



Pneumonia-Specific *Escherichia coli* with Distinct Phylogenetic and Virulence Profiles, France, 2012-2014

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Auteur	La Combe, Béatrice [1], Clermont, Olivier [2], Messika, Jonathan [3], Eveillard, Matthieu [4], Kouatchet, Achille [5], Lasocki, Sigismond [6], Corvec, Stéphane [7], Lakhal, Karim [8], Billard-Pomares, Typhaine [9], Fernandes, Romain [10], Armand-Lefevre, Laurence [11], Bourdon, Sandra [12], Reignier, Jean [13], Fihman, Vincent [14], de Prost, Nicolas [15], Bador, Julien [16], Goret, Julien [17], Wallet, Frederic [18], Denamur, Erick [19], Ricard, Jean-Damien [20]
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Résumé en anglais	In a prospective, nationwide study in France of <i>Escherichia coli</i> responsible for pneumonia in patients receiving mechanical ventilation, we determined <i>E. coli</i> antimicrobial susceptibility, phylotype, O-type, and virulence factor gene content. We compared 260 isolates with those of 2 published collections containing commensal and bacteremia isolates. The preponderant phylogenetic group was B2 (59.6%), and the predominant sequence type complex (STc) was STc73. STc127 and STc141 were overrepresented and STc95 underrepresented in pneumonia isolates compared with bacteremia isolates. Pneumonia isolates carried higher proportions of virulence genes <i>sfa/foc</i> , <i>papGIII</i> , <i>hlyC</i> , <i>cnf1</i> , and <i>iroN</i> compared with bacteremia isolates. Virulence factor gene content and antimicrobial drug resistance were higher in pneumonia than in commensal isolates. Genomic and phylogenetic characteristics of <i>E. coli</i> pneumonia isolates from critically ill patients indicate that they belong to the extraintestinal pathogenic <i>E. coli</i> pathovar but have distinguishable lung-specific traits.
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Liens

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- [4] <http://okina.univ-angers.fr/matthieu.eveillard/publications>
- [5] <http://okina.univ-angers.fr/publications?f%5Bauthor%5D=7981>
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- [25] <http://www.ncbi.nlm.nih.gov/pubmed/30882313?dopt=Abstract>

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