strain ECOR 31 isolated from leopard feces was obtained from the *E. coli* reference strain collection [7] and included as an historical strain.

Results: Genome size of the sequenced genomes was between 4.97 and 5.44 Mbp with a GC content between 50.5% and 50.9%. Number of genes is between 4886 (80//6) and 5328 (ECOR 31). Sequences were submitted to DDBJ/ENA/GenBank.

Conclusions: The sequenced genomes of semi-constitutive rdar morphotype expressing *E. coli* will shed light on the variability of the *E. coli* genome, in particular on the regulatory mechanisms of rdar biofilm formation.

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