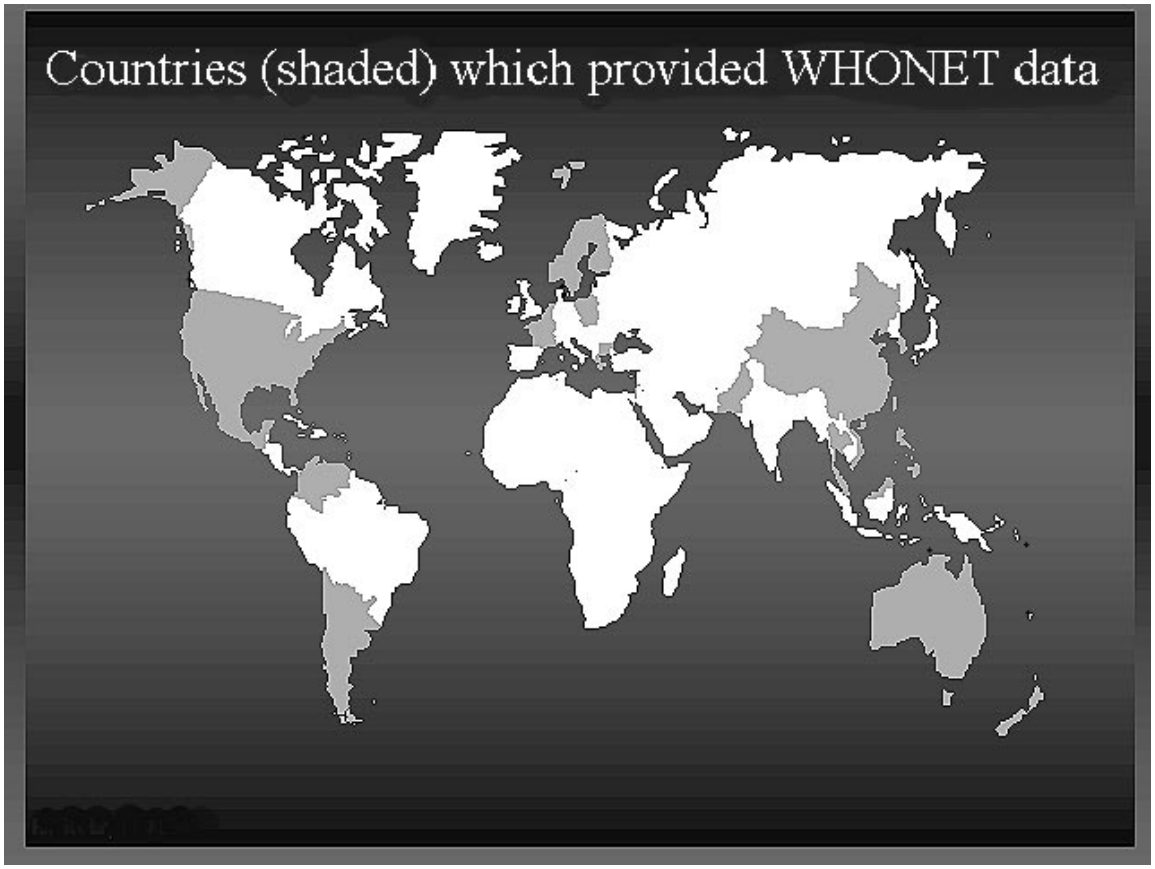
NETWORK ON ANTIMICROBIAL RESISTANCE MONITORING

Adapted from World Health Organization world wide web site (http://www.who.ch/programmes/emc/) Emerging and Other Communicable Diseases Surveillance and Control Programme (EMC).



With the establishment of the Division of Emerging and other Communicable Diseases Surveillance and Control, World Health Organization (WHO) will strengthen national and international capacity in surveillance, prevention and control of communicable diseases, in particular those that represent new, emerging and re-emerging public health problems. In this context, WHO is reinforcing its activities to establish a system for monitoring resistance of selected bacteria to specific antimicrobial agents at local, national and global levels. WHO already coordinates other international efforts for antimicrobial susceptibility surveillance, particularly in the fields of respiratory diseases, malaria and tuberculosis.

Although many countries have individual antimicrobial resistance surveillance systems, the results of epidemiological analysis are often not passed on to local physicians in a way that helps them choose the best antibiotic therapy for their patients. Locally accrued results on antimicrobial resistance testing are seldom fed back to the source laboratory or used to assess national or regional trends.

Better disease surveillance coupled with better communications systems will help physicians to use antibiotics more effectively, which in turn will facilitate detecting local and regional trends in antimicrobial resistance and control the spread of deadly bacterial infections.

In collaboration with the WHO Collaborating Centre for Surveillance of Resistance to Antimicrobial Agents in Boston, and the Nosocomial Pathogens Laboratory Branch of Centres for Disease Control (CDC) in Atlanta, WHO will strengthen the network of laboratories which collect, analyse and distribute data and results on antimicrobial resistance in bacteria of public health importance.

Over 160 laboratories in 32 countries use computer software called WHONET (developed by the WHO Collaborating Centre, Boston) to process and analyse results of antimicrobial resistance testing and provide data to the WHO Network on Antimicrobial Resistance Monitoring.

Local computer analysis of antibiotypes is the foundation for the regional and global monitoring system.

Laboratories can detect local problems in antimicrobial resistance testing, and the examination of their data will delineate the spread of drug-resistant strains. This facilitates infection control. It also explains and helps to correct the occurrence of certain types of drug resistance at selected sites. However, imbalance in the geographical distribution of the participating laboratories, problems in the supply of data, and different standardisation techniques used by the various laboratories, complicate comparison of results and the extrapolation of trends at regional and national levels.

Within the next two years, WHO plans to establish a core of about 30-50 laboratories worldwide to generate internationally verified, standardised results on trends in the susceptibility of important bacteria to specific antimicrobials. It will also encourage the use of WHONET in public health and hospital laboratories to strengthen their ability to screen bacteria for antibiotic resistance with standardised methods.

Laboratories will be assisted in conducting quality assurance and external proficiency testing - a prerequisite for collecting standardised, comparable results to detect trends and the emergence of multi-drug resistant bacteria. Training courses are planned in nine countries in Africa and Asia in 1996 and 1997. Manuals are to be produced to help microbiologists in analysing and reporting their local microbial resistance findings to physicians. Computer programs will be developed that use the antibiotic resistance data collected through WHONET to guide local decisions on the use of antibiotics.

Key regional reference laboratories will receive data from public health and hospital laboratories and develop regional summaries of trends in antibiotic resistance. WHO headquarters, in close collaboration with the regional offices and collaborating centres, will coordinate these activities. A global data bank will be established to help identify antimicrobial resistance problems of local, regional and global priority. Consensus on how to tackle these problems will be sought. These centres will initiate and coordinate appropriate control and containment measures.

The WHO network will be complemented by another WHO effort aimed at coordinating and extending the activities of several key laboratories in different parts of the world which collect, analyse and distribute gonococcal susceptibility data worldwide.

The long-term goals of these activities are to strengthen the capacities of WHO member countries to detect and contain the emergence of major multi-drug resistant bacteria and to improve standardisation of interpretation of antibiotic resistance data throughout the world..

HAEMORRHAGIC FEVERS IN AFRICA

Based on World Health Organization Fact Sheet 111 of March 1996

Infection with the haemorrhagic fever viruses is an important cause of human illness and a public health problem of global dimension. Twelve distinct viruses are associated with haemorrhagic fevers in humans. Most of them are zoonoses with the possible exception of the four dengue viruses, which may continually circulate among humans.

Haemorrhagic fever viruses are found in both temperate and tropical habitats, although the problem is of particular concern on the African continent, as shown by the recent outbreaks of yellow fever and Ebola haemorrhagic fever. They generally infect both sexes and all age groups.

Transmission to humans is frequently by the bite of an infected tick or mosquito or through aerosol transmission from infected rodent hosts. Mammals, especially rodents, appear to be important natural hosts for many haemorrhagic fever viruses. The transmission cycle for each haemorrhagic fever is distinct and is dependent on the characteristics of the primary vector species and the possibility of its contact with humans.

Apart from yellow fever, Ebola haemorrhagic fever, and dengue fever (which touches only limited parts of Africa), the major haemorrhagic fevers in Africa are:

Lassa fever, a disease that first came to light in the late 1960s after an outbreak at a mission hospital in Nigeria, during which several persons died. The natural host of the virus is a rodent that is very common in many parts of the continent, but Lassa fever appears to be restricted to West Africa. Transmission to humans is primarily by aerosol means, from rodents, or by close contact with an infected individual. It is a seasonal disease, with the incidence highest during the dry season. Nosocomial outbreaks have been especially significant in the history of Lassa fever, but recent studies indicate that relatively simple nursing precautions can eliminate most risks to hospital personnel.

Rift Valley fever, found in many areas in sub-Saharan Africa. It is normally associated with excessively heavy rainfall. The mosquito species most frequently associated with Rift Valley fever often breed in water lying in natural depressions on the African savanna and transmit the virus to vertebrates that use these sources of water. Human disease may result from either feeding

by an infected mosquito vector or by aerosol transmission, usually associated with slaughter of sick animals.

Crimean-Congo haemorrhagic fever, a disease caused by a virus which is found in many parts of Africa, the Middle East and parts of the former Soviet Union and China. This virus is transmitted primarily by ticks. Small mammals and birds are hosts of the larval and nymphal ticks, and large mammals are hosts of the adult ticks. Humans may be exposed to the virus through the bite of infected ticks or during the slaughter of infected animals. Human infection appears to be seasonal, with most cases occurring in the spring or autumn. The populations at greatest risk of infection with the virus are ranchers, shepherds, veterinarians and others who may be exposed to sick animals, and medical staff in endemic regions who may encounter acutely ill patients.

Marburg haemorrhagic fever, caused by a virus closely related to the Ebola virus. Marburg virus was first recognised during an outbreak of a severe haemorrhagic disease associated with the importation of African green monkeys from East Africa to Germany. Subsequent, isolated human cases have been reported, primarily from sub-Saharan Africa, but virtually nothing is known of the epidemiology of this disease, apart from the fact that nosocomial transmission may occur, especially after close or intimate contact.

Haemorrhagic fevers in Africa do not usually cause major epidemics. However, localised outbreaks do occur, and may have devastating effects on the local community and cause widespread concern. In addition to having high fatality rates, some also cause permanent disability, such as hearing loss following Lassa fever, or blindness following Rift Valley fever. The Division of Emerging and other Communicable Diseases, Surveillance and Control, newly established at WHO headquarters, along with the WHO Regional Office for Africa and collaborating organisations, have recognized the importance of African haemorrhagic fever viruses. Together these organisations are developing improved methods to recognise outbreaks early and thus prevent widespread infections.