



PRESS RELEASE

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High-tech consortium on track to seek out and destroy Europe's "superbugs"

10 APRIL 2010: The war against antibiotic resistance is now gaining momentum, as a consortium of 14 European institutes celebrates its first year of molecular scrutiny of the pathogens posing imminent health threats. The aim of the three year project is to exploit basic biological information to design novel, targeted strategies to control the emergence and spread of high-risk antibiotic-resistant bacteria. The TROCAR (Translational Research On Combating Antimicrobial Resistance) consortium was launched in Barcelona in February 2009 with funding from the European Commission Seventh Framework Programme under the patronage of the European Society of Clinical Microbiology and Infectious Diseases (ESCMID).

"With expertise ranging from medical microbiology to computational analysis, this network of excellence is on track to identify and target the resistant and multiresistant bacterial strains that pose the greatest health challenges in Europe", commented Giuseppe Cornaglia, Past President of ESCMID and professor at Verona University. "The results of this project could provide the scientific foundation for an early warning system such that new high-risk strains can be detected as soon as they begin to circulate in healthcare or community settings."

Antibiotic resistance is acknowledged to be one of the most serious public health threats facing Europe. Infections caused by resistant bacteria place severe social and financial burdens on European countries by causing serious, potentially untreatable illness and by complicating and lengthening hospital care for patients undergoing routine procedures. The spread of infections due to resistant bacteria from hospitals into the general population is an additional source of concern.

Efforts in recent years to stem the tide of "superbug" infections have focused on changing behaviour, such as reducing unnecessary antibiotic prescribing and increasing healthcare infection-control measures. Such approaches have resulted in some reassuring news: better infection-control policies in hospitals have stabilised or decreased rates of infection with the "superbug" methicillin-resistant *Staphylococcus aureus* (MRSA) in some European countries.

Nevertheless, MRSA remains a profound clinical and public-health challenge. In addition, many antibiotics are losing their effectiveness at an alarming rate due to the emergence of resistant strains of a range of bacteria. Alongside MRSA, the greatest impact is made by vancomycin-resistant enterococci (VRE), Gram-negative bacteria whose resistance to antibiotics results from their ability to produce certain enzymes (extended-spectrum beta-lactamases [ESBL] or metallo-beta-lactamases [MBL]), multidrug-resistant *Pseudomonas aeruginosa*, and multidrug-resistant *Acinetobacter baumannii*. Thus, these problem pathogens are the focus of TROCAR's activity.

The consortium's strategy comprises "work packages" of interdisciplinary research, drawing on expertise in the fields of medical microbiology, genomics and proteomics, molecular typing and population genetics, bacterial pathogenicity, and computational analysis.



The initial stage of TROCAR's work has been achieved. "During this first year of work, we have selected the specific bacterial strains disseminated throughout Europe that pose the most significant challenges to human health in the community and hospital settings", noted Professor Jordi Vila, TROCAR coordinator and professor at Hospital Clinic, Barcelona. He added that the strains have been sent to the TROCAR partners and genomics company, Sistemas Genómicos, which has started the process of sequencing.

TROCAR partner Roland Leclercq from the Université de Caen Basse-Normandie, explained how the isolates destined for gene sequencing were selected in the workpackage aimed at deciphering the action of vancomycin-resistant *Enterococcus faecium*. "With our colleagues from Germany (Guido Werner and Wolfgang Witte, Robert Koch Institute, Wernigerode Branch), we have chosen three isolates of *E.faecium*, two from Germany and one from France all belonging to a clonal complex CC17, a genetic subset of hospital-adapted strains. One was susceptible to antibiotics and was a commensal isolated from a patient's stools, the two others were multiply antibiotic resistant. One was responsible for a sporadic infection and the other caused a large outbreak."

Genomic and proteomic analysis will now be used to elucidate the parts of these high-risk pathogens' molecular make-up that enable them to spread, to cause severe disease, and to evade destruction by antibiotics. Data from the separate work packages will be brought together on a new bioinformatics platform, which will be used to exploit the genomics information and allow the rapid identification of emerging high-risk resistant strains in the future. In addition, it is intended that new bioinformatics tools will be developed to allow analysis of the data to detect differences between resistant strains in terms of epidemicity and propensity to persist in the human environment.

Future plans include making data on the distribution and migration patterns of high-risk antibiotic-resistant pathogens in Europe accessible on the internet.

(www.trocarproject.eu).

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