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bioMérieux connection

In this issue:

Now shipping: next-generation VIDAS® and miniVIDAS®

Redesigned with a new, modern look, bioMérieux's next-generation VIDAS® and miniVIDAS® immunoassay analyzers are now available. These new instruments are based on the same time-tested, "load and go" single-dose SPR-strip platform that laboratorians have trusted for years. We've added new features for improved reliability, workflow and security.

Both instruments have a new strip-holder prep drawer underneath the reaction sections, offer secured access to the SPR section, include a barcode reader, and allow easier access for maintenance. The larger VIDAS 30 instrument also features bioMérieux's new VIDAS PC system that provides flexible management of workflow and patient files, reliable quality control, and increased security. VIDAS PC's colorful monitor uses a user-friendly graphic interface.

Your local bioMérieux representative will be happy to give you more information.

VRSA Coming soon!

bioMérieux's Research & Development Department has developed a VITEK® 2 VRSA Screening Test that will be incorporated on VITEK 2 Gram positive susceptibility cards. U.S. Food and Drug Administration (FDA) submission and clearance are pending. We estimate that this test will be available in the summer of 2006 and will update you with further developments.

BIOMÉRIEUX

from diagnosis,
the seeds of better health

Realizing the potential of computerized 'expert' systems for interpreting antimicrobial susceptibility testing data

Charles P. Cartwright Ph.D.
Asst. Professor of Pathology & Laboratory Medicine
Asst. Professor of Medicine
University of Minnesota Medical School
Director of Microbiology
Hennepin County Medical Center, Minneapolis, MN

The process of determining the susceptibility of pathogenic bacteria to antimicrobial agents has remained remarkably unchanged in the several decades since standardized testing methods were first developed. A qualitative or quantitative assessment of the effect of a selection of clinical useful antimicrobial agents against a particular organism is performed, and the results obtained converted into interpretive categories (S, I, or R) by following the recommendations of a suitable guidance document before the completed antibiogram is conveyed to the clinician.

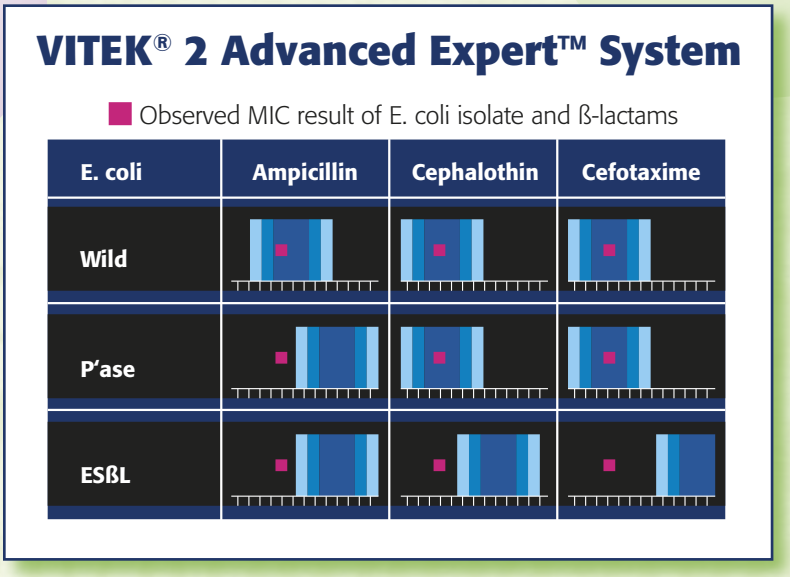
The stasis of this testing paradigm is in marked contrast to the dynamic changes that have occurred over the same time period in areas that directly impact the effectiveness and desirability of this approach. The sheer number, as well as the biological spectrum and mechanism of action, of antimicrobial agents has increased exponentially, accompanied by an equally impressive increase in the frequency and complexity of acquired antimicrobial resistance mechanisms encountered in many commonly isolated pathogens. These developments have made maintaining the validity of the simplistic 'drug vs. bug' approach increasingly difficult, and have required the generation of evermore complex testing and reporting guidelines. At the same time, major advances in biochemical and molecular biological research have made it possible to determine the underlying genotypic and phenotypic mechanisms of acquired antimicrobial resistance with increasing speed and precision. Although almost 20 years elapsed between the first description of penicillin-resistance in the 1940's and the elucidation of the mechanism of action of the staphylococcal penicillinase, the basis of vancomycin resistance in *Staph. aureus* was recently determined only a matter of weeks after the first isolate was reported. Our expanding knowledge of the genotypic and phenotypic basis of antimicrobial resistance opens up the enticing possibility of basing susceptibility testing on discernment of resistance mechanisms and extrapolation of their clinical significance rather than the traditional approach of determining an *in vitro* surrogate of *in vivo* activity for each clinically useful compound. Finally, the innumerable advancements in information technology have made computer-driven analysis, interpretation and transmission of clinical laboratory data the norm rather than the exception. The exploitation of information technology to enable our understanding of the mechanisms of antimicrobial resistance to be incorporated into the routine process of reviewing, interpreting, correcting and releasing data surely represents the future direction of antimicrobial susceptibility testing.

In its simplest form, identifying resistance mechanisms from susceptibility test results and then using such information to detect erroneous or misleading test results is already used to by all laboratories. An example of this is the suppression of all beta-lactam drugs if a staphylococcal isolate is determined to be resistant to oxacillin. The necessity for some form of interpretive review of results is also universally accepted. The prerequisites for this approach to work on a broader basis are firstly that organisms be identified accurately and that organism identity be linked to interpretation of susceptibility test results, secondly that both the number and type of antimicrobials tested provide sufficiently probative information for resistance mechanisms to be discerned from the results obtained (i.e. that sufficient key indicator antimicrobials are tested) and thirdly, and most importantly, that standardized interpretive rules for identifying patterns of resistance consistent or inconsistent with organism identifications are developed and applied. Software applications designed to assist with such interpretative analyses of susceptibility test results have for some time been an almost universal feature of commercial testing systems.

Most commercial, first-generation, 'expert review' applications have been designed to essentially mimic the approach taken by human reviewers of susceptibility test results, and this severely constrains their potential utility. Quantitative analytical data (i.e. MIC values) generated by the susceptibility test systems that these

software packages are linked to is typically bypassed, and only the interpretive categories into which results are placed are scrutinized. While this is often necessary to make manual results review manageable, and to enable the same interpretive decision making process to be used with qualitative and quantitative test systems, it markedly decreases the interrogative sensitivity of any 'expert' software program. Simply put, if significant differences in the MIC distribution frequencies for certain antimicrobials occur that, although they correlate with the presence of a given resistance mechanism, fail to result in a change in the categorical interpretation of those MIC results, the potential presence of such resistance will pass undetected by the expert. Detection of certain ESßL-producing organisms is an excellent example of this phenomenon, as is inducible clindamycin-resistance and vancomycin-resistance in *Staph. aureus.* First generation 'expert' systems are also typically designed to look only for markedly aberrant results in certain key 'indicator' antimicrobial agents by the application of rules employing simple conditional logic, i.e. IF antibiotic X is R, THEN antibiotic(s) Y and/or Z could/should also be R. This approach is useful in certain limited situations where an alteration in the interpretive category of a key drug is only ever attributable to a single resistance mechanism and always carries the same implications for other antimicrobials on the panel (intrinsic resistance to aminopenicillins in *Klebsiella pneumoniae* for example), but is of little value in situations where multiple different mechanisms can have the same effect on the indicator drug while impacting other drugs in markedly different ways. Given the increasing complexity of antimicrobial resistance mechanisms for certain drug classes and organisms (e.g. beta-lactams and *Enterobacteriaceae*) this situation is becoming commonplace, and thus the specificity of first generation 'expert' systems is often less than optimal. Finally, and perhaps most importantly, because only the results of certain indicator drugs trigger the 'firing' of the aforementioned conditional rules, the global validity of antimicrobial test results is not assessed. A biologically implausible result for a given antimicrobial that fails to impact one of the conditional rules is, therefore, only detected upon manual review of all test results by a human expert. First generation 'expert' systems thus provide only limited, largely adjunctive, assistance to the technologist, are defined by and operate entirely within the historical paradigm of susceptibility testing, and provide no real framework for future development.

The VITEK® 2 Advanced Expert™ System (AES) represents a radical departure from first-generation 'expert' systems in that it is not designed to duplicate the historical approach to reviewing susceptibility test results but rather to utilize a novel approach that maximally exploits the information gained about an organism when quantitative testing of a large panel of antimicrobial agents is performed. In brief, the AES consists of a large database of MIC value distributions for each antimicrobial agent and organism that can be tested and identified on its companion system (VITEK 2 and related instruments). Each MIC distribution is further delineated in the database by the particular corresponding antimicrobial resistance phenotype. Thus, for example, there are multiple MIC distributions in the database for E. coli and ampicillin, each of which corresponds to a different resistance phenotype for this pairing of organism and antimicrobial agent (e.g. wild-type, acquired penicillinase, ESßL etc). When a susceptibility assay is finalized by the analytical testing system (VITEK 2), every MIC value determined in that test is used to interrogate the AES database to match the obtained results with expected results for antimicrobial resistance phenotypes potentially present in that particular organism. Upon completion of this analysis, a report is generated that lists the most probable phenotypes for each drug class or sub-class tested, in essence a 'virtual phenogram'. Only when this process has been completed, and each test result determined to be consistent with a recognized phenotype, are the results converted into interpretive categories and reported. The AES represents, therefore, the first attempt to move toward replacing conventional 'bug vs. drug' testing with an approach that seeks to discern underlying resistance mechanisms present in organisms and then extrapolate the utility, or lack thereof, of clinically indicated agents from resultant composite phenotypes. This system does not disregard the analytical data generated by quantitative testing systems in favor of simplistic S, I, or R designations, but exploits the added layer of information provided by MIC values, so that even if expression of a resistance mechanism changes the MIC frequency distribution of a drug or drugs on the testing panel entirely within a single interpretive category the phenotype associated with that change can still be identified. Furthermore, results generated for every drug



Realizing the Potential of Computerized 'Expert' Systems, continued on page 7.

VITEK® 1 & VITEK® 2 software updates coming soon

bioMérieux is committed to delivering annual software updates to VITEK® 1 and VITEK® 2 users. Software updates contain a variety of modifications and improvements for the VITEK 1 and VITEK 2 systems. For example, software updates may contain:

- Firmware updates that will improve instrument reliability
- Analysis software for new antibiotics
- Analysis software to improve a current antibiotic's performance
- Analysis changes for ID cards
- An update to the Expert rules or Advanced Expert™ System (AES) database
- Software bug fixes

New antibiotics in the software may be pending clinical trials and FDA clearance. By delivering the antibiotic in the software pre-FDA clearance, bioMérieux can quickly deliver the antibiotic on new cards once it is cleared by the FDA. This allows us to shorten the delivery time for new antibiotics.

VITEK 1 Software Version 10.01 shipments have already begun. This software update provides several enhancements to improve workflow and enhance reporting capabilities. There will be:

- M-39 compliance with regard to duplicate-free antibiograms
- Daptomycin reporting capabilities. This antibiotic will be available on GPS cards in the 2nd quarter of 2006*. Daptomycin provides physicians with an additional choice with which to treat infections due to increasingly problematic and resistant *Staphylococcus aureus* infections (both methicillin sensitive and methicillin resistant).
- Taxonomy modifications for Gram negative species to reflect current scientific nomenclature
- Updated quality control ranges
- New VITEK Expert System™ rules added to clarify antibiotic reporting and nomenclature changes

Please contact your Customer Service Representative to request your copy of Version 10.01 if it has not yet arrived in your laboratory. Remember that this update is only suitable for VITEK 1 users with CC2 and higher computers.

You get SXT with this update!

VITEK 2 Software Version 4.02 will be available December 2005. This much-anticipated software provides:

- SXT reporting capabilities for *Staphylococcus aureus*. A new VITEK 2 card – the AST-GP63 card will be required to report SXT. After you have installed the 4.02 software, contact your Customer Service Representative to order the AST-GP63 card (product number 22101).
- The Cefoxitin Screening Test.* This will be on VITEK 2 GPS cards in the 2nd quarter of 2006.
- Daptomycin reporting capabilities. VITEK 2 cards with this antibiotic will be available in the 2nd quarter of 2006.
- M-39 compliance with regards to duplicate-free antibiograms.
- Firmware and software modifications that will improve the reliability of the instrument.
- The software analysis for the NH card (for speciation of Neisseria, Haemophilus and other fastidious organisms) will be included in Version 4.02. The NH cards will be available in the 1st quarter of 2006.
- An additional 31 phenotypes were added to the AES database, including newly described resistance mechanisms for specific species.

VITEK 2 AST-GP63 22101 Gram positive
Ampicillin
Ciprofloxacin
Clindamycin
Erythromycin
Gatifloxacin
Gentamicin
Gentamicin High Level Synergy
Levofloxacin
Linezolid
Moxifloxacin
Nitrofurantoin
Oxacillin
Penicillin
Quinupristin/Dalfopristin (Synercid)
Rifampin
Streptomycin High Level Synergy
SXT (Trimethoprim-sulfamethoxazole)
Tetracycline
Vancomycin

*Pending successful clinical trial, submission and clearance by the FDA

Why pharmacists back STELLARA™: an interview with J. Kelly Martin, Pharm.D.

J. Kelly Martin, Pharm.D., is the regional pharmaceutical care manager for the Franciscan Health System in Tacoma, Washington. He is also a clinical assistant professor at the University of Washington School of Pharmacy. Recently, Dr. Martin evaluated the usefulness of bioMérieux's STELLARA™ clinical intervention and patient monitoring software, powered by TheraDoc®. He explains his findings in the following interview with the *bioMérieux Connection*.

bioMérieux Connection: Where did you perform your evaluation of the STELLARA system?
Dr. Martin: At St. Joseph Medical Center in Tacoma, Washington. St. Joseph is a member of the Franciscan Health System with 330 beds. It's generally cited as one of the top 100 hospitals in the United States.

bioMérieux Connection: Why did you perform the evaluation?
Dr. Martin: It was part of our ongoing effort to deliver the best patient care through patient safety initiatives. We decided recently that we should implement an intelligent patient therapy management system. STELLARA seemed to fit the requirements.

bioMérieux Connection: Was there a particular impetus behind the move to intelligent patient therapy management?
Dr. Martin: Yes, ADEs – adverse drug events.

bioMérieux Connection: You've said that adverse drug events not only endanger lives but also lead to a significant waste of time and money. Can you expand on that?
Dr. Martin: Studies appearing in the *Journal of the American Medical Association* and the *American Journal of Health-System Pharmacy* show that adverse drug events add between $2,200 and $4,000, on average, to the cost of a hospital stay. The Alliance for Pharmaceutical Care has demonstrated that correcting drug errors adds $1.60 to every dollar spent on medication in the U.S.

bioMérieux Connection: The hospital had used another bioMérieux system to help reduce ADEs. Tell us about that.
Dr. Martin: We carried out a two-and-a-half-year project using the TheraTrac® 2 system. When the technology was upgraded to a Web-based application platform with advanced functionality, we were asked to participate in clinical trials to see if the success we'd had with TheraTrac could be improved upon with STELLARA.

bioMérieux Connection: In a nutshell, can you tell us what STELLARA is?
Dr. Martin: It's clinical intervention and patient monitoring software that provides knowledge-enriched, infectious-disease specific recommendations to clinicians for medication treatment management based on individual patient profiles, integrated lab results and hospital formularies.

bioMérieux Connection: What are the differences between TheraTrac and STELLARA?
Dr. Martin: We found that STELLARA provided more depth, versatility and mobility via PDAs and laptop PCs. Also, STELLARA gave us real-time connectivity with the hospital's pharmacy systems and other bioMérieux systems, such as BacT/ALERT® and VITEK®. STELLARA has given us a more complete view of the patient that includes all results provided by the laboratory information system. STELLARA can also access the Internet for reference citations associated with therapy or best-practice recommendations. The software can even provide up to 90 automatic alerts, such as when a drug interaction is likely, and that increases the opportunity for timely intervention, decreasing the chance of an ADE.

bioMérieux Connection: That's impressive at the individual patient level. Does STELLARA have a role in the larger picture of infection control and antibiotic management?
Dr. Martin. Definitely. With STELLARA, our clinicians have access to data across the hospital or health system. They can identify trends in bacteria and antibiotic susceptibility and resistance in the local environment.

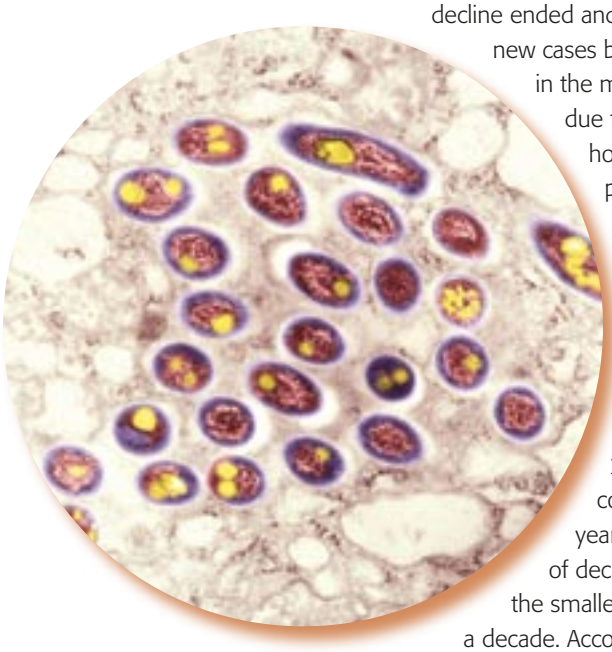
bioMérieux Connection: Is STELLARA a one-size-fits-all system?
Dr. Martin: Not at all. STELLARA comes in four levels – called étages – that provide four levels of functionality.

bioMérieux Connection: How do the four étages differ?
Dr. Martin: Étage 1 is a stand-alone PDA application. It combines the system's Antibiotic Wizard™, which is an integrated infectious disease knowledge base using the institution's own antibiograms and antibiotic formulary, and the Dose Assistant™, which is an antibiotic intervention tool that also uses the institution's formulary. This étage also allows aggregation of patient data on a HIPAA-compliant web server, antibiotic intervention documentation, actionable results for optimizing antibiotic medication management and handheld software downloaded from a user-specific website.

Why Pharmacists Back STELLARA, continued on page 8.

Mycobacteria

Tuberculosis (TB) is one of the oldest recorded human afflictions and is still one of the biggest killers among infectious diseases. Tuberculosis morbidity and mortality rates continued to decline in the 20th century in the developed world, thanks to better public health measures, vaccines, and the development of antibiotics. However, this decline ended and numbers of new cases began to increase in the mid-1980s due to increased homelessness and poverty in the developed world and to the emergence of AIDS.[1] US rates of tuberculosis reached an all-time low in 2004; however, compared with years past, the rate of decline was one of the smallest in more than a decade. According to the Centers for Disease Control and Prevention's (CDC)'s latest data from the National TB Surveillance System, there were 14,511 TB cases reported in 2004. The overall case rate – 4.9 per 100,000 people – was the lowest ever recorded since 1953, when national reporting began. While the decline in case rate from year to year has decreased on average 6.8%, between 2003 and 2004 the decline was only 3.3%.[4]



Outside of the US, cases are concentrated in Southeast Asia - more than half of the cases in the world are in India, Pakistan, Bangladesh, Indonesia and the Philippines. Already, TB cases are increasing 10% per year in Africa because of HIV. There were nearly 2 million new TB cases in Africa in 1999, with two-thirds of those also infected with HIV. Experts estimate that the number of TB cases in Africa will reach 3.3 million by 2005 and surpass 4 million shortly thereafter.[4]

Even while the incidence of tuberculosis fell, the incidence of nontuberculosis Mycobacteria became more prevalent. Before the AIDS epidemic, disease caused by nontuberculosis Mycobacteria was pulmonary, confined to cervical lymph nodes, limited to the skin, or in rare cases, disseminated. After the AIDS epidemic, the situation became very different with up to 25 to 50% of AIDS patients in the US and Europe being infected with nontuberculosis Mycobacteria.[2]

Mycobacteria tuberculosis, the causative agent of tuberculosis, is most commonly isolated from respiratory specimens. Most TB infections are initiated by the respiratory route of exposure.[1] The most common nontuberculosis Mycobacteria isolated in the clinical laboratory is Mycobacteria avium. Other Mycobacteria sometimes isolated include M. kansasii, M. marinum, and M. intracellulare. These bacteria, especially in AIDS and immunocompromised patients, may be disseminated and can be isolated from a variety of specimens including blood.[2]

Isolation of Mycobacteria is often difficult for the laboratory due to safety requirements, difficulty in culling the Mycobacteria from other organisms normally present in specimens such as sputum, and the exceptionally long growth period required for the organism isolation. Specimens such as sputum, urine, and stool must be digested and decontaminated before inoculation onto Mycobacteria culture media.

The BacT/ALERT® microbial detection system, in addition to testing blood and sterile body fluid (SBF), and platelet sterility testing, also allows culturing for Mycobacteria from various specimen types. The Mycobacteria blood (MB) bottle is available for Mycobacteria testing from blood specimens. The Mycobacteria Process (MP) bottle is available for testing other specimens including SBF and those specimens requiring a decontamination/digestion procedure before inoculation.

The BacT/ALERT MB bottle was designed to recover Mycobacteria from blood. The bottle contains 29 ml of Middlebrook 7H9 media, supplements to enhance growth, SPS to prevent clotting of blood, and a lysing agent to lyse red blood cells and release intracellular organisms. Decontamination/digestion is not required when culturing blood in the MB bottle.

The MP bottle was developed to recover Mycobacterium from specimens other than blood. The MP bottle, with a removable closure, contains 10 ml of Middlebrook 7H9 media in an atmosphere of CO_2 nitrogen, and oxygen. Use of the MP bottle may often require decontamination and digestion of the specimen before the bottle is inoculated. Many specimens submitted for isolation of Mycobacteria, such as sputum and gastric lavage, contain mucus. Mycobacteria, as well as contaminating flora, are often present but trapped within the mucus. Liquefaction is achieved by adding chemicals which, when vortexed with the specimen, break down the mucus and release the organisms. Most specimens received for culture of Mycobacteria also contain various amounts of organic debris and a variety of contaminating, normal, or transient bacterial flora. The chemical decontamination process usually kills these bacteria while allowing recovery of the Mycobacteria. The high lipid content of the acid-fast

bacillus cell wall makes the Mycobacteria more resistant to both the acid and alkaline decontaminating agents. However, reagents used in this process can be toxic to the Mycobacteria as well as the contaminating flora. A balance must be found to maximize the elimination of the contaminating flora, and minimize the killing of the Mycobacteria.[3] Strict adherence to the timed killing period is necessary to maximize recovery.[5]

Sodium hydroxide, the most commonly used decontaminant, also serves as a mucolytic agent but must be used cautiously because it is only somewhat less harmful to tubercle bacilli than to the contaminating organisms. The stronger the alkali, the higher its temperature during the time it acts on the specimen. The longer it is allowed to act, the greater will be the killing action on both contaminants and Mycobacteria.[6] After decontamination, the specimen is inoculated into the MP bottle and the bottle is subsequently incubated in the BacT/ALERT incubator.

In addition, Mycobacteria Antibiotic Supplement (MAS) is added to the MP bottle to reduce the occurrence of breakthrough contamination. This antibiotic supplement contains 6 antibiotics to inhibit the growth of normal bacterial flora. Prior to inoculation with specimen, 0.5 ml should be added to each MP bottle. Once the specimen is inoculated into the bottle, gently inverting the bottle several times assures maximum performance by effectively mixing the specimen with the MAS.

There are many processing methods and commercial reagents in use around the world and most are acceptable for use with the BacT/ALERT MP Process bottles. Regardless of the method used, however, the most critical steps are:

1. Decanting completely after centrifugation
2. Re-suspending the pellet in sterile 0.067M phosphate buffer, pH 6.8
3. Establishing a neutral pH of the re-suspended pellet
4. Using no more than the recommended 0.5 ml MAS per bottle

For further information about Mycobacteria testing with the BacT/ALERT 3D, please contact your local bioMérieux representative or visit us at www.biomerieux-usa.com

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3. Mandell, G L, et al., Principles and Practices of Infectious Diseases, ed. 6, p. 224 – 228.
4. http://www.infectiousdiseasenews.com/200504/frameset.asp
5. Cernoch, P L; Enni, R K; Saubolle, M A; Wallace, R J; Weissfeld, AS (ed); Laboratory Diagnosis of the Mycobacterioses; Cumulative Techniques and Procedures in Clinical Microbiology. Washington D.C., American Society of Microbiology 1994, p. 8.
6. Pfyffer, G E; Brown-Elliott, B A; Wallace, R J; Murray, P R; Baron, E J; Pfaller, M A; et al. (ed); Mycobacterium: General Characteristics, Isolation, and Staining Procedures; Manual of Clinical Microbiology. Washington D.C., American Society for Microbiology, 2003, ed. 8, p. 544.

Realizing the Potential of Computerized 'Expert' Systems, **continued from page 3.**

on the panel are analyzed, thus subtle variations in patterns of MIC values that help distinguish different resistance phenotypes can also be discerned, markedly improving the specificity of categorization over that of first generation systems. Perhaps even more importantly, the requirement that each drug tested yields a result compatible with a known resistance phenotype means that by default each and every susceptibility test is analyzed by AES for its biological validity, enabling perfectly acceptable results, in addition to potential testing errors and highly unusual results, to be identified without the rate-limiting requirement of human intervention.

Some significant issues remain to be resolved, however, before the full potential of systems such as the AES can be realized. The limitations of the technology currently used to generate antimicrobial susceptibility data are considerable, and this significantly impacts the scope of post-analytic analyses.

For expression of acquired resistance mechanisms to be detected by AES or similar applications, changes in MIC frequency distribution for one or more drugs on the testing panel of sufficient scale to enable differentiation from other valid phenotypes must occur. It may well be that the ideal drugs for differentiating resistance phenotypes in this way are not typically used clinically, or that the useful MIC range for detecting a particular phenotype is beyond that used to assign conventional interpretive breakpoints. Maximizing the utilization of AES-type constructs is, therefore, a considerable challenge when the input data is generated by test systems engineered to function using the current testing paradigm where generating MIC values around approved breakpoints on clinically useful antimicrobials is adequate. The second issue is the pervasiveness of the concept that the conventional 'drug vs. bug' approach to susceptibility testing is the only legitimate one, and must be preserved as the de facto gold standard in perpetuity. It is my opinion that a strong belief in the conventional approach to testing stifles the investigation of creative approaches to improving test performance. Fortunately, our burgeoning ability to determine the genetic basis for resistance has already begun to challenge this view. I believe that all microbiologists would now concede that direct detection of the mecA gene has supplanted conventional susceptibility testing as the optimal technique for identifying methicillin-resistant staphylococci. While complete genotypic determination of antimicrobial resistance in the routine laboratory remains only a remote possibility, even in the medium to long term, elucidation of phenotypic manifestations of acquired resistance genes, via computational analysis of MIC results, using systems like the AES is very much within the realm of possibility in the immediate short term. In my opinion, the availability of computerized data analysis systems like the AES affords us an irresistible opportunity to undertake the most significant examination of how antimicrobial susceptibilities could and should be determined since the first tentative standards for testing were proposed well over forty years ago.

Why Pharmacists Back STELLARA, continued from page 4.

bioMérieux Connection: How do you improve on that?

Dr. Martin: With Étage 2, 3 and 4. For example, Étage 2 gives you all the features of Étage 1 but adds a desktop and PDA application with secure access from any web browser. It also features four automated microbial alerts and the ability to export data to desktop software applications.

bioMérieux Connection: What about Étage 3 and 4?

Dr. Martin: Étage 3 gives you 25 more pre-programmed alerts plus antibiotic intervention recommendations with decision logic and references, individualized patient rosters and a wireless PDA option. Étage 4 has 90 pre-programmed alerts and alert subscription management.

bioMérieux Connection: So how did the trial go?

Dr. Martin: We chose STELLARA for our patient monitoring software in all three of our system's hospitals. We found the system aligns with Franciscan's primary and secondary initiatives for reducing ADEs and improving patient safety, managing related costs, such as those associated with medication management, IV-PO switching, appropriateness of antimicrobial therapy regimens, and reducing length of stay.

bioMérieux Connection: How does STELLARA fit with today's emphasis on pay for performance?

Dr. Martin: STELLARA software will be important to creating better records for our health system, and that's critical in a pay for performance environment. Already our clinical interventions increased 9 percent just between December 2004 and February 2005, compared to the same period a year earlier. But our census was up only 2 percent. That's a real increase in clinical interventions and it's a direct result of STELLARA's ability to identify additional opportunities for pharmacists to make interventions.

Meet the BacT/ALERT® customer service representatives

Our customer service representatives are ready to serve you.

Back row: Art Laperre (SE), Robert Dyke (SE), Joe GIllmore (SE), Mike Stefan-Donovan (SE), Suzanne Dameron (AS), J.R. Holmes (SE) and Danny Woodward (SE).

Middle row: Shannon Lewis (SE), Dale Moore (SE), Tracy Williams (SE) and James Rice (SE).

Front row: Denise Campbell (SE), Marie Snyder (AS), Stephanie Vick (AS), Rhonda Choquette (SE) and Patti Katsikis (AS).

AS = Application Specailist
SE = System Engineer

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