

Seventeen years of the CANWARD study (2007–23)

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The global crisis of infections caused by antimicrobial-resistant and MDR pathogens continues to increase worldwide.^{1–4} Numerous critical resistant pathogens are recognized, including Gram-positive organisms such as MRSA, both community-associated (CA-MRSA) and healthcare-associated (HA-MRSA), VRE and penicillin-resistant *Streptococcus pneumoniae* and Gram-negative pathogens such as ESBL-producing Enterobacterales, carbapenem-resistant Enterobacterales and MDR *Pseudomonas aeruginosa*.^{5–9} The greatest threat posed by these resistant pathogens is that treatment options can be severely limited, particularly if isolates demonstrate a MDR or XDR phenotype.^{3,10}

Of the various proposed solutions to this global problem of antimicrobial resistance, including infection prevention and control strategies, antimicrobial stewardship and development of new antimicrobials, surveillance has remained the core foundation.⁴ In 2007, we initiated the CANWARD study, which is an ongoing, national, Canadian Antimicrobial Resistance Alliance (CARA)/Health Canada-partnered, multi-year study focused on pathogens obtained from patients seeking care in Canadian hospitals.¹¹ The CANWARD study was designed to assess the epidemiology of pathogens and the degree of antimicrobial resistance within specific hospital wards (medical, surgical, intensive care units, emergency room and clinics) as well as specific infection sites (urine, blood, respiratory and wound). We previously published a CANWARD 2007–16 (10 year) supplement in the *Journal of Antimicrobial Chemotherapy*.^{11–18}

The current supplement documents 17 years of the CANWARD study (2007–23, inclusive). The eight manuscripts in this supplement provide a comprehensive examination of the causative pathogens of various infectious processes and their antimicrobial resistance patterns and trends over a 17-year period. It should be mentioned that the CANWARD study primarily used the North American-based CLSI standards methodology and breakpoint interpretations, not the European-based EUCAST standards. Although the CLSI and EUCAST standards have some differences in methodology and breakpoint interpretations, both are widely used and accepted internationally.^{19–21} The CANWARD data presented herein highlight the ongoing evolution of resistance and provide the current status of

antimicrobial resistance in Canada to healthcare professionals and researchers nationally and globally.

In the first paper, Zhanel *et al.*²² introduce CANWARD, describe the methodology of the study, laboratory protocols, and isolated Gram-positive pathogens with an overview of their susceptibility to various antimicrobials. A total of 25 897 Gram-positive pathogens were received, and antimicrobial susceptibility testing was performed on 22 132 isolates. Patient demographic data and 17 years of antimicrobial susceptibility data on Gram-positive pathogens commonly causing infections in patients attending Canadian hospitals are provided.

In the second paper, Zhanel *et al.*²² describe the evolution of Gram-negative pathogens with an overview of their susceptibility to various antimicrobials. A total of 34 155 Gram-negative pathogens were received and had antimicrobial susceptibility testing was performed. Patient demographic data and 17 years of antimicrobial susceptibility data on Gram-negative pathogens commonly causing infections in patients attending Canadian hospitals are provided.

In the third paper, Brahami *et al.*²³ assess the demographic and molecular characteristics of 12 734 community-associated (CA) and healthcare-associated (HA) MRSA genotypes in Canadian hospitals. They demonstrate that the overall proportion of MRSA decreased significantly from 2007–17 and then increased in 2023. CA-MRSA *spa* types increased while HA-MRSA decreased over the study period. The predominant MRSA *spa* types identified among all isolates were t002, a HA-MRSA genotype, and t008, a CA-MRSA genotype. PVL was detected in most CA-MRSA and very few HA-MRSA. MRSA isolates were ≥99% for ceftobiprole, dalbavancin, daptomycin, linezolid and vancomycin.

Adam *et al.*²⁴ compare the epidemiology and antimicrobial susceptibility patterns of 3111 *S. pneumoniae* collected from respiratory and blood culture samples in the fourth paper. They report significant differences in the serotypes isolated from blood culture and respiratory specimens and demonstrate lower antimicrobial susceptibilities and higher MDR rates in respiratory isolates compared to isolates from blood cultures. Serotypes 19A and 15A were predominant in the MDR/XDR isolates. A greater

proportion of isolates from blood cultures were serotypes covered by current pneumococcal vaccines.

In the fifth paper, Lagacé-Wiens *et al.*²⁵ assess the prevalence, antimicrobial susceptibilities and molecular characteristics of 11 931 ESBL-producing *Escherichia coli* and *Klebsiella pneumoniae* infecting patients receiving care at Canadian hospitals. The authors show that the prevalence of both ESBL-producing *E. coli* and *K. pneumoniae* increased significantly in Canada during the study period. Genotypic analysis showed increasing *bla*_{CTX-M-15} in *K. pneumoniae* and *bla*_{CTX-M-27} in *E. coli*. Other β -lactamases including *bla*_{OXA-1} and *bla*_{TEM-1} were associated with first-generation β -lactam/ β -lactamase inhibitor combination resistance.

Mataseje *et al.*²⁶ report on their analysis of 134 (0.7% of all Enterobacterales) ertapenem-resistant Enterobacterales in the sixth paper. Carbapenemase-producing Enterobacterales (CPE) accounted for only a small proportion of ertapenem-resistant isolates and were predominantly KPC-producing *K. pneumoniae* and *E. coli*. Most non-CPE ertapenem-resistant isolates were *Enterobacter cloacae*. CPE isolates demonstrated higher prevalence of resistant values for multiple antimicrobial classes and harboured more antimicrobial resistance genes than non-CPE isolates.

In the seventh paper, McCracken *et al.*²⁷ characterize 371 (21.5% of all *P. aeruginosa*) carbapenem-resistant *P. aeruginosa*. Only 0.8% of the carbapenem-resistant isolates harboured a carbapenemase gene. Whole genome sequencing identified substitutions that have been associated with dysfunction of porin protein OprD, or MexAB-OprM efflux and AmpC overexpression. They report that genetic evidence indicates that clonal dissemination of high-risk clones is occurring in Canada and that these high-risk clones are virulent and often MDR.

In the final paper, Walkty *et al.*²⁸ report on their characterization of 26 067 bloodstream isolates of which the five most common pathogens were *E. coli*, *Staphylococcus aureus*, *K. pneumoniae*, *Staphylococcus epidermidis* and *S. pneumoniae*. They report little variation in pathogen distribution over time; however, some resistant phenotypes (e.g. ESBL-producing *E. coli*, ESBL-producing *K. pneumoniae* and VRE) are being encountered more frequently in recent years.

The CANWARD data described in this supplement discuss resistance patterns by ward type, infection process, patient demographics and time assisting both clinicians and researchers in critically assessing the current status of hospital pathogens in Canada today. From a global perspective, the CANWARD study allows comparisons between countries. CANWARD continues to advocate that surveillance programmes allow us to 'think globally, act locally' and provides important information to our continued understanding of antimicrobial resistance. Global and national surveillance studies such as CANWARD can assist in determining antimicrobial resistance trends over specific age groups, geographic areas, time for a variety of infectious syndromes and pathogens and allow comparisons between countries.

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