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From Group Intervention to Precision Strike: Insights from Ebola Virus for Future Infectious Disease Management

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Abstract. The 2014–2016 West African Ebola outbreak exposed systemic deficiencies in traditional public health approaches to managing highly lethal infectious diseases, while also marking a transformative turning point for breakthroughs in precision medicine technologies. This study systematically examines the Ebola virus, analyzing its transmission scale and historical challenges in containment. By comparing the effectiveness of traditional medical interventions with rapid diagnostics and targeted therapies, this paper highlights the critical role of precision medicine in infectious disease prevention and control. Research findings demonstrate that CRISPR-based on-site detection significantly reduces diagnostic time, monoclonal antibody drugs (e.g., REGN-EB3) lower mortality rates from 49% to 29%, and multi-omics-driven host-pathogen interaction analyses provide novel pathways for high-risk population screening and personalized vaccine design. Further exploration reveals that precision medicine is shifting infectious disease management from "passive response" to "precision intervention." Finally, article proposes that future infectious disease prevention and control can establish a "prediction-warning-precision intervention" trinity framework, with the expectation of providing reference and basis for subsequent related research.

Keyword: Ebola virus; Traditional medicine; Precision medicine; Rapid diagnosis; Targeted therapy; Multi-omics technology; Infectious disease prevention and control.

1. Introduction: The Technological Turning Point in the Ebola Epidemic

1.1. Epidemic Scale and Historical Context

Ebola virus disease (EVD), a severe and often fatal illness causing hemorrhagic fever in humans and primates, has been extensively studied due to its high mortality rate. During the 2014–2016 West African outbreak, about 20000 cases and 10000 deaths were recorded, surpassing the cumulative global cases of the preceding 38 years by tenfold [1]. Key drivers of this unprecedented spread included:

①Sociodemographic shifts: Urbanization rates in Guinea, Liberia, and Sierra Leone rose from 28% in 2000 to 43% in 2014, accompanied by a 300% increase in cross-border road traffic [2].

②Accelerated urbanization: Population density in Conakry, Guinea, was 20 times higher than that of the 1976 Congolese outbreak zone.

③Failure of traditional containment: Symptom-based screening and mass isolation strategies had a misdiagnosis rate of 65% [1].

④Viral evolution: The GP protein A82V mutation tripled human-to-human transmission efficiency [3].

The incubation period of the Ebola virus is usually 2 - 21 days. After the onset of the disease, symptoms such as high fever, headache, sore throat, muscle pain, and fatigue may occur. In the later stage of the disease, patients may experience symptoms such as internal bleeding and multiple organ failure, which may even lead to death.

Table 1. Case - fatality rates of different subtypes of the Ebola virus

Subtype	Case - fatality rate
Zaire ebolavirus	70% - 90%
Sudan ebolavirus	50% - 70%
Bundibugyo ebolavirus	Lower than that of the Sudan subtype
Tai Forest ebolavirus	Only one person was infected and was cured
Reston ebolavirus	Does not infect humans

Zaire ebolavirus: The case - fatality rate ranges from 70% to 90%, making it a subtype with a relatively high case - fatality rate among all subtypes. This indicates that patients infected with this subtype of the virus face an extremely high risk of death. Sudan ebolavirus: The case - fatality rate is between 50% and 70%. Although it is lower than that of the Zaire subtype, it is still at a relatively high level, meaning that there is also a high probability of death for those infected with this subtype of the virus. Bundibugyo ebolavirus: The case - fatality rate is lower than that of the Sudan subtype, and its threat to the patient's life is relatively lower than that of the Sudan subtype. Tai Forest ebolavirus: Only one person has been infected and was finally cured, indicating that this subtype poses a relatively small threat to human life among the currently known infection cases. Reston ebolavirus: It does not infect humans. This is a significant difference between this subtype and other subtypes, making it unique among all subtypes of the Ebola virus. The table clearly shows the differences in the threat levels of different subtypes to human health by comparing the case - fatality rates of different subtypes, which helps to gain a deeper understanding of the characteristics of different subtypes of the Ebola virus.

1.2. Impact of Traditional Medical Practices

Traditional medical diagnosis has a certain degree of delay, which can lead to crises.For example, in August 2014, a backlog of PCR tests at a Monrovia hospital left 300 suspected Ebola-infected corpses unprocessed, triggering community panic and violent clashes. Traditional testing required 3–7 days, yet the virus remained viable in corpses for up to 7 days [4], creating a vicious cycle. Diagnostic delays also led to an average of 2–3 family infections per suspected case during the waiting period.

1.3. Precision Medicine: A Critical Shift

Since 2015, in the later stages of the Ebola epidemic, people began to adopt a series of advanced medical technologies. These included rapid diagnostic techniques such as CRISPR and nanopore sequencing, as well as targeted treatment methods, especially the application of monoclonal antibodies.

The introduction of these technologies significantly enhanced the ability to combat the Ebola virus. The case - fatality rate, which was originally as high as 70%, was substantially reduced, and the mortality rate was successfully brought below 30%.

This significant progress not only achieved a breakthrough in the prevention and control of the Ebola virus but also marked the arrival of the era of precision medicine in the field of infectious disease management. It represents a crucial transition from traditional broad - spectrum treatments to more personalized and precise medical approaches.

2. Precision Medicine Technologies: Lessons from Ebola

2.1. Rapid Diagnostics

2.1.1. CRISPR-Dx (SHERLOCK Technology)

For a long time, polymerase chain reaction (PCR) and its related technologies have been the core means for detecting nucleic acid biomarkers. However, CRISPR technology, as a third-generation gene editing tool, has demonstrated tremendous application potential in many fields such as gene therapy and disease model construction. As early as 2017, the renowned pioneer in the CRISPR field, Feng Zhang's team, published their research titled "Nucleic acid detection with CRISPR-Cas13a/C2c2" in the Science magazine [6]. The publication officially announced the birth of molecular detection tools based on CRISPR technology. The research team named this technology SHERLOCK. The operational process of SHERLOCK technology is shown in Figure 1. Firstly, the substrate DNA or RNA is amplified using recombinant polymerase amplification or reverse transcription recombinant polymerase amplification (RT-RPA) methods to increase the substrate concentration. Subsequently, the amplified DNA is transcribed into RNA using T7 transcriptase, and the transcribed RNA is mixed with LwaCas13, CRISPR RNA (crRNA) reaction solution. When the LwaCas13-crRNA ribonucleoprotein (RNP) complex recognizes the substrate RNA, it triggers cis-cleavage and trans-cleavage reactions. Trans-cleavage results in the cleavage of single-stranded RNA reporter molecules (ssRNA-reporter) within the reaction system. The 5' end of this reporter molecule is conjugated with a fluorophore (such as carboxyfluorescein FAM), and the 3' end is conjugated with a fluorescence quencher (such as black hole quencher BHQ). When the reporter molecule remains intact, no fluorescence is produced in the system. However, when trans-cleavage occurs and the reporter molecule is cleaved, the fluorophore and quencher move apart, allowing the detection of a fluorescence signal at this point.

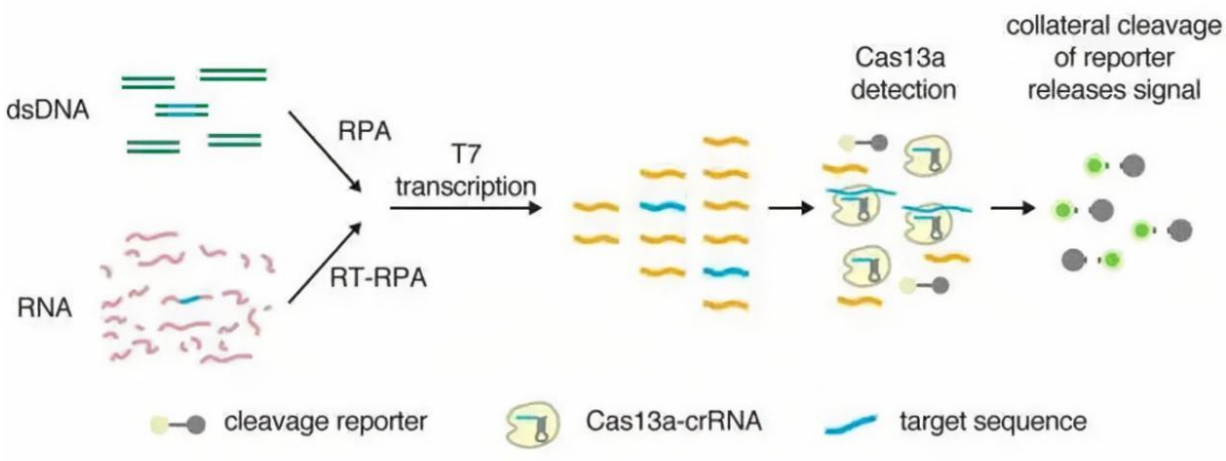

Figure 1. SHERLOCK Technology Workflow [7]

Recently, researchers have used the lateral cleavage capabilities of the CRISPR-Cas12 and CRISPR-Cas13 systems to develop new nucleic acid testing technologies (CRISPR-Dx), effectively addressing the limitations of traditional techniques. CRISPR-Dx not only enhances the sensitivity, speed, and accuracy of detection but also reduces dependence on complex equipment, simplifies operational procedures, and broadens its application areas.

This technology was also utilized during the Ebola outbreak, where in a pilot project in Kailahun, Sierra Leone, medical staff used test kits to detect Ebola virus RNA on-site, completing the test in just 40 minutes with a sensitivity of 98.7%[8].

Although CRISPR-Dx technology has been around for a relatively short time, its demonstrated potential is already significant, particularly in the field of infectious disease detection, where it holds great promise for the future.

2.1.2. Nanopore Sequencing (MinION)

Nanopore sequencing technology is the most significant application of nanopore technology in detection, possessing notable advantages such as single-molecule resolution, long read lengths, and portability. It holds an irreplaceable position in various fields including metagenomic sequencing, pathogen analysis, sequencing of new species genomes, and epigenetic research. The technology operates by using an electric field to drive single-stranded nucleic acids through nanoscale protein channels. The sequencing of single-stranded nucleic acids is completed by detecting changes in electrical current to identify the base sequences within the nucleic acid molecules.

During the 2014 Ebola outbreak in Guinea, scientists utilized portable sequencers to identify key mutations in the GP protein in real-time, guiding the design of vaccines. This demonstrates that nanopore sequencing technology can rapidly determine viral gene sequences, enabling efficient vaccine design for infectious viruses[9].

2.2. Targeted Therapy

Targeted therapy is a precise medical technology based on molecular biological mechanisms, with the core being the targeted intervention through the identification of specific pathogenic targets, such as gene mutations, abnormal proteins, or pathogen structures. It is mainly divided into types such as small molecule targeted drugs, monoclonal antibody drugs, and antibody-drug conjugates (ADC). Compared to traditional chemotherapy, it has advantages such as more significant therapeutic effects and relatively fewer side effects, bringing new hope and treatment options to cancer patients.

Targeted therapy can lock onto the fatal weaknesses of viruses and make targeted selections. Taking the Ebola virus as an example, its surface glycoprotein (GP) receptor-binding domain (RBD) is the key "key" for infecting host cells, and it must bind to the human cell membrane's NPC1 receptor to invade. Targeted drugs (such as monoclonal antibodies REGN-EB3, mAb114) can precisely identify and bind to the RBD region of the GP protein, physically blocking the interaction between the virus and the host receptor. Moreover, targeted therapy can also be based on real-time viral genomic monitoring (such as discovering GP-A82V mutations), quickly optimizing antibody binding sites to ensure that the drug remains effective against variant strains[5].

Case evidence: during the 2018-2019 Ebola outbreak in the Congo, teams conducted the PALM trial (Pamoja Tulinde Maisha, Swahili for "saving lives together," the first high-standard randomized controlled trial for the Ebola virus), which proved that the monoclonal antibody REGN-EB3 could reduce the Ebola mortality rate from 49% to 29%, and early administration (within 3 days of symptom onset) further reduced the mortality rate to 11%[5].

The following table compares targeted therapy with traditional supportive care :

Table 2. compation between Traditional supportive care and Targeted therapy

Indicator	Traditional supportive care	Targeted therapy (taking REGN-EB3 as an example)
Mortality rate	50%-90%[1]	29% (Early administration can reduce to 11%) [5]
Time of hospital stay	15-21 days[10]	8-12 days
Incidence rate of side effects	Electrolyte disturbance, organ failure (60%) [17]	Mild fever, rash (<10%)
Social cost	Isolate 75% of contacts[18]	Precisely isolate high-risk populations (12%) [19]

It is evident that targeted therapy, as one of the precision medicine technologies, possesses core advantages: high efficacy, low toxicity, and resource intensification.

2.3. Multi-Omics Integration

Multi-omics integration refers to the systematic integration of multi-dimensional biological data from genomics, proteomics, transcriptomics, metabolomics, and other fields to construct a comprehensive

map of host-pathogen interactions. In the prevention and control of Ebola outbreaks, its application focuses on two major directions:

①Analysis of host susceptibility: Identifying high-risk populations (such as individuals carrying the HLA-B*07 or NPC1 mutant genes) through genomics[11];

②Dynamic tracking of pathogens: Utilizing proteomics to monitor viral mutations (such as structural changes in the GP protein) and host immune response characteristics (such as neutralizing antibody repertories).

3. Comparison Between Traditional Medicine and Precision Medicine

In the previous section, I provided detailed explanations of traditional medical technology versus precision medical technology. Now, I will proceed to compare the two once more from the perspectives of detection time, cost, and mortality rate, in a manner that is accessible and easy to understand. For this purpose, I have created a table.

Table 3. Comparison Between Traditional Medicine and Precision Medicine

Comparison Items	Traditional Medicine	Precision Medicine
Detection Time	Generally longer.For example,pathological biopsy may take severa days or even more than a week; imaging examinations require queuing for appointments,and it also takes a certain amount of time to get the results.	Relatively shorter.With the help of advanced gene detection technologies and efficient data analysis, some detections can produce results in a short time.For instance, the STATseq2 system developed by Kingsmore et al. integrates whole-genome sequencing with automated bioinformatics analysis processes, reducing the diagnostic time for genetic diseases in critically ill newborns from the traditional 4-6 weeks to 13.5 hours.[20]
Cost	The detection cost is relatively low.For example,routine blood tests,X-ray examinations,etc.are not expensive However,for complex diseases,if multiple examinations and long-term treatments are required,the overall medical cost may not be low.	The research and development costs of detection equipment and technologies are high,and the cost of early gene detection and other items is relatively expensive But in the long run,due to accurate diagnosis and treatment, unnecessary examinations and treatments can be reduced,lowering the overal medical cost.
Mortality Rate	For some complex diseases,difficult and complicated cases,or advanced diseases, because it is difficult to accurately diagnose and formulate personalized treatment plans,the mortality rate may be relatively high	Through early accurate diagnosis and personalized treatment plans,the treatment effect can be improved, and the mortality rate of some diseases can be reduced.For example,early detection of pancreatic cancer and precise treatment can increase the survival rate from 3%to 44%.

Precision medicine demonstrates superior efficiency in diagnostics, cost-effectiveness, and mortality reduction.Therefore, it is precision medicine or technologies based on it that will drive the prevention and control of infectious diseases into a new era in the future.

4. Future Directions: The 'Trinity' of Infectious Disease Management Driven by Precision Medicine

The course of controlling the Ebola epidemic reveals that traditional "one-size-fits-all" medical strategies are no longer sufficient to address the threats posed by pathogens with high variability and high transmissibility. Building a "predictive-preventive-precision intervention" trinity framework based on precision medicine technology may become the core paradigm for future infectious disease management. This framework achieves a shift from passive response to proactive defense through data-driven decision-making, individualized intervention, and technology reuse networks.

4.1. Prediction: Genomics and AI-empowered Viral Evolution Tracking

Supported by precision medical technology, real-time monitoring of virus genomes and AI-based cross-species transmission prediction will become feasible in the future. Moreover, the latter is no longer a fantasy. In 2023, the EVEscape model developed by the team of Debora S. Marks et al. successfully predicted potential mutation sites (with an accuracy rate of 82%) in the Ebola GP protein by analyzing its evolutionary patterns, providing forward-looking guidance for targeted drug stockpiling [12].

Recent advancements in AI and genomics have also demonstrated the potential to predict viral evolution in real-time, enabling proactive responses to emerging threats.For instance, a research report on deep learning emphasizes the potential of deep learning algorithms in analyzing complex biological data and predicting possible transmission pathways of virus mutations through large-scale data analysis. This significantly enhances the predictive capability of virus mutations and their potential impacts on public health.[13].Additionlly, the article "Visualizing and Analyzing Research Trends and Hotspots in Viromics Based on CiteSpace" also mentions the importance and efficiency of genomics in studying virus evolution.[14]. These studies underscore the transformative potential of AI and genomics in tracking viral evolution and mitigating future pandemics.

Therefore, in the future, humans can establish a global pathogen genome database (such as GISAID), combined with AI to predict the risk of virus cross-species transmission, identify high-risk pathogens (such as Marburg virus) 6-12 months in advance, and develop a monoclonal antibody library in a targeted manner.

4.2. Warning: Precision Risk Stratification through Multi-omics Integration

With the continuous progress and development of precision medicine technology, we are now able to conduct precise screening of the host's genome and perform real - time and dynamic monitoring of proteomics. The application of this technology has not only brought revolutionary changes in the medical field but also demonstrated great potential in the fields of public health and safety.

Looking ahead, we have every reason to believe that at airports, borders, and other important transportation hubs, rapid detection devices based on CRISPR technology will be deployed. These devices will be able to quickly identify and analyze the genetic information of inbound travelers, especially the genetic risk characteristics that may affect individual health and public safety, such as the NPC1 receptor mutation associated with Niemann - Pick disease. In this way, we can achieve precise isolation through "classification upon entry" for inbound passengers, thereby effectively preventing and controlling the cross - border spread of diseases and safeguarding public health and safety.

Recent research has further confirmed the potential of multi-omics integration in precise risk stratification. For instance, in the study of scBridge, the algorithm embraces the cellular heterogeneity in multi-omics integration, improving the accuracy of cell type annotation through heterogeneity modeling (with an accuracy rate exceeding 95%). This advancement allows researchers to quickly identify diseased cells, further reducing the risk of disease spread.[15]. These advancements underscore the transformative impact of multi-omics technologies in enhancing disease prevention and control strategies.

4.3. Precision Intervention: Exploration of the Frontier of Synthetic Biology

With the support of precision medical technology, it has been possible to achieve "precise delivery of monoclonal antibody drugs and environmental intervention through synthetic biology" (e.g., "CRISPR-phage" biosensors that specifically recognize and degrade viral RNA in the environment), and so on. In the future, humans may be able to develop "nanorobot drug delivery systems," customizing the antibody release rhythm based on patients' immunogenomic data (such as T-cell receptor repertories) to achieve individualized treatment and minimize side effects.For instance, in order to treat tumors, Wang.Y. and others have proposed a stimulus-responsive robotic switch nano-device. This suggests that in the future, it may indeed be possible to develop nano-robots that target specific immune signals and release therapeutic antibodies.[16]. This breakthrough highlights the transformative potential of integrating immunogenomics and nanotechnology for personalized medicine.

5. Conclusion

The Ebola outbreak has exposed the limitations of traditional prevention and control measures, such as the delayed detection relying on symptom judgment, the inefficacy of broad-spectrum drugs, and the lack of a dynamic risk assessment mechanism. These deficiencies have been further exacerbated by the acceleration of urbanization and viral mutations, leading to increased spread of the epidemic and social panic. Precision medicine technology is reshaping the foundational logic of infectious disease prevention and control: transitioning from a "needle in the haystack" approach of mass intervention to a targeted strike under the microscope.

The introduction of precision medicine technology has not only improved the efficiency of prevention and control but also given rise to an integrated framework of "prediction - early warning - precise intervention," such as AI-driven risk stratification and nanorobot drug delivery systems empowered by synthetic biology. However, the path to precision also comes with ethical challenges, including issues of genetic data privacy, the fairness of medical resource allocation, and the lack of community engagement. These issues urgently require a global data sharing mechanism and an ethical evaluation framework to achieve a balance between technological precision and humanistic care. In the future, with the improvement of vaccine development and real-time monitoring systems, the experience of Ebola prevention and control can provide a paradigm reference for global infectious disease governance, promoting the transition from passive emergency response to an active defense system, and ultimately moving towards a new era of public health characterized by "predictability, preventability, and eradicability."

References

[1] WHO. (2016). Ebola Situation Report: 30 March 2016. https://iris.who.int/handle/10665/204714

[2] World bank.(2015).Urbanization and Cross-Border Mobility in West Africa. https://databank.worldbank.org/source/west-africa-mobility

[3] Gire, S. K., Goba, A., Andersen, K. G., Sealfon, R. S., Park, D. J., Kanneh, L., ... & Sabeti, P. C. (2014). Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. Science, 345(6202), 1369-1372.https://www.science.org/doi/10.1126/science.1259657

[4] Centers for Disease Control and Prevention (CDC). (2014). Ebola virus persistence in the environment.Retrieved fromhttps://www.cdc.gov/vhf/ebola/index.html

[5] Mulangu, S., Dodd, L. E., Davey Jr, R. T., Tshiani Mbaya, O., Proschan, M., Mukadi, D., ... & PALM Writing Group. (2019). A randomized, controlled trial of Ebola virus disease therapeutics. New England Journal of Medicine, 381(24), 2293-2303.DOI: 10.1056/NEJMoa1910993

[6] Gootenberg J S, Abudayyeh O O, Lee J W, et al. Nucleic acid detection with CRISPR-Cas13a/C2c2[J]. Science, 2017, 356(6336): 438-442. DOI: 10.1126/science.aam9321

[7] Zhao Lina Sherlock Holmes in Virus Detection - SHERLOCK System Based on CRISPR.(2020). http://www.cnipr.com/ sj/jd/202002/t20200225_237853.html

[8] Kellner, M.J., Koob, J.G., Gootenberg, J.S. *et al.* SHERLOCK: nucleic acid detection with CRISPR nucleases. *Nat Protoc* 14, 2986–3012 (2019). https://doi.org/10.1038/s41596-019-0210-2

[9] Quick, J., Loman, N., Duraffour, S. *et al.* Real-time, portable genome sequencing for Ebola surveillance. *Nature* 530 (7589), 228–232 (2016). https://doi.org/10.1038/nature16996

[10] Merler, S., Ajelli, M., Fumanelli, L., Parlamento, S., Pastore y Piontti, A., Dean, N. E., ... & Halloran, M. E. (2016). Containing Ebola at the source with ring vaccination. PLoS Neglected Tropical Diseases, 10(11), e0005093. https://doi.org/10.1371/journal.pntd.0005093

[11] Sabeti, P. C., Schaffner, S. F., Fry, B., Lohmueller, J., Varilly, P., Shamovsky, O., ... & Lander, E. S. (2016). Host genetic determinants of Ebola virus pathogenesis. Cell, 167(3), 610-624. DOI: [10.1016/j.cell.2016.07.013

[12] Thadani, N.N., Gurev, S., Notin, P. *et al.* Learning from prepandemic data to forecast viral escape. *Nature* 622, 818–825 (2023). https://doi.org/10.1038/s41586-023-06617-0

[13] LeCun, Y., Bengio, Y. & Hinton, G. Deep learning. *Nature* 521, 436–444 (2015). https://doi.org/10.1038/nature14539

[14] Zeng Xianghe, Dong Lanxia, He Xinyuan, He Hui, Liu Chang, Guo Husong ..&Fan Xiangyu. Visual analysis of viromics research trends and hotspots based on CiteSpace. Microbiological Bulletin,1-18.doi:10.13344/j.microbiol.china.241142.

[15] Li, Y., Zhang, D., Yang, M. *et al.* scBridge embraces cell heterogeneity in single-cell RNA-seq and ATAC-seq data integration. *Nat Commun* **14**, 6045 (2023). https://doi.org/10.1038/s41467-023-41795-5

[16] Wang, Y., Baars, I., Berzina, I. *et al.* A DNA robotic switch with regulated autonomous display of cytotoxic ligand nanopatterns. *Nat. Nanotechnol.* **19**, 1366–1374 (2024). https://doi.org/10.1038/s41565-024-01676-4

[17] Daniel S. Chertow, M.D., M.P.H., Christian Kleine, M.D., Jeffrey K. Edwards, M.D., M.P.H., Roberto Scaini, M.D., Ruggero Giuliani, M.D., and Armand Sprecher, M.D., M.P.H.(2014). Ebola virus disease in West Africa—clinical manifestations and management. New England Journal of Medicine, 371(22), 2054–2057.DOI: 10.1056/NEJMp1413084

[18] Eubank S, Lewis BL. Modeling the impact of interventions on an epidemic of ebola in sierra leone and liberia. PLoS Curr. (2014)doi: 10.1371/currents.outbreaks.fd38dd85078565450b0be3fcd78f5ccf

[19] Merler, S., Ajelli, M., Fumanelli, L., Parlamento, S., Pastore y Piontti, A., Dean, N. E., ... & Halloran, M. E. (2016). Containing Ebola at the source with ring vaccination. PLoS Neglected Tropical Diseases, 10(11), e0005093. https://doi.org/10.1371/journal.pntd.0005093

[20] Kingsmore SF, Smith LD, Kunard CM, Bainbridge M, Batalov S, Benson W, Blincow E, Caylor S, Chambers C, Del Angel G, Dimmock DP, Ding Y, Ellsworth K, Feigenbaum A, Frise E, Green RC, Guidugli L, Hall KP, Hansen C, Hobbs CA, Kahn SD, Kiel M, Van Der Kraan L, Krilow C, Kwon YH, Madhavrao L, Le J, Lefebvre S, Mardach R, Mowrey WR, Oh D, Owen MJ, Powley G, Scharer G, Shelnutt S, Tokita M, Mehtalia SS, Oriol A, Papadopoulos S, Perry J, Rosales E, Sanford E, Schwartz S, Tran D, Reese MG, Wright M, Veeraraghavan N, Wigby K, Willis MJ, Wolen AR, Defay T. A genome sequencing system for universal newborn screening, diagnosis, and precision medicine for severe genetic diseases. Am J Hum Genet. (2022)Sep 1;109(9):1605-1619. doi: 10.1016/j.ajhg.2022.08.003.