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Commentary

Vector vs. victim: The complexity of vector-borne diseases

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DESCRIPTION

In the complex web of ecosystems, there exists a silent force capable of transmitting deadly diseases from one host to another – vectors. These vectors, often small and inconspicuous creatures such as mosquitoes, ticks, and flies, play a significant role in the transmission of pathogens that cause a *myriad* of illnesses in humans, animals, and plants (Bakker et al., 2005).

Defining vector-borne diseases

Vector-borne diseases are infectious diseases transmitted to humans and animals through the bite of infected arthropods, such as mosquitoes, ticks, sandflies, and fleas, or through other vectors like snails and freshwater snails. These vectors serve as carriers for pathogens, including bacteria, viruses, and parasites, facilitating their transmission from one host to another (Chelbi-Alix et al., 2006).

Common vector-borne diseases

Vector-borne diseases encompass a diverse range of illnesses, each with its unique characteristics and geographic distribution. Some of the most common vector-borne diseases include:

Malaria: Transmitted by Anopheles mosquitoes infected with Plasmodium parasites, malaria remains a major public health concern, particularly in tropical and subtropical regions (Finke et al., 2005).

Dengue fever: Spread by *Aedes* mosquitoes, dengue fever is characterized by high fever, severe joint and muscle pain, and in severe cases, hemorrhagic fever and shock syndrome.

Lyme disease: Transmitted by the bite of infected ticks, particularly the black-legged tick in North America and the sheep tick in Europe, Lyme disease can lead to symptoms such as fever, rash, arthritis, and neurological complications (Garcia et al., 1999)

Zika virus: Transmitted primarily by *Aedes* mosquitoes, *Zika virus* infection during pregnancy can cause congenital *Zika* syndrome, characterized by microcephaly and other neurological abnormalities in infants.

Chikungunya: Spread by *Aedes* mosquitoes, chikungunya causes symptoms such as fever, joint pain, rash, and in some cases, long-term joint pain and arthritis (Marissen et al., 2005).

Impact of vector-borne diseases

Vector-borne diseases pose significant threats to human health, causing millions of cases and hundreds of thousands of deaths worldwide each year. In addition to the direct impact on human health, these diseases can have far-reaching social, economic, and ecological consequences, including:

Economic burden: Vector-borne diseases impose a substantial economic burden on affected individuals, families, healthcare systems, and economies at large, through healthcare costs, lost productivity, and reduced agricultural output (Morin et al., 2017).

Healthcare systems: Outbreaks of vector-borne diseases can overwhelm healthcare systems, particularly in resource-limited settings, where access to healthcare services and diagnostic tools may be limited.

Travel and trade: Vector-borne diseases can spread across borders through international travel and trade, posing challenges for global health security and requiring coordinated efforts to prevent and control their transmission.

Climate change: Environmental factors such as temperature, humidity, and precipitation play a significant role in the distribution and abundance of vectors and the pathogens they transmit. Climate change can alter these factors, potentially affecting the geographic range and seasonality of vector-borne diseases (Nadin-Davis et al., 2011).

Prevention and control strategies

Preventing and controlling vector-borne diseases require integrated, multidisciplinary approaches that encompass surveillance, vector control, community engagement, and capacity building. Key strategies include:

Vector control: Implementing measures to reduce vector populations and interrupt transmission, such as insecticide-treated bed nets, indoor residual spraying, larval control, and environmental management.

Surveillance: Establishing robust surveillance systems to monitor vector populations, disease incidence, and antimicrobial resistance, enabling timely detection and response to outbreaks (Ogino et al., 2016).

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Health education: Raising awareness among communities about vector-borne diseases, their transmission, and preventive measures can empower individuals to protect themselves and their families from infection (Qureshi et al., 2023).

Research and innovation: Investing in research to develop new tools and strategies for vector control, diagnostics, and treatment can enhance our ability to prevent and control vector-borne diseases effectively.

International collaboration: Promoting collaboration and knowledge sharing among countries, regions, and international organizations is essential for addressing the transboundary nature of vector-borne diseases and strengthening global preparedness and response capabilities (Rieder et al., 2011).

Vector-borne diseases represent a complex and dynamic challenge to global health security, affecting millions of people worldwide and posing significant threats to economies, ecosystems, and livelihoods. By understanding the biology of vectors, the pathogens they transmit, and the socioenvironmental factors that influence their distribution and abundance, we can develop effective strategies to prevent and control vector-borne diseases. Through sustained investment, innovation, and collaboration, we can strive to reduce the burden of these diseases and protect the health and well-being of communities around the world.

REFRENCES

- Bakker AB, Marissen WE, Kramer RA, Rice AB, Weldon WC, Niezgoda M, Hanlon CA. et al. (2005). Novel human monoclonal antibody combination effectively neutralizing natural rabies virus variants and individual *in vitro* escape mutants. Journal of virology. Jul;79(14):9062-8.
- Chelbi-Alix MK, Vidy A, Bougrini JE, Blondel D. (2006).Rabies viral mechanisms to escape the IFN system: The viral protein P interferes with IRF-3, Stat1, and PML nuclear bodies. Journal of interferon & cytokine research. 26(5):271-280.

- 3. Finke S, Conzelmann KK. (2005).Replication strategies of rabies virus. Virus research. 111(2):120-131.
- 4. Garcia LS. (1999). Classification of human parasites, vectors, and similar organisms. Clinical infectious diseases. 29(4):734-736.
- Marissen WE, Kramer RA, Rice A, Weldon WC, Niezgoda M, Faber M, Slootstra JW. et al. (2005). Novel rabies virus-neutralizing epitope recognized by human monoclonal antibody: Fine mapping and escape mutant analysis. Journal of virology. Apr 15;79(8):4672-4678.
- Morin B, Liang B, Gardner E, Ross RA, Whelan SP. (2017) . An *in vitro* RNA synthesis assay for rabies virus defines ribonucleoprotein interactions critical for polymerase activity. Journal of virology.91(1): 10-128.
- Nadin-Davis SA, Real LA. (2011). Molecular Phylogenetics of the Lyssaviruses—Insights from a Coalescent Approach. Advances in virus research. 79:203-38.
- Ogino M, Ito N, Sugiyama M, Ogino T. (2016). The rabies virus L protein catalyzes mRNA capping with GDP polyribonucleotidyltransferase7 activity. Viruses.8(5):144.
- Qureshi YM, Voloshin V, Facchinelli L, McCall PJ, Chervova O, Towers CE, Covington JA, Towers DP. (2023). Finding a Husband: Using Explainable AI to Define Male Mosquito Flight Differences. Biology. 12(4):496.
- Rieder M, Brzózka K, Pfaller CK, Cox JH, Stitz L, Conzelmann KK. 2011. Genetic dissection of interferon-antagonistic functions of rabies virus phosphoprotein: Inhibition of interferon regulatory factor 3 activation is important for pathogenicity. Journal of virology. 85(2):842-852.