

Virtually all practices had a computer (79 [99%] of 80), Internet access (70 [88%] of 80), and email (53 [75%] of 71). Most (68 [91%] of 75) were comfortable using a Web-based application to submit case reports. However, because Internet access and email may not be universal, multiple modes of communication must be utilized. Furthermore, of 81 respondents, 29 (36%) indicated lack of time, and 24 (30%) indicated lack of staff as a barrier to online reporting. Therefore, the reporting system should be efficient.

Rabies, bovine tuberculosis, and West Nile virus, all zoonotic diseases, were listed by >50% of the 79 respondents as 1 of the 6 diseases they felt were most important in Michigan. Simultaneous tracking of human and animal diseases was considered useful by 32 (84%) of 38 respondents because animals are sentinels of human (zoonotic) disease and by 7 (18%) respondents because of the threat of agroterrorism. In general, respondents are aware of the importance of animal disease reporting to public health.

In Michigan, the human and animal disease reporting systems are similarly structured, although there is no local level animal health agency (Figure). These similarities can provide the basis for a system that is functionally appropriate to track diseases in humans and multiple animal species and meet multiple agency surveillance objectives.

Overall, this group of Michigan veterinarians considers developing a Web-based disease reporting system as useful as long as the following issues are addressed: 1) quality case report feedback; 2) access to correct and coordinated human and animal disease information; and 3) computer system reliability and efficiency. Based on the results of this study, the second phase of this project, construction of the animal disease surveillance portion of Michigan's reporting system, will be implemented with continued input from local, state, and federal stakeholders.

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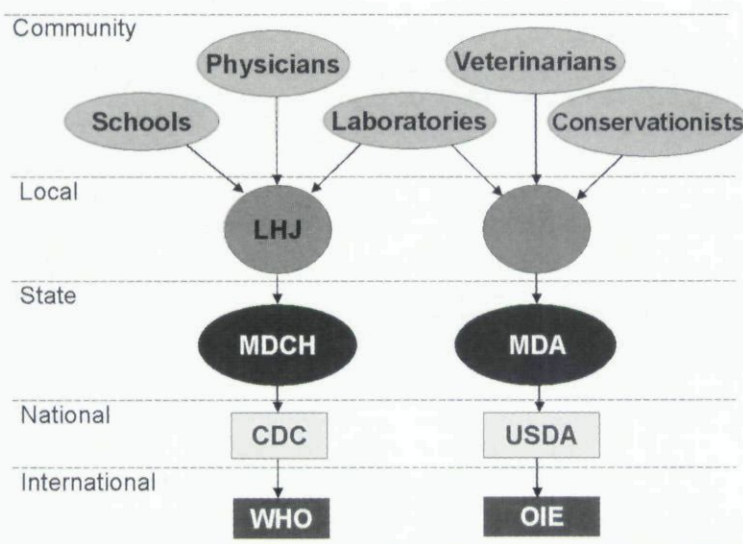


Figure. Comparison of Michigan human and animal disease reporting system structures. LHJ, Local Health Jurisdiction; MDCH, Michigan Department of Community Health; CDC, Centers for Disease Control and Prevention; WHO, World Health Organization; MDA, Michigan Department of Agriculture; USDA, US Department of Agriculture; Animal Plant Health Inspection Service, Veterinary Services; OIE, Office International Epizooties.

VanB-VanC1 *Enterococcus gallinarum*, Italy

To the Editor: We report detecting a *vanB* determinant in *Enterococcus gallinarum* in poultry in Italy. High-level *vanA*-mediated glycopeptide resistance has been described for *E. gallinarum* and *E. casseliflavus* (1–4), and *vanB*-mediated vancomycin resistance has been frequently described for *E. faecalis* and *E. faecium*. However, *vanB*-mediated resistance in isolates of *E. gallinarum* has been described only in sporadic nosocomial cases of infection or colonization (5,6).

In January 2005, a study of contamination by foodborne organisms in

slaughtered broiler carcasses was conducted in Sicily. To detect glycopeptide-resistant enterococci (GRE), each carcass was placed in a bag with 100 mL sterile buffered peptone water and shaken vigorously for 60 sec. After overnight incubation at 37°C, 0.5 mL rinsate was added in duplicate to 5 mL ethyl violet azide broth (Oxoid, Basingstoke, United Kingdom) with 4 mg/L vancomycin. Broth cultures were further incubated at 37°C for 48 h, and 0.1 mL aliquots were spread onto duplicate plates of VRE (commercial denomination product, Oxoid) agar.

A vancomycin-resistant isolate of *E. gallinarum* was identified in a carcass from a broiler farm in eastern Sicily. The biochemical tests of API 20 Strep (bioMérieux, Marcy l'Etoile, France) and motility test at 30°C were used to characterize the isolate at the species level. The MICs of vancomycin and teicoplanin were 64 µg/mL and 1 µg/mL, respectively. The isolate was subjected to a multiplex polymerase chain reaction followed by an endonuclease cleavage of amplicons by *MspI* (Invitrogen, Carlsbad, CA, USA) as previously described (7) to detect *van* gene determinants; this process demonstrated a simultaneous presence of *vanC1* and *vanB* determinants.

E. gallinarum and the other motile enterococci are thought to infrequently cause infection. However, the recent involvement of *vanC1-vanA E. gallinarum* in person-to-person spread in a long-term-care facility (8) and in an intensive care unit (2), along with identification of *vanC1-vanB* isolates in some patients treated with prolonged courses of glycopeptides (5,6), suggests reassessment of their possible pathogenic role.

For the first time, 1 isolate of *E. gallinarum* has been found harboring the *vanB* gene in poultry. Our findings confirm that *E. gallinarum* can capture the genetic determinants of high-level glycopeptide resistance, proba-

bly under selective pressure conditions that do not permit survival of a host organism with constitutive low-level resistance (3). Previous studies have demonstrated that *E. gallinarum* can transfer these determinants to *E. faecium* by conjugation (2).

The role of food animals as reservoirs of GRE and the causes of their persistently high prevalence in poultry carcasses in some European countries are being investigated (9). Moreover, the public health risk associated with consumer exposure to GRE when handling raw animal foods is poorly understood. In Europe, the food chain is thought to be the major source of GRE since avoparcin was used as a food additive for animals until the European Union ban in 1997. Previous studies in Italy showed that avoparcin withdrawal successfully reduced GRE contamination of poultry meat products (10). However, our finding, 7 years after the European Union ban, highlights that resistance genotypes in motile enterococci should be closely monitored (11).

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