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Infectious Agents And Disease In Clinical Laboratory, Role Of Nurses, Pharmacist To Increase Awareness; Review

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Abstract:

The occurrence and dissemination of infectious diseases with the potential to cause pandemics have transpired throughout human history. Throughout history, there have been significant outbreaks of bacterial infectious diseases including plague, cholera, and tuberculosis. In more recent times, viral infectious diseases such as influenza and the most recent COVID-19 pandemic, which began in late 2019, have spread worldwide and resulted in millions of deaths. Pandemics sometimes arise from infectious diseases that are caused by zoonotic infections, which originate from animals such as cattle, wildlife, or companion animals. The essential role of the microbiology laboratory in diagnosing infectious diseases necessitates a strong and collaborative relationship between the physician/advanced practice provider and the microbiologists, who contribute immense value to the healthcare team.

Introduction:

Each stage of the infection process can be prevented by a separate set of defense mechanisms. The process of infection can be broken down into substages. At the beginning of the process, a new host is exposed to infectious particles that have been shed by an individual who is already sick. There are a lot of factors that

determine an infectious agent's infectivity outside of the host, including its number, route, method of transmission, and stability. Certain infections, such as anthrax, are transmitted by the transmission of spores that are highly resistant to heat and drying. On the other hand, other pathogens, such as the human immunodeficiency virus (HIV), are only transmitted through the exchange of bodily fluids or tissues because they are unable to persist as infectious agents outside of the body [1].

The epithelium surface is the one via which the initial interaction with a new host takes place. There is a possibility that this is the skin or the mucosal surfaces of the respiratory, gastrointestinal, and urogenital tracts that are found internally. Following the establishment of contact, an infectious agent is required to establish a focal point of infection. In order to accomplish this, the organism must first adhere to the epithelial surface, and then colonize it, or penetrate it, in order to replicate within the tissues. During this stage, innate immunity is able to repel a significant number of bacteria. NK cells are activated in response to intracellular infections, and as a result, a local inflammatory response and generated cytokines and chemokines can recruit additional effector cells and molecules to the site of an infection, thereby preventing the spread of pathogens into the bloodstream. For the purpose of distinguishing between microbial and host cell surfaces, as well as between infected and normal cells, these innate immune responses make use of a wide range of receptors that are encoded in the germline. They are not as effective as adaptive immune responses, which are able to afford to be more powerful due to the fact that they are specific to antigens. On the other hand, they have the ability to either stop an infection from developing or, if that is not possible, to contain it while an adaptive immune response is being developed [2]. Unless the agent is able to travel from the initial site of infection or can generate toxins that can spread to other areas of the body, sickness will not emerge until a microbe has successfully established a site of infection in the host. In the event that this occurs, the harm that is caused will be minimal. By directly extending the focal point of infection through the lymphatic system or the bloodstream, extracellular infections are able to disseminate throughout the body. The transmission of infectious agents through the bloodstream typically takes place only after the lymphatic system has been unable to cope with the weight of the infectious agent [3]. It is necessary for pathogens that are obligatory to be found inside of cells to move from one cell to another. They can do this either through direct transfer from one cell to the next or through release into the extracellular fluid and reinfection of cells that are both adjacent and distant. A great many of the organisms that cause food poisoning are capable of causing pathology without moving into the tissues. They do not directly cause any pathology, but they do release toxins that cause damage either in situ or after they have crossed the epithelial barrier and entered the circulation [4]. They do this by establishing a site of infection on the epithelial surface in the lumen of the gut.

The majority of infectious agents exhibit a high degree of host specificity, meaning that they only cause disease in a single or a small number of closely related species. It is not understood what factors determine the host specificity of each and every agent; nonetheless, one of the most important factors is the requirement for attachment to a specific cell-surface molecule at the desired location. The majority of diseases have a restricted host range since it is typically necessary for them to engage in various interactions with host cells in order to support replication. There is a field of study known as molecular pathogenesis that encompasses the molecular mechanisms of host specificity; however, this book does not cover this particular area of research [5].

Review:

Numerous publications discussed topics such as the diversity of bacteria, epidemiology, and the resistance of bacteria to antimicrobials. One study found new Mycobacterium ulcerans genotypes in Buruli ulcer endemic communities in Ghana and Côte d'Ivoire by employing VNTR profiling. These communities were located in both countries. The findings of this molecular epidemiology investigation showed that there is evidence of the possible transmission of M. ulcerans from the environment, specifically water bodies from aquatic plants, to humans through open lesions on the skin. The phenotypic and molecular characterisation of a hypervirulent Klebsiella pneumoniae strain K54-ST29 that caused a multi-system infection in a diabetic patient was reported by another researcher. In East Asia, there is a particular concern regarding the community-acquired illness that is caused by hypervirulent K54 K. pneumoniae in conjunction with diabetes. Streptococcus suis is a zoonotic pathogen that is responsible for invasive infections in both people and pigs worldwide. Additionally, a recent study described the genetic characterisation of the clonal complex 221/234 of Streptococcus suis serotype 24 that was obtained from human patients. The antimicrobial resistance genes, pathotyping, virulence-associated gene profiles, and minimum core genome typing of the strains were evaluated and classified in accordance with the results of the analysis. Regarding the transmission of infections, and more specifically the transmission of tick-borne pathogens, an article that explored the function of ranged horses in the eco-epidemiology of Rickettsia raoultii infection in China was written according to a hypothesis and theory. It was shown that R. raoultii gene sequences were present in both the ticks of horses and the horses themselves. In the field of epidemiology, a study that was carried out in hospitals located in Seesen, Germany, reported the risk factors of patients who were experiencing diarrhea for having an infection caused by Clostridium difficile. The use of diuretics and a diet that was deficient in vegetables were listed as two of the key factors that were identified [6,7,8,9].

Within the Research Topic, there were five publications that focused on antimicrobial-resistant organisms and the methods that can be utilized to counteract their dissemination and emergence. Several different plasmids bearing blactx-m antibiotic resistance genes that encode extended-spectrum beta-lactamases were found to be present in a uropathogenic Escherichia coli ST405 isolate, according to a major study that detailed the genomic characterisation of the bacteria. The presence of two different blactx-m variants inside the same strain raises the probability that further blactx-m variants will develop for the first time. One of these research revealed the identification of bacterial drug-resistant cells by the convolutional neural network in transmission electron microscopy pictures. This was in reference to the detection of bacteria that are resistant to antimicrobials. In terms of classifying cells and distinguishing between enoxacin-resistant and enoxacin-sensitive cells on the basis of differences in bacterial cell envelopes, the suggested method demonstrated a high degree of accuracy. Concerning antibiotic resistance, Neisseria meningitidis is yet another bacterial infection that should be taken into consideration. The epidemiology of meningococcal disease in a single study, as well as the carriage, genotypic features, and antibiotic resistance of N. meningitidis isolates in Zhejiang province, China, throughout the period of 2011–2021. In the context of antimicrobial chemotherapy, a study advocated the use of active surveillance cultures and procalcitonin in conjunction with clinical data to guide empirical antimicrobial therapy in hospitalized medical patients who were diagnosed with sepsis. A mini-study was conducted on gold-derived compounds as

potential novel antimicrobial agents. This review was one of the potential methods that may be utilized to battle the growth and spread of germs that are resistant to antimicrobials. Gold complexes, with their antibacterial properties that span a broad range and their one-of-a-kind mechanisms of action, appear to be particularly important among the several families of derivatives that have been explored [10,11,12,13].

The topics of virulence factors, pathogenicity mechanisms, infection models, immune response, and infectious pathology were discussed in a number of the submitted publications. A single study examined the existing body of knowledge concerning the virulence mechanisms of Mycobacterium abscessus and the implications these processes have for the development of vaccines. The continuation of study into the pathogenesis of M. abscessus is essential for the development of vaccines and therapies that are both safe and effective in the future, with the goal of reducing the occurrence of this newly discovered disease on a global scale. The preceding one discussed the pathogenesis of leprosy as well as the modification of the cellular response to Mycobacterium leprae. In addition, a recent study examined the cross-talk that occurs between the intestinal epithelium and Salmonella Typhimurium. The study focused on the methods that S. Typhimurium has developed in order to cross the intestinal epithelium, get access to sub-epithelial or systemic areas, and survive the host's defense mechanisms. A mouse model of septic arthritis caused by Staphylococcus aureus was used by another researcher to investigate the role that Staphylococcus aureus lipoproteins play in triggering bone regeneration. It has been hypothesised that the action is mediated by the lipid-moiety of the lipoproteins, which is mediated by monocytes and macrophages. Through the utilization of a murine model of infection, researchers in the field of microbial pathogenesis have demonstrated that the increased vascular permeability that occurs as a result of the spread and invasion of Vibrio vulnificus in the wound infection exacerbates the potentially deadly necrotizing disease that is produced by this pathogen. A connection has been established between an infection with Helicobacter hepaticus and chronic hepatitis and fibrosis in BALB/c mice. A significant investigation was conducted to analyze the mechanism that underlies the mouse model of hepatocellular carcinoma generated by H. hepaticus. The findings of this study demonstrated that infection with H. hepaticus enhances the advancement of liver preneoplasia through the activation and accumulation of high-mobility group box-1 (HMGB1). Controlled human infection models, also known as CHIMs, have been utilized to provide vital insights into the etiology of diseases, the interaction between hosts and pathogens, and the evaluation of vaccinations. The purpose of CHIMs is to fully comprehend the human response to enteric infections, specifically enteric fevers caused by typhoidal Salmonella spp., with a particular emphasis on the contributions of CHIMs to uncover the complex immunological responses to these organisms and to provide insights into the factors that determine protective immunity [14,15].

Towards the end of 2019, the COVID-19 disease, which is caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), emerged and quickly spread throughout the human population all over the world. It became the first major pandemic of the 21st century, affecting hundreds of millions of people and causing millions of deaths. A number of variants have emerged in multiple successive waves over the course of three years, which has prompted health and government authorities to implement severe preventative measures, such as lockdowns for a number of months. This is a situation that

was not previously known to the population of the entire world, and it has led to critical economic situations in a number of countries. On the other hand, this pandemic and the research that has been linked with it have made a significant contribution to the expansion of our knowledge regarding all elements of a viral infectious disease, as well as to the quick development of new diagnostic, therapeutic, infectious disease preventive, and vaccine techniques [16].

The identification of indicators of new SARS-CoV-2 variants in individuals with secondary immunodeficiency was the subject of a recent study that addressed the topic. Immunodeficient people are one of the vulnerable groups that are shown to be the most susceptible to this virus. Chronic infections that occur in the presence of anti-COVID-19 medications have the potential to lead to the evolution of the virus in the host. Amino acid alterations were found in a wide range of viral proteins, including spike proteins and other proteins that play a role in the pathogenesis of the virus. It was discovered that some of them have recurrent de novo modifications, and these changes have the potential to play a role in the pathogenesis and progression of SARS-CoV-2. Several groups investigated the immunological responses of COVID-19 convalescent patients to SARS-CoV-2 peptides, specifically antibody and T cell responses. Their findings shed light on the potential role that humoral immune responses and cytotoxic T cell responses to certain peptides could have in the pathogenesis of SARS-CoV-2. In relation to the transmission of SARS-CoV-2, an integrated analysis was reported, which revealed the characteristics and impacts of SARS-CoV-2 transmission from mother to child. It has been claimed that the possibility of SARS-CoV-2 being transmitted from mother to child through the placenta is substantially lower, at approximately 3%. However, the virus can be transmitted through the air at a rate of up to 15% each transmission. Within the scope of the research conducted by [17,18], cellular and viral-associated variables that contribute to this transmission were studied.

Conclusion:

It is necessary for the pathogen to first colonize the skin or the internal mucosal surfaces of the respiratory, gastrointestinal, or urogenital tracts in order to create an infection. After this, the pathogen must then overcome or bypass the innate immune responses that are connected with the epithelia and the tissues that lie beneath the epithelia. In the event that it is successful in doing so, it will trigger an adaptive immune response, which will begin to exercise its effects after a number of days and will typically eradicate the infection. Because pathogens are so different from one another in terms of their lives and the ways in which they cause disease, the immune system of the host must be able to mount a defense against them that is similarly varied. For the purpose of preventing malaria in tourists, antimalarial medications are frequently used in conjunction with personal protective measures. Additionally, there are set standards for the administration of antibiotic prophylaxis prior to surgical procedures. Recognition and management of patients who have underlying diseases and disorders that can decrease host barriers to infection is another key component in the prevention and control of infections. This is because these individuals are more likely to be susceptible to infection.

References:

1. Abubakar, U., and Tangiisuran, B. (2020). Nationwide survey of Pharmacist's involvement in antimicrobial stewardship program in Nigerian Tertiary Hospitals. J. Glob. Antimicrob. Resist. 21, 148–153. doi: 10.1016/j.jgar.2019. 10.007

2. Alsan, M., Schoemaker, L., Egglestn, K., Kammili, N., Kolli, P., and Bhattacharya, J. (2015). Out-of-pocket health expenditures and antimicrobial resistance in low- and middle-income countries. Lancet Infect. Dis. 15, 1203–1210. doi: 10.1016/ S1473-3099(15)00149-8
3. Bessesen, M. T., Ma, A., Clegg, D., Fugit, R. V., Pepe, A., Goetz, M. B., et al. (2015). Antimicrobial Stewardship Programs: Comparison of a Program with Infectious Diseases Pharmacist Support to a Program with a Geographic Pharmacist Staffing Model. Hosp. Pharm. 50, 477–483. doi: 10.1310/hpj5006-477
4. Bilal, A.II, Tilahun, Z., Gebretekle, G. B., Ayalneh, B., Hailemeskel, B., and Engidawork, E. (2017). Current status, challenges and the way forward for clinical pharmacy service in Ethiopian public hospitals. BMC. Health Serv. Res. 17, 359. doi: 10.1186/s12913-017-2305-1
5. Bishop, P. A., Isache, C., McCarter, Y. S., Smotherman, C., Gautam, S., and Jankowski, C. A. (2020). Clinical impact of a pharmacist-led antimicrobial stewardship initiative evaluating patients with Clostridioides difficile colitis. J. Investig. Med. 68, 888–892. doi: 10.1136/jim-2019-001173
6. Brink, A. J., Messina, A. P., Feldman, C., Richards, G. A., Becker, P. J., Goff, D. A., et al. (2016). Antimicrobial stewardship across 47 South African hospitals: an implementation study. Lancet Infect. Dis. 16, 1017–1025. doi: 10.1016/S1473- 3099(16)30012-3
7. Charani, E., Smith, I., Skodvin, B., Perozziello, A., Lucet, J. C., Lescure, F. X., et al. (2019). Investigating the cultural and contextual determinants of antimicrobial stewardship programmes across low-, middle- and high-income countries-A qualitative study. PLoS One 14, e0209847. doi: 10.1371/journal.pone.0209847
8. EI Hajj, M. S., Al-Saeed, H. S., and Khaja, M. (2016). Qatar pharmacists' understanding, attitudes, practice and perceived barriers related to providing pharmaceutical care. Int. J. Clin. Pharm. 38, 330–343. doi: 10.1007/s11096-016-0246-0
9. Ellis, K., Rubal-Peace, G., Chang, V., Liang, E., Wong, N., and Campbell, S. (2016). Antimicrobial stewardship for a geriatric behavioral health population. Antibiotics 5, E8. doi: 10.3390/antibiotics5010008
10. Piret J., Boivin G. (2021). Pandemics throughout history. Front Microbiol. 11, 631736. 10.3389/fmicb.2020.631736
11. Broder K.R., Cortese M.M., Iskander J.K., Kretsinger K., Slade B.A., Brown K.H., Mijalski C.M., Tiwari T., Weston E.J., Cohn A.C., Srivastava P.U., Moran J.S., Schwartz B., Murphy T.V. Preventing tetanus, diphtheria, and pertussis among adolescents: use of tetanus toxoid, reduced diphtheria toxoid and acellular pertussis vaccines recommendations of the Advisory Committee on Immunization Practices (ACIP) MMWR Recomm. Rep. 2006;55:1–34.
12. Brunkard J.M., Robles Lopez J.L., Ramirez J., Cifuentes E., Rothenberg S.J., Hunsperger E.A., Moore C.G., Brussolo R.M., Villarreal N.A., Haddad B.M. Dengue fever seroprevalence and risk factors, Texas-Mexico border, 2004. Emerg. Infect. Dis. 2007;13:1477–1483.
13. Burke R.L., Kronmann K.C., Daniels C.C., Meyers M., Byarugaba D.K., Dueger E., Klein T.A., Evans B.P., Vest

K.G. A review of zoonotic disease surveillance supported by the Armed Forces Health Surveillance Center. Zoonoses Public Health. 2012;59:164–175.

14. Cann K.F., Thomas D.R., Salmon R.L., Wyn-Jones A.P., Kay D. Extreme water-related weather events and waterborne disease. Epidemiol. Infect. 2013;141:671–686.
15. EFSA . EFSA; Parma, Italy: 2011. Tracing Seeds, in Particular Fenugreek (Trigonella foenum-graecum) Seeds, in Relation to the Shiga Toxin-Producing E. coli (STEC) O104:H4 2011 Outbreaks in Germany and France. Technical Report on request of European Food Safety Authority, Question No EFSA-Q-2011-00817, issued on 05 July 2011.
16. Engelthaler D.M., Mosley D.G., Cheek J.E., Levy C.E., Komatsu K.K., Ettestad P., Davis T., Tanda D.T., Miller L., Frampton J.W., Porter R., Bryan R.T. Climatic and environmental patterns associated with hantavirus pulmonary syndrome, Four Corners region, United States. Emerg. Infect. Dis. 1999;5:87–94.
17. Erlanger T.E., Weiss S., Keiser J., Utzinger J., Wiedenmayer K. Past, present, and future of Japanese encephalitis. Emerg. Infect. Dis. 2009;15:1–7.
18. Faria N.R., Rambaut A., Suchard M.A., Baele G., Bedford T., Ward M.J., Tatem A.J., Sousa J.D., Arinaminpathy N., Pepin J., Posada D., Peeters M., Pybus O.G., Lemey P. HIV epidemiology. The early spread and epidemic ignition of HIV-1 in human populations. Science. 2014;346:56–61.