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Maddalena Dilucca, Giulio Cimini, Andrea Giansanti



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## Essentiality, conservation, evolutionary pressure and codon bias in bacterial genomes

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**Abstract** Essential genes constitute the core of genes which cannot be mutated too much nor lost along the evolutionary history of a species. Natural selection is expected to be stricter on essential genes and on conserved (highly shared) genes, than on genes that are either nonessential or peculiar to a single or a few species. In order to further assess this expectation, we study here how essentiality of a gene is connected with its degree of conservation among several unrelated bacterial species, each one characterised by its own codon usage bias. Confirming previous results on *E. coli*, we show the existence of a universal exponential relation between gene essentiality and conservation in bacteria. Moreover, we show that, within each bacterial genome, there are at least two groups of functionally distinct genes, characterised by different levels of conservation and codon bias: i) a core of essential genes, mainly related to cellular information processing; ii) a set of less conserved nonessential genes with prevalent functions related to metabolism. In particular, the genes in the first group are more retained among species, are subject to a stronger purifying conservative selection and display a more limited repertoire of synonymous codons. The core of essential genes is close to the minimal bacterial genome, which is in the focus of recent studies in synthetic biology, though we confirm that orthologs of genes that are essential in one species are not necessarily essential in other species. We also list a set of highly shared genes which, reasonably, could constitute a reservoir of targets for new anti-microbial drugs.

**Keywords** Bacteria · Essentiality · Conservation · Selective pressure · Codon bias

M. Dilucca  
Dipartimento di Fisica, "Sapienza" University of Rome, 00185 Rome, Italy  
E-mail: maddalena.dilucca@roma1.infn.it

G. Cimini  
IMT School for Advanced Studies, 55100 Lucca, Italy  
Istituto dei Sistemi Complessi (ISC)-CNR, 00185 Rome, Italy

A. Giansanti  
Dipartimento di Fisica, "Sapienza" University of Rome, 00185 Rome, Italy  
INFN Roma1 unit, 00185 Rome, Italy

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