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Impact of Bovine on the Threat of Transmitted by Viruses Illness on Humans: Review

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Abstract

A meta-analysis of relevant scientific literature examined the frequent bovine leukemia virus (BLV) discovered in human samples. By doing searches in five different databases, we were able to locate publications that covered a broad range of academic fields. The literature was written in three different languages: Spanish, Portuguese and English. While we were collecting data from a variety of groups utilizing a comprehensive and simple search method, two researchers double-checked the criteria for inclusion and exclusion. There were 800 objects that we discovered, but only twenty of them were suitable for inclusion. The total virus frequency was 28%, with a range of 18% to 38%; there was a lot of variation in the frequencies measured between investigations. Additional investigation into the mechanism of infection and potential role in disease development is warranted in light of the virus's presence in many human biological samples.

Keywords: Bovine, viruses, bovine respiratory disease (BRD), bovine leukemia virus (BLV)

INTRODUCTION

A major problem in the cattle production systems, bovine respiratory disease (BRD) affects young animals and calves on a global scale. The illness is complex as well as multifaceted, with host, pathogen and environmental variables are playing a role in its development. The rise in BRD-related morbidity and death has persisted despite the development of more effective therapeutic and preventative drugs, enhancements to management and environmental optimization initiatives (1). There needs to be a reevaluation of BRD management options due to recent studies showing that mass therapy and vaccination provide partial control of the illness. The current state of BRD, current preventive measures and future state of security upgrades will be used to demonstrate the case for this programme (2). One innovative strategy for lowering and preventing BRD is the Norwegian BRSV and BCoV control programmers. The coder is a model of this method. It discusses possible stumbling barriers for programmers and draws attention to any significant differences between Norwegian and similar locations (3). Enzootic bovine leukosis, caused by the BLV, is on the rise in several nations but has been eradicated. More people are interested in finding ways to manage BLV in cow herds that the economic effect of BLV has been recognized. The recent advances in BLV epidemiology, diagnostics and disease control approaches, propose new topics for study, all of which have contributed to a better knowledge of the illness and its control strategies (4). The poxvirus genus Capri-poxvirus, which contains the closely related sheep pox and goat pox viruses, is the causative agent of lumpy skin disease (LSD). Although water buffalo have been known to have the disease, cattle are the most common victims. Despite the disease's supposed significance, no research has detailed the causes of its incidence on farms or the financial burdens it places on Kenyan livestock caretakers (5). To allocate scarce resources for cattle disease management on a farm and nationwide, these studies are crucial for guiding control methods. The value of lost income or the extra expenses of illness management are examples of indirect losses. The value of lost income includes the usage of less-than-ideal breeds and the inability to access local and worldwide markets. At the same time, additional expenses can arise from vaccinations, vaccine distribution, movement restrictions, diagnostic testing and culling animals (6). Diseases like brucellosis, which affect people all over the globe, have their roots in the rise of agricultural civilizations and the role of animal husbandry in those societies. Two organizations consider it a major zoonosis threat: the FAO and the WHO. To control this illness, it is beneficial to use monitoring, restrict delivery and handle reservoirs. Through the use of accurate diagnostic technologies, mass vaccination of huge populations and regular culling of animals that tested positive for Brucella, some nations have managed to bring the illness under control to some degree (7). The lack of competent immunological animals, along with improper vaccination and inaccurate diagnosis, increases the risk of disease escalation owing to increased virulence, host hopping and greater transmission across species. Earlier on, when domestic animals were kept in close quarters with their owners and handlers, contaminated dairy as well as other animal products were a major source of transmission for both bovine brucellosis and its zoonotic human version (8). This disease has expanded its host range, jumped from host to host have been transmitted across species as a result of both animal domestication and the anthropogenic adaptability of wild animals. Brucellosis has evolved into a devastating illness that can infect people and a wide range of animal species due to the pathogen's ability to alter its genes to target specific host immune response systems. This has led to significant economic losses throughout the years. Brucellosis manifests severely in humans because humans are dead-end hosts (9). It is possible to ease the execution of control and preventative operations related to BVDV at the farm level by determining the epidemiology and mitigating variables that influence production losses caused by BVDV (10, 11). The objective of this research was to examine the relationship between the amount of money lost in output due to BVDV infections in cattle coupled with the impact of various epidemiological parameters and mitigation strategies, as shown in Figure (1).

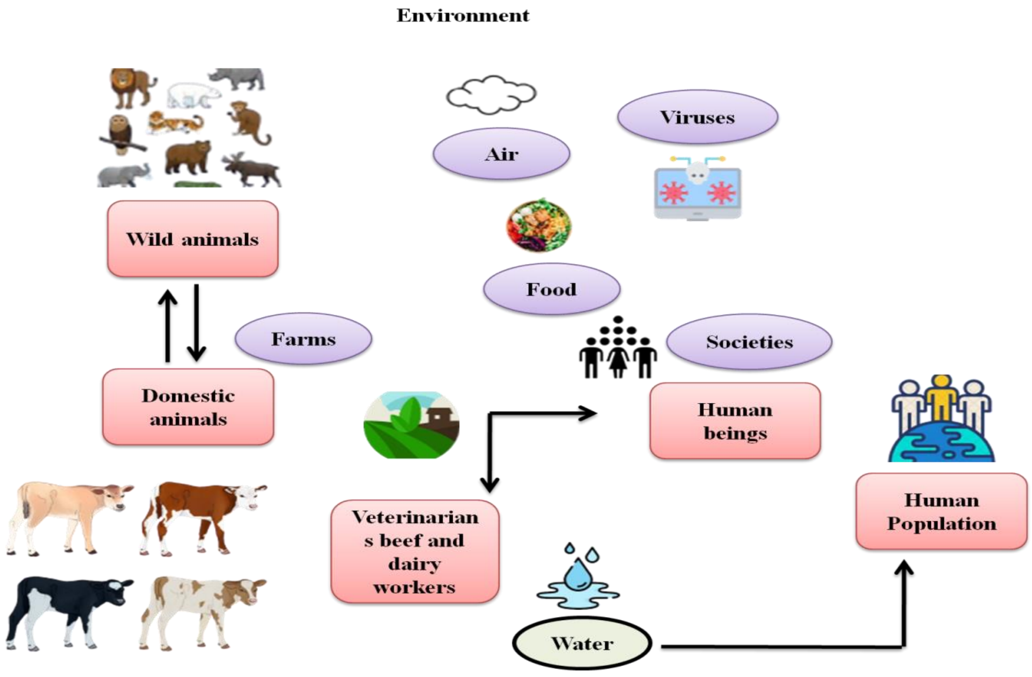

Figure (1). Vectors that might spread viruses

(Source: https://www.bing.com/images/search?view=detailV2&insightstoken=bcid_r82N-WdKwG8GHg*ccid_zY35Z0rA&form=ANCMS1&iss=SBIUPLOADGET&selectedindex=0&id=954222739&ccid=zY35Z0rA&exph=384&expw=512&vt=2&sim=1**)**

BLV causes B-cell lymphosarcoma EBL consuming EBL-positive livestock is forbidden in Japan. BLV-infected cattle with high pro-viral loads must be detected, isolated and eliminated early to avoid BLV transmission. Compare milk sEV micro-RNA (miRNA) patterns to identify BLV-prone animals (12, 13). A number of factors, including genetics, the environment and processing techniques, have the potential to influence the biochemical composition of BC and the supplements it contains. Extensive study has been conducted on BC and its derivatives. Clinical tests have shown that BC products are safe for human consumption, do not cause any adverse effects and they are well tolerated (14, 15). Ticks are effective vectors of infectious diseases because of a number of variables, such as their apparent promiscuity in host selection and the length of time they remain attached. Many different types of viruses, bacteria along with protozoa can be transmitted to humans and other animals via ticks (16). Compared to other parts of the globe, the Caribbean had less tick and tick-borne illness monitoring. Serological testing and polymerase chain reaction (PCR) are the current diagnostic tools used to identify parasites and bacteria that cause illnesses in dogs and animals. Patients in the nation have reported cases of a tick-borne rash that is similar to southern tick-associated rash illness (STARI), which can happen after a tick bite. It has been suggested that the Tacaribe virus, which was first found in bat and mosquito samples from these islands, is really carried by ticks (17). Mastitis is one of the most prevalent and difficult infections to treat in dairy cattle. This condition manifests as an inflammation of the udder tissues from several causes, such as physical trauma, chemical irritation, or infection. Although bovine mastitis has been around for a long time, it is difficult to manage due to its multi-factorial nature and complicated etiology (18). One way in which mastitis might harm human health is by giving rise to dangerous bacteria and viruses that are resistant to antibiotics. Finding effective ways to manage mastitis is an ongoing challenge for researchers. Disease prevention is the primary goal of farm management techniques (19). This involves better diagnostic and treatment processes, stricter sanitation standards and experienced staff to detect even mild udder or milk abnormalities. New technologies like genomics and proteomics-based diagnostics, vaccines and immune modulators-based prophylaxis, gene therapy and probiotic metabolic byproducts like bacteriocins can help to comprehend this complicated condition (20).

METHODS

Bovine populations can influence the spread of viruses to people. Viruses that infect only bovines, like cattle, can really infect humans if they find a suitable host. There is a concern for public health about bovine populations since they can help spread infections to people. It is crucial to closely observe and take precautions against zoonotic diseases because of the potential transmission via close contact with diseased livestock.

Study design

The first person searched through the literature in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) 2020 standards. As seen in Figure (2), the data was quantitatively synthesized.

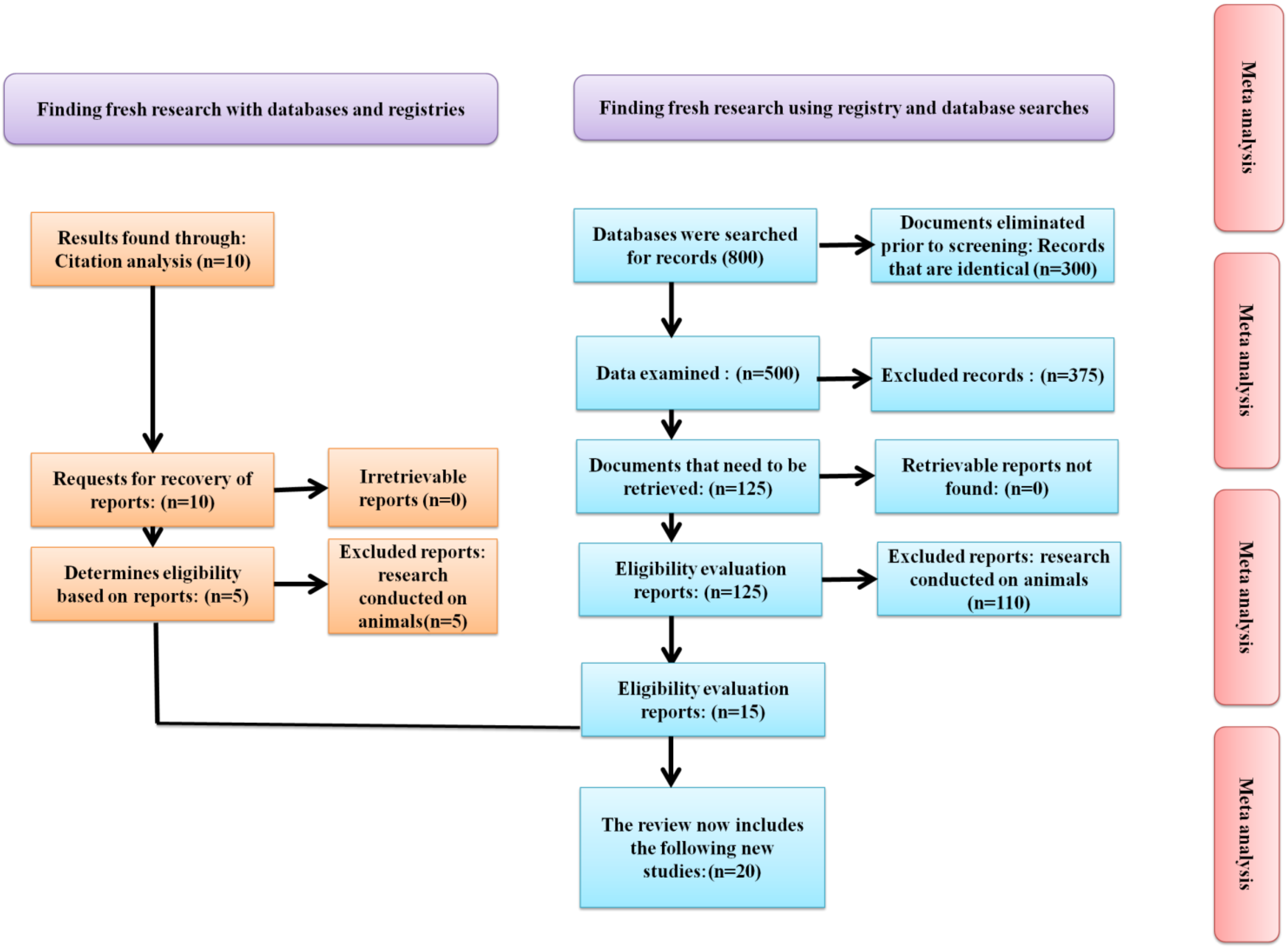

Figure (2). Flow of PRISMA

(Source: author)

Selection criteria

The articles that met the criteria were analyzed by looking at their titles, authors, years, locations of production, publishing, research populations, identification procedures, targets as well as samples used evaluation numbers and positive responses. Using the PRISMA 2020 statement checklist, two researchers found, filtered and assessed data. Methods outlined in strengthening the reporting of observational studies in epidemiology (STROBE) have been used to determine the approach. This editing guide provides a framework for conducting methodological reviews of descriptive research.

Search strategy

The following databases were searched for this information: Science Direct, Google Scholar, Scielo, PubMed, LILACS and Scopus. The indexed mesh terms include "humans," "risk factors," "prevalence," "Leukemia Virus, Bovine" and their Portuguese along with Spanish equivalents**.** Themed Subject Headings and the Thesaurus of Health Sciences were used to verify the keywords. Nine distinct search techniques in six databases were born from the combination. To find relevant results, they used the following search terms: "leukemia virus, bovine" plus "prevalence" plus "humans" in PubMed, "leukemia virus, bovine" plus "risk factors" plus "humans" in Scopus and "leukemia virus, bovine" plus "epidemiology" plus "humans" in LILACS.

RESULTS

It incorporated terms from nine search techniques in six databases: LILACS (n =150), Google Scholar (n =200), Science Direct (n =30), Scopus (n =150), Scielo (n =70) and PubMed (n =200). This initial search yielded 800 items. The deleted 500 duplicate documents. Two researchers independently assessed 500 papers' titles, keywords and abstracts. Research review articles and reports in languages other than Spanish, Portuguese and English were excluded. Neither were virus-wide reports. To read the whole content, the picked 125 papers met inclusion conditions. The excluded 110 studies that identified the virus or indicated risk factors in animal samples or agricultural products, leaving 15 carefully selected pieces. The present study contains five publications identified by reading the 15 preselected papers and reviewing their bibliographies. Finally, we examined 20 articles, as shown in Table (1).

Table (1). Information overview of the 20 publications evaluated

(Source: author)

Ref. no	**Title**	**Publication information: Journal name**	**Year**	**Site**
[21]	Prevalencia de anticuerpos contra el VLB in Colombian women.	Undergraduate dissertation	2021	Colombia
[22]	Human breast tissues contain many oncogenic viruses before developing breast cancer (BC).	Infectious Agents	2021	Australia
[23]	BC and BLV were associated, although the two viruses did not co-infect.	Cancer	2019	USA
[24]	Among Australian women, BLV is associated with BC and can be detected in its early stages.	PLoS One	2021	Australia
[25]	BLVDNA is associated with BCin women from South Brazil.	Scientific Reports	2021	Brazil
[26]	The presence of BLV in breast tissue in Argentinian women is linked to cell proliferation and prognostic indicators.	Multidisciplinary Cancer Investigation	2019	Argentina
[27]	Genomic sequencing of 51 breast cancers found that the tumours lack BVLDNA.	Retro virology	2023	Mexico / USA
[28]	DNA detection of BLVemtecidosmamarios in humans.	Master's Thesis	2022	Brazil
[29]	BLV Molecular Detection in BC Patients	Scholarena Journal of Cancer Science	2023	Sudan
[30]	Blood-borne virus found in humans	BMC infectious diseases	2023	USA
[31]	Iranian women's breast tissue and blood contain BLV	Microbial Pathogenesis	2022	Iran
[32]	Highly positive BLV levels in BC patients	PLoS One	2020	Brazil

[33]	A case-control study of BC risk factors in Colombian women exposed to BLV.	PLoS One	2022	Colombia
[34]	Water buffalo BLV prevalence	Revista Mexicana De CienciasPecuarias	2020	Colombia
[35]	Lack of BLV in buffy coats of BCpatients in Alabama, USA.	Microbial Pathogenesis	2023	USA
[36]	We learn more about BLV's zoonotic potential from the fact that its haplotypes are co-circulating in people, animals and food.	Int J Environ Res Public Health	2023	Colombia
[37]	Molecular study of BLV-BClinks	Scientific reports	2023	Pakistan
[38]	Human breast tissue has BLV DNA, which is hereditarily linked to the cow virus.	One Health	2023	Brazil
[39]	BLV: evaluation of human ensangrevirus presence and in silico analysis of involved cell receptors.	Master's Thesis	2021	Colombia
[40]	BLV with potential zoonotic evidence	Doctoral thesis	2020	Colombia

Human peripheral blood (43%), breast tissue specimens treated in neutral formalin (51%) and paraffin-embedded breast tissue (3.0%), among others, were screened for BLV (21). The researchers found a 94% association between BLV in breast tissues and blood. Human BLV antibody serology has shown conflicting findings. Materials were tested using nested PCR to target taxes, env, pol, gag and LTR genes. The research investigated the whole BLV genome. Others detected viruses using molecular and serological approaches (22, 23). Only one study employed probe-based qPCR, a compassionate and specific molecular approach used for comparing gene expression of particular genes, to detect BLV. This research, like others, did not look at gene expression. Using qPCR and WSG, the researchers were unable to detect BLV in the peripheral blood samples of cancer patients. No inhibitory controls or negative controls were provided to assess the functioning of the detection assay (24). Two investigations found no beneficial outcomes in identifying specific viral gene fragments by extensive genome sequencing (25). Possibly, whole genome sequencing identifies viral DNA, which can be too little (<1% of reads) to identify without amplification (26). The Nested PCR method enhances the sensitivity and specificity of regular PCR. This approach was the most utilized in the reviewed studies (30.1%), with varying favorable rates, as shown in Table (2).

Table (2). Variability in BLV Detection: Method, Population and Sample Impact

(Source: author)

Ref. no	**Features of the population**	**procedure**	**n**	**populace**	**example**	**Frequency of positive samples**
[21]	Leukemia patients	AGID assay	359	Selfless individuals	P.B. / Milk	1%
[22]	Selfless individuals	Complement fixation test	193	Selfless individuals	P.B. / Milk	1%
[23]	Selfless	257	75.3%	Selfless	P.B. /	Immunoblotting

	individuals			individuals	Milk	
[24]	Normal (control)	PCR in situ	90	Recipients of breast augmentation procedures	BTFFP	256%
	malevolent (cases)	-	-	-	-	23.5%
[25]	Preventative medicine	PCR	43	Syndrome of chronic tiredness	P.B.	1%
	Chronic fatigue syndrome case-patient	-	-	case-patient	-	-
[26]	Cases	Southern blot	294	Kids with ALL or NHL	B.M. and P.B./	1%
	Control group	-	-	Healthy kids	milk	-
[27]	malevolent (cases)	Nested PCR	518	Leukemia patients	B.M.	1%
	Cases of lung cancer	-	163	Cases of lung cancer	BTFFP	-
[28]	Selfless individuals	Nested PCR	78	Selfless individuals	P.B./ Cell fraction & serum	10%
[29]	malevolent (cases)breast cancer	Immunoperoxidase	57	Recipients of breast augmentation procedures	BTFFP	8%
[30]	Normal (control)	PCR	107	Recipients of breast augmentation procedures	BTFFP	46%
	malevolent (cases)	-		-		36%
[31]	Slaughterhouse workers	ELISA	455	Slaughterhouse workers	P.B./ Cell fraction & serum	14%
		AGID assay	29	-	-	8%
		PCR		-	-	1%
[32]	Normal (control)	PCR in situ	240	Recipients of breast augmentation procedures	BTFFP	30%
	malevolent (cases)	-	-	-	-	60%
	Premalignant	-	-	-	-	39%
	NA	IHC	237	-	-	6%

		IHC	216	-	-	17%
[33]	Normal (control)	PCR in situ	45	Recipients of breast augmentation procedures	BTFFP	36%
	malevolent (cases)	-	-	-	-	75%
[34]	Volunteer women	ELISA	227	Volunteer women	P.B./ Serum	1%
[35]	sequences of DNA extracted from whole genomes of healthy breast tissues	WSG	71	Recipients of breast augmentation procedures	BTFFP	1%
	sequences of DNA extracted from whole genomes of healthy breast tissues	-	-	--	-	-
[36]	Normal (control)	PCR in situ	217	Recipients of breast augmentation procedures	BTFFP	21%
	malevolent (cases)	-	-	-	-	58%
	Premalignant	-	-	-	-	35%
	malevolent (cases)	-	-	-		81%
[37]	BC patients	PCR	53	Recipients of breast augmentation procedures	BTFFP	3.9%
[38]	Blood donors	20	0%	Blood donors	P.B./ Cell fraction	PCR
[39]	Normal (control)	106	45%	Recipients of breast augmentation procedures	BTFFP	PCR
	malevolent (cases)		35%			
[40]	Normal (control)	92	65%	Recipients of	BTFFP	PCR

				breast augmentation procedures		

Possible reasons for a negative result include insufficient viral loads, target gene partial deletion or polymorphism, or the "hit-and-run virus" phenomenon, in which a virally altered cell is in detectable due to unintentional virus loss during cell division (27). The studies' findings are very diverse ($I^2 = 99\%$). Hence, a random-effects model was used to evaluate the global impact. The frequencies of virus identification varied between samples and procedures. According to the research design, as seen in Figure (3), each analysis was carried out independently (28).

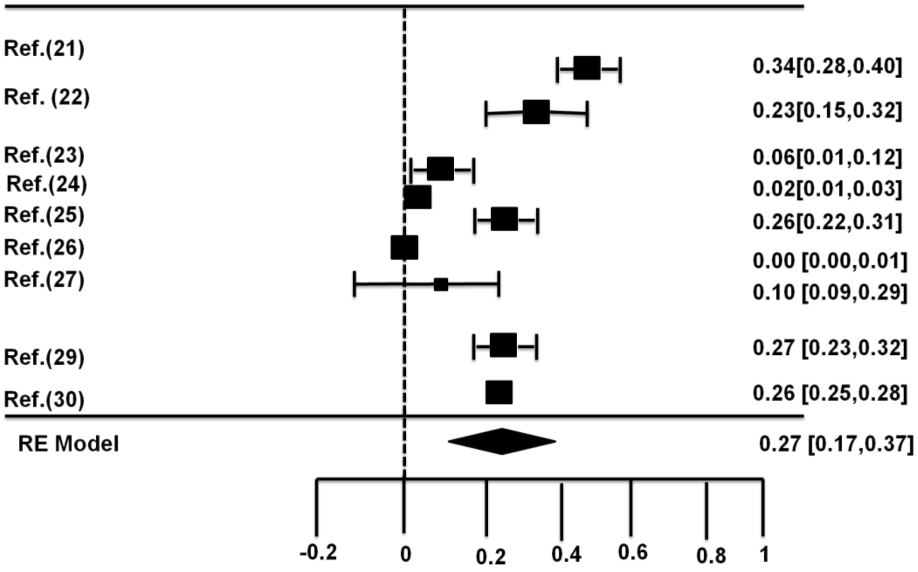

Figure (3). BLV Prevalence: A Global and Local Perspective from Nine Studies

(Source: author)

Note: The above figure shows the estimations of each research, with positivity ranging from 2% to 88%; 8 studies showed positivity of more than 51%, 16 had 3 to 42% and the total estimate was 28% with a range of 18 to 38%. No positive instances were found in 8 studies. Research without data from the four gray literature publications found that BLV-positive rates declined 3%, from 28% to 26%, with a confidence range of 15% to 36%.

The studies evaluated found BLV more prevalent in BC tissues than normal or benign tissues. Cancer is more probable from infectious agents in noncancerous tissues before cancer development. These samples were taken 4-11 years before BLV-positive breast tumors (29). It determined the impact of comparing favorable outcomes between BC patients and controls in thirteen trials by analyzing log chances and calculating odds ratios. Two studies had pessimistic point estimates, indicating a lesser probability of being positive, whereas nine studies found significant findings. A greater positive chance (30) was associated with the remaining 10. Being positive increases the risks by around 1.08 when cancer is present. The likelihood of being positive was 2.90 times higher in BC patients compared to healthy individuals, with values ranging from 1.86 to 4.55, as shown in Figure (4).

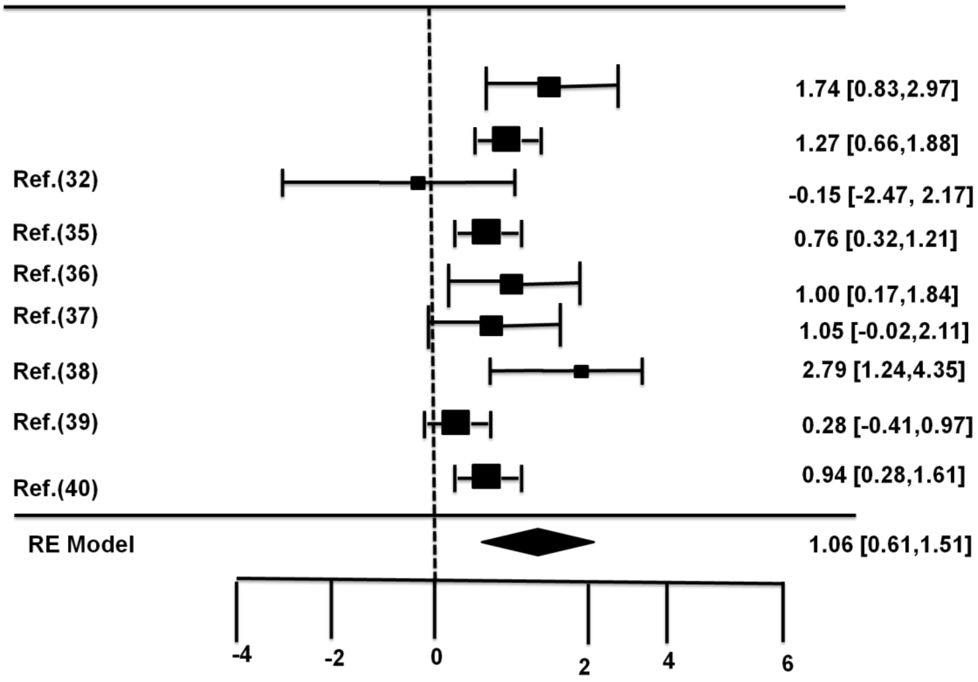

Figure (4). Statistical Analysis of 7 Analyzed Studies' Individual and Global Data Log

(Source: author)

Note: Cancer raises the incidence of BLV in the majority of studies (10/7), as seen in the figure. With a global OR of 2.889 (1.85-4.54) according to the logarithmic odds estimation, cancer-stricken women were more likely to test negative for the influenza virus than cancer-free women.

DISCUSSION

BLV rates in the investigated groups varied depending on demographic characteristics, sample size and diagnostic procedure. One study found that a BLV nested-PCR test was 96% positive in BC patients and 60% positive in undiagnosed patients (31). The majority of molecular biology techniques are exact and delicate. Reducing the likelihood of cross-contamination, in-situ PCR stops DNA from escaping control cells and human tissues. Rinsing removes impurities amplified by polymerase chain reaction, while amplified DNA inside cells stays there (32). BLV detection methods target pro-viral DNA targets such as pol, LTR, env, tax and gag. Some studies employ many targets to enhance viral detection, whereas others use one. Integrating into host cells and destroying genomes is a significant immune system evasion strategy (33). The 70 BC tissue samples analyzed utilizing whole genome sequencing did not have BLV. What went wrong with the negative genome sequencing is unknown. PCR is more sensitive than whole genome sequencing. Therefore, BLV must be in every cell and tissue. Retroviruses account for about 1% of genomes and they are 11–13 kb. A tiny sample can be contaminated and contain few virus genome copies (34). Serologic tests like AGID and complement fixation identified no BLV in early human samples. Negative results can be from sensitive reagents and processes (35). Serological testing can identify antibodies against p24 and gp51. Each subtype of virus has its unique envelope glycoprotein. It is possible that the studied area's BLV sub-species do not have the monoclonal antibodies epitome, which might affect infected humans or cattle (36). Although there are limits when using antibody detection to validate BLV infections, it is utilized to identify viral diseases (37).

The study did not investigate how BLV enters people. Some have suggested raw milk drinking as a transmission route, although the research did not control for it. BLV is common in beef and dairy herds, making human-cattle transmission possible. Many individuals have eaten raw milk and meat despite pasteurization and grilling beef to avoid the virus (38). According to this study, BC tissues exhibited higher BLV prevalence than normal or benign tissues. This research suggests this corona virus causes breast cancer. Causation in any condition requires numerous steps, starting with relationship between the diseases. Other demographic research must confirm this link (39). BLV prevalence studies differ by country due to lifestyle, diet, age, sample size and detection techniques. The presence of BLV in human samples requires further investigation into its transmission mechanism and disease development (40).

CONCLUSION

This systematic study aimed to assess the effect of cattle on human health in terms of vector-borne illnesses. Our analysis indicates that cattle can raise human VBD exposure risk, but there is evidence for their positive health benefits. We hypothesized seven methods from the literature on how cattle might affect human VBD exposure risk, influenced by ecological circumstances, vector taxa and environmental variables. However, several pathways need to be studied more and need additional research. Future research should explore the interactions between cattle, people, wildlife and vectors to create practical solutions to protect humans as well as animals from VBDs that reduce harmful environmental impacts**.**

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