DO ORGANIC, CONVENTIONAL, AND INTENSIVE APPROACHES IN LIVESTOCK FARMING HAVE AN IMPACT ON THE CIRCULATION OF INFECTIOUS AGENTS? A SYSTEMATIC REVIEW, FOCUSED ON DAIRY CATTLE

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ABSTRACT

A common thought is that extensive and organic breeding systems are associated with lower prevalence of infections in livestock animals, compared to intensive ones. In addition, organic systems limit the use of anti-microbial drugs, which may lead to lower emergence of antimicrobial resistances (AMR). To examine these issues, avoiding any a priori bias, we carried out a systematic literature search on dairy cattle breeding. Search was targeted to publications that compared different types of livestock farming (intensive, extensive, conventional, organic) in terms of the circulation of infectious diseases and AMR. A total of 101 papers were finally selected. These papers did not show any trend in the circulation of the infections in the four types of breeding systems. However, AMR was more prevalent on conventional dairy farms compared to organic ones. The prevalence of specific pathogens and types of resistances were frequently associated with specific risk factors that were not strictly related to the type of farming system. In conclusion, we did not find any evidence suggesting that extensive and organic dairy farming bears any advantage over the intensive and conventional ones, in terms of the circulation of infectious agents.

1. INTRODUCTION

It is a common view that intensive livestock farming facilitates the circulation of infectious agents within herds, possibly facilitating spill-over events of infections from animals to humans and the diffusion of emerging infectious diseases (EID) [1]. Factors that are expected to facilitate the circulation of infections in intensive management are: high density and numerosity of animals; movement of animals (or animal-derived products) to food-processing industries (or markets); sub-optimal animal welfare conditions [2]. However, this view has been called into question, at least for some types of farming management systems (FMS) [1,3]. In addition, reliable opinions on this topic requires that intensive and extensive FMS are precisely defined [1]. Intensive animal farming typically ensures a higher production per unit area [1]. Intensive farming is thus expected to reduce the extension of the land used to support animal breeding, for a given amount of produce (e.g., milk, meat, eggs). Furthermore, intensive livestock farming is frequently based on large herds, with animals placed in dense aggregations, as opposed to extensive farming in which herds are generally small, and animals not over crowded [4]. Therefore, according to [1], but differently from other views (e.g. [4]), extensive farming increases the risk of circulation of infectious agents, since it is associated with the fragmentation of farming into small holdings, with higher number of animals in a given area, in order to obtain the same production that is achieved in intensive farming with fewer animals. The fragmentation of the farming system may increase contact with wildlife and the sylvatic environment. Thus, while it has been suggested that intensive farming is associated with increased circulation of infectious agents, an alternative hypothesis is that extensive breeding is more likely to favour infections in livestock. This issue can also regard organic farming, defined by specific requirements that differ among countries, and which shares some features with extensive systems, such as the space available to animals or the fact that high production yield is generally not a primary goal in either system. In addition, extensive farming is generally assumed to be associated with a high level of animal welfare, similar to organic farming [5,6]. In turn, animal welfare is thought to be associated with increased resistance to infectious agents [7].

Along with the scientific literature, non-specialist publications (e.g. news publications, magazines and web sites devoted to scientific dissemination) have also discussed the "pros" and "cons" of intensive and conventional farming, at times in the absence of solid scientific evidence. The issue is thus well suited to be addressed through systematic analyses of the literature. A systematic review implies that search keys and inclusion and exclusion criteria are defined *a-priori*, in order to obtain unbiased retrieval of relevant publications. Systematic reviews are frequently performed according to the PRISMA protocol [8]. The resulting scientific literature is then examined to build a general, unbiased view of the topic, rather than an "advocacy publication".

In this systematic review we focused on dairy cattle farming, to evaluate the current knowledge on the circulation of infectious agents and the diffusion of antimicrobial resistance in relation to the type of management system. We specifically defined the search keys to retrieve publications in which the different types of managements (intensive and extensive; conventional and organic) have been directly compared. Furthermore, the circulation of infectious agents in herds, in terms of both acute and chronic infections, may impact on the quality of animal-derived foods. Therefore, a systematic review, or metanalysis, to determine whether the prevalence of infections in herd is influenced by the type of management systems might also provide indirect information on the quality of food production, and in this specific case, quality of milk and milk-derived products, as recently emphasized by the Food and Agriculture Organization of the United Nations [9]. The present metanalysis is not specifically addressed to livestock veterinary practitioners and stakeholders of milk production chain, whose interest is likely focused on specific risk factors associated with cattle infections. Rather, the aim is to target those “non-specialist” readers such as journalists, science communicators, and politicians, who have the responsibility to inform the general public, orienting (and taking) decisions on laws and regulations. Indeed, the issue of intensive and extensive production (or conventional and organic) is hotly debated in governmental institutions (e.g. [10]), non-governmental organizations (e.g. [11]), and newspapers (e.g. [12]). In this context, the public deserves information based on unbiased reports to prevent the creation and circulation of ideological positions. The purpose of this article is thus to respond to this need for information, with a search on the scientific literature that is not biased by preconceptions.

2. METHODS

In this study, we followed the PRISMA guidelines [8] and carried out the bibliographic search on the Scopus database (search day: 4/3/2023). Literature retrieval strategy consisted in the search for publications in which dairy cattle management systems have been compared. Specifically, the type of searched comparisons was as follows: intensive VS extensive (IvsE) or conventional VS organic (CvsO). The different types of management systems were compared in relation to the following: 1) infectious agents (IA) or infectious diseases (ID); 2) antimicrobial resistance/susceptibility (AMR/AMS). The search terms were selected according to synonyms present in the literature. In addition, we assumed that publications focused on anti-parasitic and antimicrobial drug use (AMU) might provide results relevant to the issues of IA/ID and AMR/AMS, and we thus included terms related with the use of these drugs (even though the specific issue of AMU was out of the scope of this study). The following search terms and Boolean operators were used; the two query strings are reported below. Two query strings were used rather than combining all search terms into a single string in order to obtain two separate outputs for IvsE and CvsO.

((TITLE-ABS-KEY (intensive*) AND TITLE-ABS-KEY (cow) OR TITLE-ABS-KEY (cattle) AND TITLE-ABS-KEY (milk) OR TITLE-ABS-KEY (dairy) OR TITLE-ABS-KEY (cheese) AND TITLE-ABS-KEY (infect*) OR TITLE-ABS-KEY (parasit*) OR TITLE-ABS-KEY (pathogen*) OR TITLE-ABS-KEY (zoono*) OR TITLE-ABS-KEY (microb*) OR TITLE-ABS-KEY (vir*) OR TITLE-ABS-KEY (protozo*) OR TITLE-ABS-KEY (mico*) OR TITLE-ABS-KEY (fungi*) OR TITLE-ABS-KEY (nematod*) OR TITLE-ABS-KEY (helmint*) OR TITLE-ABS-KEY (antibiotic*) OR TITLE-ABS-KEY (antimicrobial*) OR TITLE-ABS-KEY (amr) OR TITLE-ABS-KEY (antiparasit*) OR TITLE-ABS-KEY (drug*) AND TITLE-ABS-KEY (extensive*) OR TITLE-ABS-KEY (pastur*) OR TITLE-ABS-KEY (graz*)))

((TITLE-ABS-KEY (conventional*) AND TITLE-ABS-KEY (cow) OR TITLE-ABS-KEY (cattle) AND TITLE-ABS-KEY (milk) OR TITLE-ABS-KEY (dairy) OR TITLE-ABS-KEY (cheese) AND TITLE-ABS-KEY (infect*) OR TITLE-ABS-KEY (parasit*) OR TITLE-ABS-KEY (pathogen*) OR TITLE-ABS-KEY (zoono*) OR TITLE-ABS-KEY (microb*) OR TITLE-ABS-KEY (vir*) OR TITLE-ABS-KEY (protozo*) OR TITLE-ABS-KEY (mico*) OR TITLE-ABS-KEY (fungi*) OR TITLE-ABS-KEY (nematod*) OR TITLE-ABS-KEY (helmint*) OR TITLE-ABS-KEY (antibiotic*) OR TITLE-ABS-KEY (antimicrobial*) OR TITLE-ABS-KEY (amr) OR TITLE-ABS-KEY (antiparasit*) OR TITLE-ABS-KEY (drug*) AND TITLE-ABS-KEY (organic*)))

Outputs generated by the two query strings were subjected to the same eligibility criteria and the same PRISMA procedure. The inclusion criteria were: (1) a publication must be an original study, in which conventional management was compared to organic management (CvsO), or intensive management was compared to extensive management (IvsE), of dairy cattle farms; (2) results must refer to: the presence, prevalence, or incidence of an infectious agent or infectious disease; the use of antimicrobials; the presence of drug-resistant (AMR) or drug-susceptible (AMS) microbes or parasites (where "drug" is intended as an antimicrobial product).

The exclusion criteria were as follows: publications classified as reviews, or other types of secondary studies such as book chapters, conference publications, notes and incomplete text articles. The full texts of all potentially relevant studies were downloaded in their entirety. A further round of screening was applied through careful reading of the abstracts (carried out by three co-authors independently, who subsequently discussed the doubtful cases), in order to collect and identify all those studies that met the eligibility criteria, gradually excluding those identified as "not pertinent for some classified reasons" ** as described in the PRISMA flow chart (Fig. 1).

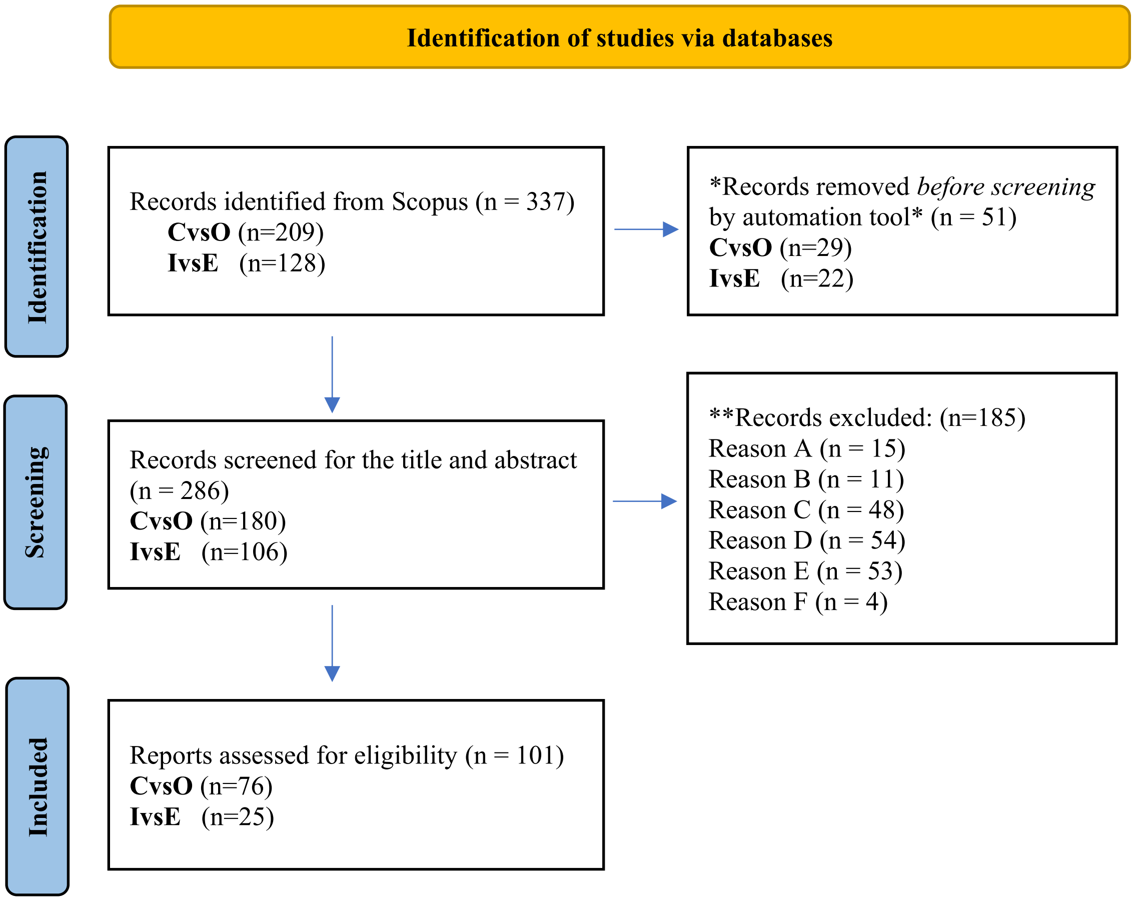

Figure 1. PRISMA flow chart presenting the results of the searching strategy and the exclusion process.* An automatic filter was applied to automatically exclude publications classified as “note”, “conference publications”, “book chapter”, “review”. ** A manual operation to identify publications defined “not pertinent” for the follow reasons (A, B, C, D, E, F); A: items focused on the issue of “consumer perception” or “farming policy”; B: items that did not refer to “dairy cow” (e.g., those focused on dairy buffalo or other dairy animals); C: items that did not perform, in the same study, a direct comparison CvsO or IvsE; D: the terms “extensive “intensive” “organic”, “conventional” did not refer to the farming management system; E: items that did not compare CvsO or IvsE according to eligibility criteria nº 2; F: publications classified as “note”, “conference publications”, “book chapter”, “review”.

3. RESULTS AND DISCUSSION

3.1. Overall results

A total of 336 items were retrieved from the Scopus platform. According to pre-defined eligibility criteria, as reported in the PRISMA flow-chart (Fig. 1), we finally selected 101 publications, 77 dealing with the comparison CvsO, and 25 with IvsE (one publication addressed both comparisons). We emphasize that part of these publications presented two or more studies, focused on different ID/IA or on both ID/IA and AMR. Therefore, the total number of studies (132) was higher than the number of publications (101). These 132 studies are reported in Tables 1-3, indicated as study numbers Sn1-Sn132, with the corresponding references. Also in the main text, the quoted studies will be referred to by indicating the Sn code, as reported in the Tables. The countries where the studies had been conducted and year of publication are reported in supplementary material (Tab S1 – S3). In total, 102 studies focused on f ID/IA and 30 on AMR. A higher number of studies was focused on CvsO (73 on ID/IA; 27 AMR), compared with IvsE (29 on ID/IA; 3 AMR). The countries where the studies had been conducted are also presented in figures 2 and 3 present. Comparative studies on IvsE were mainly conducted in Mediterranean and sub-Saharan countries, Far East Asia, and South America, while studies on CvsO were mainly conducted in North and South America, North and Central Europe, and Mediterranean countries. Studies on AMR/AMS came mainly from CvsO comparisons, mostly from North America and Europe. The two major ID groups that had been investigated in both CvsO and IvsE are: 1) intra-mammary infections (IMIs), with 31 studies (3 IvsE and 28 CvsO), mainly from North America and Europe and 2) gastrointestinal parasitic infections (GPIs), with 20 studies (4 IvsE and 16 CvsO) mainly from European countries. A full report and discussion on IMIs and GPIs can be found below in the main text. For the remaining IDs/IAs, for which the number of studies is limited, a complete list is reported below, with results and comments summarized in the supplementary material (Tab. S4). In general, the different dairy FMS (C, O, I, E) do not always appear to be associated with the incidence or prevalence of a given infection or disease. Furthermore, most of the studies did not clearly define the criteria for the attribution of a farm to the O or C group, even if several of the studies referred to the national transposition of the FAO guidelines on organic farms [13]. Similarly, different studies classified I and E farms based on different criteria. Furthermore, a number of studies evaluated the risk factors associated with the prevalence/incidence of IDs, IAs or AMR, with less attention to the relevance of these risk factors in relation to the type of farming management systems (FMS) in terms of C, O, I, E. However, since the goal of this study was to contribute to the public debate on animal welfare and ecological sustainability issues associated with the different FMS, we will only report briefly on the specific risk factors (RFs).

Tab. 1. Comparative studies on the presence of infectious diseases or infectious agents (ID/IA), in intensive versus extensive management (IvsE, on the left) and conventional versus organic management (CvsO, right), in which the investigated ID/IA coincide.

ID/IA	IvsE		CvsO	
	Sn	ref	Sn	ref
GPIs**	**Sn3-Sn6**	[57-60]	**Sn21-Sn36**	[14,18,25,40,45-56]
IMIs*	**Sn5-Sn7**	[42-44]	**Sn32-Sn59**	[14-41]
Campylobacter	**Sn8**	[72]	**Sn60, Sn61**	[70,71]
Ectoparasite	**Sn9**	[73]	**Sn62-Sn64**	[49,24,25]
MAP***	**Sn10;Sn11**	[64,65]	**Sn65-Sn67**	[61-63]
Mycosis	**Sn12**	[74]	**Sn68**	[74]
Urogenital Inf.	**Sn13**	[69]	**Sn69, Sn70**	[29,34]
Viruses	**Sn14-Sn15**	[64,68]	**Sn71, Sn72**	[66,67]

*IMIs, Intra Mammary Infections; **GPIs, Gastrointestinal Parasitic Infectious; ***MAP, *Mycobacterium avium subspecies paratuberculosis*, **Sn**, **study number;** ID/IA, infectious disease/infectious agent; ref, reference

Tab. 2. Comparative studies on the presence of infectious diseases or infectious agents (ID/IA), in intensive versus extensive management (IvsE, on the left) and conventional versus organic management (CvsO, right), in which the investigated ID/IA do not coincide.

IvsE			CvsO		
ID/IA	Sn	ref	ID/IA	Sn	ref
Anaplasma	**Sn73**	[93]	Aero. Spor. Bact.**	**Sn84**	[84]
Brucella	**Sn74, Sn75**	[89,90]	Lameness	**Sn85-Sn88**	[15,25,29,34]
Chlamidia	**Sn76, Sn77**	[64,91]	*Listeria* sp.	**Sn89, Sn90**	[83,31]
Coxiella	**Sn78**	[92]	Pneumonia	**Sn91, Sn92**	[29,34]
Neospora	**Sn79**	[64]	*Salmonella* sp.	**Sn93-Sn97**	[31, 79-82]
Tuberculosis	**Sn80-Sn83**	[85-88]	STEC*/ STEB*	**Sn98-102**	[31, 75-78]

*STEC, Shiga Toxigenic *Escherichia coli*; *STEB, Shiga Toxigenic Encoding Bacteria; **Aero. Spor. Bact., Aerobically Spore-forming Bacteria; **Sn**, **study number**; ID/IA, infectious disease/infectious agent; ref, reference

Tab. 3. Comparative studies of antimicrobial resistance/antimicrobial susceptibility (AMR/AMS) in infectious diseases or infectious agents (ID/IA) in intensive versus extensive management (IvsE, on the left) and conventional versus organic management (CvsO, right)

IvsE			CvsO		
ID/IA	Sn	ref	ID/IA	Sn	ref.
E. coli	**Sn103**	[94]	*E. coli*	**Sn106-Sn114**	[19,76;96-103]
Pasteurellaceae	**Sn104**	[94]	*Campylobacter*	**Sn115, Sn116**	[113,71]
MCGT**	**Sn105**	[95]	IMIs***	**Sn117-Sn125**	[30,32,39,41,104-108]
			Listeria spp.	**Sn126**	[83]
			MCGT**	**Sn127-Sn129**	[109-111]
			Salmonella spp.	**Sn130, Sn131**	[19,112]
			STEC*	**Sn132**	[98]

*STEC, Shiga Toxigenic *Escherichia coli;* **MCGT, Microbial Community Gene Transfer; ***IMIs, Intra Mammary Infections; **Sn**, **study number**; ID/IA, infectious disease/infectious agent; ref, reference

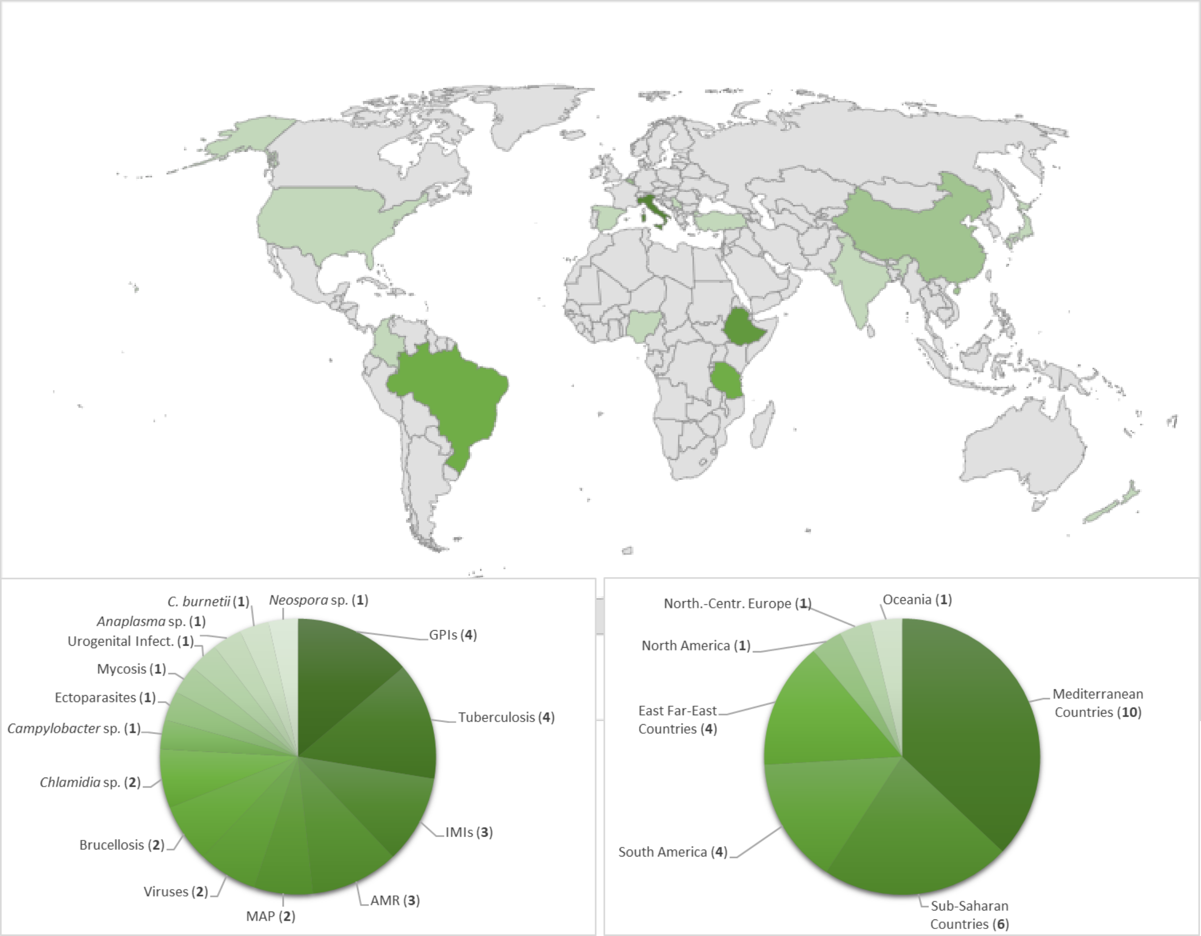

Fig. 2. Countries where IvsE investigations have been conducted and relative prevalence of the studies on the different ID/IA or on AMR.

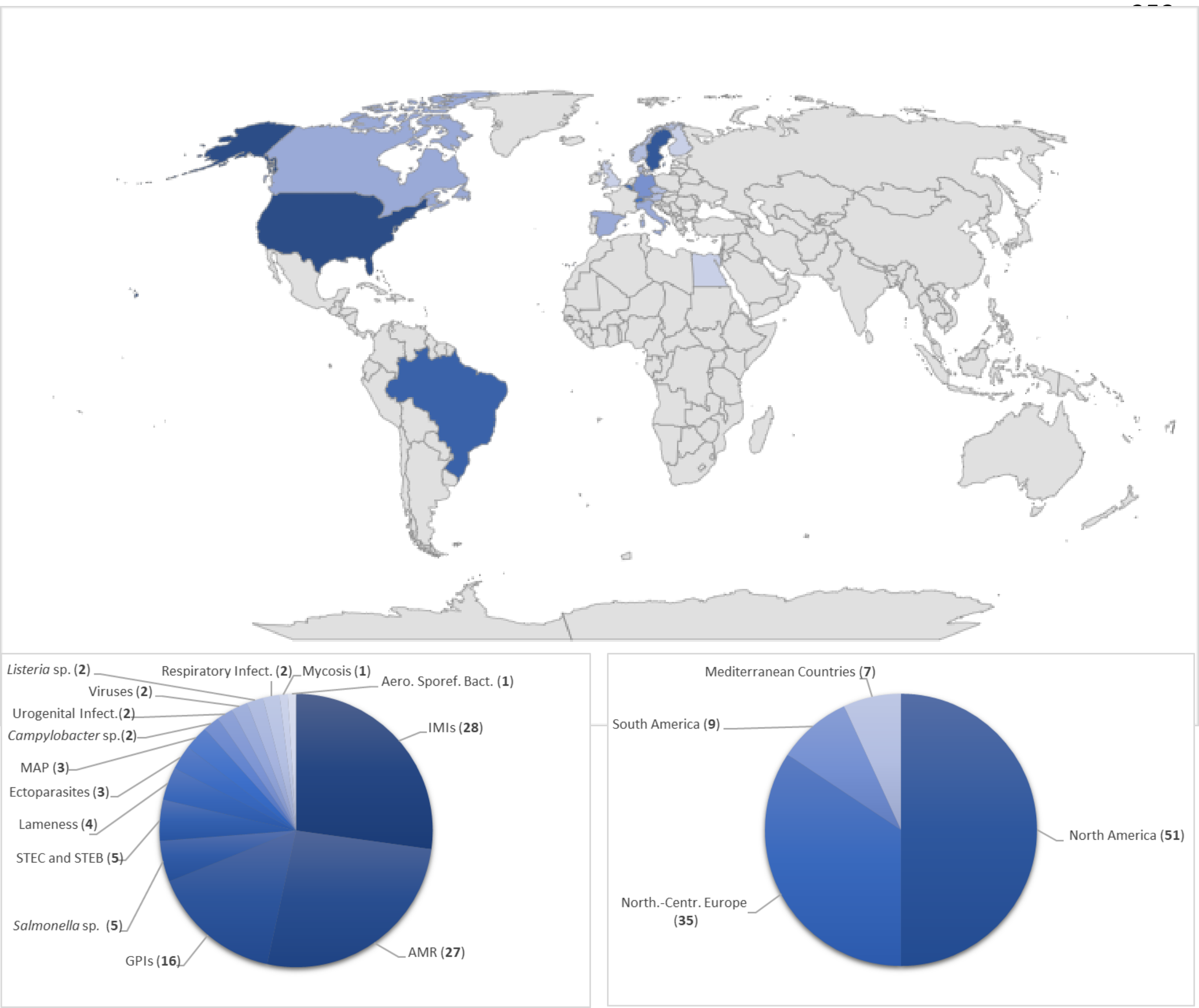

Fig. 3. Countries where CvsO investigations have been conducted and relative prevalence of the studies on the different ID/IA or on AMR.

3.2. Intramammary infections

Thirty-one studies focused on IMIs were retrieved. Twenty-eight of these dealt with CvsO (Sn32-Sn59) [14–41]; three with IvsE (Sn5-Sn7) [42–44].

Eight out of the 28 studies on CvsO didn't report any significative difference between C and O (Sn32; Sn35; Sn40; Sn44; Sn46; Sn49; Sn57; Sn58), six studies reported a higher prevalence/incidence of IMI in C (Sn38; Sn41; Sn42; Sn47; Sn52; Sn59); one study reported a higher prevalence/incidence of IMI in O (Sn56). Among the remaining 13 studies, six were focused on the risk factors associated with IMI (see below); seven highlighted apparently contrasting results. Sn55 recorded higher somatic cell counts (SCCs) in organic farms at day 31 DIM (day in milking), which were however similar to that of conventional herds at 102 DIM; in addition, higher prevalence of non-agalactiae streptococci was recorded at both 31 DIM and102 DIM in O compared to C, but the prevalence of coagulase-negative staphylococci was lower in O at 102 DIM. These fluctuations in cellular and microbial counts were not associated with clinical or sub-clinical mastitis. Similarly, in Sn41, higher counts of mesophilic and coliform bacteria were found in milk samples from O, but with no significant correlations with IMIs. A Norwegian study (Sn50) highlighted a higher proportion of dried off quarters in O vs. C, but did not find any difference in the number of quarters positive for mastitis bacteria, even if lower SCC in O cows was noted. Another study conducted in Sweden (Sn33) reported higher prevalence of IMI in C, even though bulk milk SCCs was higher in O. A German study (Sn51) didn't report any difference in bulk milk SCCs, but reported a higher portion of organic vs. conventional individual cows with SCC > 150,000 at both 3 months before and 3 months after the dry period. A study conducted in the USA (Sn48) monitored several farms for three years during the transition from C to O, highlighting a higher incidence of mastitis in O at parturition, but no differences at dry-off. Finally, Sn39 reported that the incidence rate of clinical mastitis was higher in C compared to O (23.7 vs. 13.2 cases per 100 cows per year), however, bulk tank SCC tended to be lower in C.

Among the three retrieved studies on IvsE, in one the prevalence of mycotic mastitis in China was higher under extensive management (Sn6). One study, focused on *S. aureus* biofilm-producer strains in different regions of Serbia, didn't find any differences under intensive or semi-extensive dairy farms (Sn5). Finally, a study conducted in the USA (Sn7) focused on the risk factors associated to grazing management.

Part of the studies retrieved with the query string for CvsO (namely: Sn34, Sn44, Sn47, Sn53, Sn54) were focused on the risk factors associated with IMI, and only to a lesser extent on the effects of the type of management, C or O, on the prevalence or incidence of these infections. Highlighted risk factors include: lactation number, farming part time, poor cleanliness of udders, size of the herd, use of mineral feed supplements, irregular milking intervals, milk urea concentrations, water temperature for washing the milking system, bedding area, timing of antibiotic treatments in relation to dry period (C only), hygiene, extent in the use of external resources, number of people responsible for mastitis treatment, age of the premises, percentage of cows with three or fewer quarters, use of fore stripping, proactive detection of mastitis during postpartum (and thus treatment), and stall barn housing. In addition, environmental temperature and duration of the infection in positive cows were associated with the incidence of mycotic mastitis (Sn6). Evidence for the role of genetic susceptibility to IMI was also reported in Sn36. A reduction in the risk of mastitis was associated to regular access to pasture, automatic milking shut-off and access to feed immediately after milking (Sn34). None of these factors appear to be specifically associated with C, O, I, E. However, they represent important leverage points for management towards healthier animals in terms of rational grazing (e.g., through rotational grazing rather than confined grazing) that are not specifically linked to intensive or extensive FM (Sn7).

3.3. Gastrointestinal parasitic infections

Twenty studies focused on GIPs were retrieved. Sixteen of these dealt with CvsO (Sn16-Sn31) [14,45–47,18,48,49,25,50–54,40,55,56], while the remaining four dealt with IvsE (Sn1-Sn4) [57–60].

Three out of 16 studies comparing CvsO (Sn21, Sn24, Sn25) didn't report any significative difference, four studies reported a higher GPIs in conventional farming (Sn16, Sn18, Sn19, Sn30), five studies reported a higher GPIs in organic farming (Sn22, Sn23, Sn27, Sn29, Sn31), and the remaining four studies (Sn17, Sn20, Sn26, Sn28) were focused on risk factors associated to GPIs, not strictly related with the type of management. Studies on *Cryptosporidium* spp. infection provided apparently contradictory results. According to Sn24, there was no difference in the prevalence in either calves or cows; however, another study (Sn28) found higher levels of parasite shedding in organic farms, but a variety of factors not strictly related with the type of management might be associated with parasite shedding. Studies focused on fascioliasis (Sn21; Sn27), reported no significant difference between the two management types, while another (Sn18) detected significantly lower prevalence in O farms, probably due to continuous exposure to the parasite, leadings to better resilience (Sn16). Studies considering *Ostertagia ostertagi* highlighted contrasting results: two studies (Sn25; Sn29) found no correlation between infection and FMS, while another (Sn27) reported the opposite. Studies on the lungworm *Dictyocaulus viviparus* also reported contrasting results: Sn30 detected *D. viviparus* only on C, while Sn27 reported a prevalence of 18% in O and 9% in C herds. Interestingly, infected conventional herds were located near infected organic herds. Two studies (Sn22; Sn23), conducted in North and South America, reported a significatively higher prevalence of strongyle-type fecal eggs on O farms, while a German study (Sn19), highlighted a significantly higher prevalence C farms and pointed out the risk factors associated to seasonality. Another German study (Sn20) considered the issue of bovine genetics as a risk factor for parasitic infections, not strictly related to different FMS, even if particular genetic traits could be preferred in relation to the type of farming. Moreover, as highlighted in a Danish study (Sn17), estimations GPIs can also vary in relation with the type diagnostic method used.

Two out of four studies comparing IvsE reported higher GPIs on extensive farms (Sn2, Sn4), one reported higher GPIs in intensive farming, but also considered other risk factors (Sn1), while the other was focused only on risk factors (Sn3). Sn2 (conducted in Spain) reported a higher prevalence of *Ostertagia ostertagi* in EvsI, but the different environmental contexts could explain this result. Similar findings came from Sn4 (conducted in Italy) that compared two intensive farms (located in the Po River Valley) with an extensive farm (in an Alpine Mountain region), but again the differences in the sampling areas could represent an important confounding factor. Sn1, conducted in Ethiopia, highlighting a lower prevalence for cryptosporidiosis in IvsE; however, the authors note that the infection was significantly associated not only with the FMS but also with same others RFs like farm location, herd size, source of drinking water, weaning age, presence of bedding, pen cleanness and cleanness of hindquarters. Sn3, conducted in Tanzania, showed that prevalences of nematodes and flukes vary widely with geographic location and grazing management, further highlighting that several RFs not specifically related to the type of farming, (e.g. communal grazing and watering management practices) play a role in the circulation of parasitic worms.

3.4. Miscellaneous of retrieved IDs/IAs with limited comparative studies

This paragraph presents a complete list of the IDs/IAs for which the number of comparative studies is limited. Results and comments are summarized in the supplementary material (Tab S4).

IDs/IAs present on both CvsO and IvsE: five studies on MAP (Sn65-Sn67 CvsO [61–63]; Sn10-Sn11 IvsE [64,65]), four studies on viral infections (Sn71-Sn72 CvsO [66,67], and Sn14-Sn15 IvsE [64,68]), three studies on urogenital infections (Sn69-Sn70 CvsO [29,34], and Sn13 IvsE [69]), three studies on *Campylobacter* sp., (Sn60-Sn61 CvsO [70,71], and Sn8 IvsE [72]), four studies on ectoparasites (Sn62-Sn64 CvsO [49,24,25], and Sn9 IvsE [73]), two studies on zoonotic dermatophyte (Sn12 CvsO [74], and Sn68 IvsE [74]).

IDs/IAs present only on CvsO: Shiga Toxigenic *E. coli* (STEC) and Shiga Toxigenic Bacteria (STEB) (Sn98-Sn102) [31,75–78], Lameness (Sn85-Sn88) [15,25,29,34], Salmonella sp. (Sn93-Sn97) [31,79–82], pneumonia (Sn91-Sn92) [29,34], Listeria sp. (Sn89-Sn90) [83,31] and aerobic spore-forming bacteria (Sn84) [84].

IDs/IAs present only on the IvsE: tuberculosis (Sn80-Sn83) [85–88], Brucellosis (Sn74-Sn75) [89,90], *Chlamidia* sp. (Sn76-Sn77) [64,91], *Coxiella burnetii* (Sn78) [92], *Neospora* sp. (Sn79) [64], and *Anaplasma marginale* (Sn73) [93].

3.5. Antibiotic resistance/susceptibility (AMR/AMS)

Among the 30 studies retrieved, 27 compared CvsO (Sn106-Sn132) and three IvsE (Sn103-Sn105). In general, a higher circulation of AMR genes was found on conventional and intensive FMS.

AMR/AMS in CvsO. Ten studies on AMR/AMS strains of *Escherichia coli* (Sn106-Sn114, Sn132) [94,19,95–99,76,100,101] were retrieved . Six were conducted in the USA. Sn113 didn’t find any significant difference across FMS for the abundance of *E. coli* O157 virulence marker genes, antimicrobial susceptibility profiles, and genotypes. On the contrary, Sn107 found significantly more abundant resistance genes in animals bred on conventional farms, but no significant differences in carcasses or beef trimmings. *E. coli* strains isolated from fecal samples showed a significantly higher resistance to seven out of 17 antimicrobial molecules on conventional farms (Sn114). Furthermore, AMR was strongly influenced by animal age, geographical region (dairy-intense flat land or more extensive foothill pasture) and whether cattle were raised for dairy or beef (Sn111). Sn112 assessed the association between age of cattle, and AMR/AMS in *E. coli* phylogroups isolated from both FMS. Here the authors used a hierarchical log-linear modeling approach that accounts for additional confounding factors, resulting in more robust relationships; The study provided evidence of clonal resistance (ampicillin) and genetic hitchhiking (tetracycline), reporting a significant association between low multidrug resistance, organic herds and numerically dominant phylogroup B1 strains, suggesting that the genetic composition of the herds may influence the AMR/AMS. Additionally, authors estimated that it would take from three to 15 years to have a significant change in bacterial populations passing from conventional to organic farming. Another study (Sn132) found a significantly higher proportion of non-susceptible spectinomycin in Shiga Toxigenic *E. coli* (STEC) isolates from conventional farms. Resistance to sulphadimethoxine in calves (but not in adult milking cows) was significantly higher on conventional farms. Multidrug resistant (MDR) patterns were more commonly found in non-O157 STEC vs. O157 STEC and the percentage of MDR on the two farm types was similar. A Swedish study (Sn108) found little significant difference for resistance to single antimicrobials on conventional farms. Most conventional herds had a rather high proportion of isolates resistant to at least one antimicrobial, but MDR strains were rare. A study conducted in Czech Republic (Sn110), revealed a higher prevalence of *E. coli* isolates producing an extended-spectrum beta-lactamase (ESBL) on conventional farms compared to organic ones. A Swiss study (Sn106) didn't find any significative difference in the AMR of *E. coli* strains isolated from young dairy calves, but did report that the ESBL-producing Enterobacteriaceae were more prevalent in conventional farms.

Nine studies on AMR/AMS on IMIs were retrieved (Sn117-Sn125) [102,103,30,32,104–106,39,41]. Three out the four studied conducted in USA (Sn125, Sn121, Sn122), found that *S. aureus* isolates from milk samples from C were significantly more resistant for the majority of tested antimicrobial molecules (Sn121, Sn125). Sn122 found that AMR of IMIs-associated pathogens were more common in C, yet the prevalence of bacteria responsible for mastitis was higher on O (with the exception of coliforms). Finally, a high proportion of sulfadimethoxine-resistant isolates were observed in both FMS, and were higher on O. Another study from USA (Sn119) was focused on the conversion process from conventional to organic management over a 3-year period; coagulase-negative staphylococci (CNS) were the most prevalent bacteria responsible for mastitis. They were significantly less resistant to β-lactam antibiotics after herd transitioned to O. AMR significatively decreased for ampicillin, cephalothin, cloxacillin, and penicillin for CNS, but not for *S. aureus*. This suggests that cessation of antibiotic use, in combination with organic management, reduced AMR of mastitis bacteria, even if the prevalence of *S. aureus* did not change significantly as herds transitioned from conventional to organic FMS. Similar results were reported in a Belgium study (Sn124) which found that the three most frequently isolated pathogens (*Streptococcus uberis*, *Staphylococcus aureus* and *Streptococcus dysgalactiae*) were significantly more resistant to antimicrobials on C. On the contrary, a Norwegian study (Sn120), did not find a significant difference in penicillin resistance against coagulase-negative staphylococci isolated from sub-clinically infected quarters, while a Swiss study (Sn123), found that AMR of *Staphylococcus* spp. and *Streptococcus* spp. was not significantly different in CvsO, except for *S. uberis,* which tended to have more single gene resistance on OvsC ones. Finally, a Brazilian study (Sn117), on *Staphylococcus* strains sampled in Minas Frescal cheese found no significant prevalence related to FMS.

Three studies on AMR/AMS in microbial communities and gene transfer phenomena MCGT (Sn127-Sn129) [107–109]. A Canadian study (Sn127) analyzed publicly available metagenomics data, showing that organic practices are generally associated with lower prevalence of AMR Genes (AMRGs). Sn129 affirmed that the abundance and diversity of ARGs in feces was significantly higher in conventional vs. organic herds. All manure storage and soil samples had a diversity (albeit low abundance) of AMRGs conferring resistance to several antibiotics. Antimicrobial use on farms significantly influenced specific groups of AMRGs in feces, but not in manure storages or soil samples. Similar results from a Spanish study (Sn128), based on the monitoring AMRGs and mobile genetic elements (MGEs) in different types of comparisons (amended vs. unamended, CvsO, slurry vs. fresh or aged manure), found that the spread of AMRGs-MGEs cannot be inferred directly from any of the individual comparisons (including CvsO).
Two studies on AMR/AMS in *Salmonella* strains (Sn130, Sn131) [19,110]. (both conducted in the USA). Sn130 found significantly higher circulation of AMRGs on C, but differences in carcasses or beef trimmings were not significant. Sn131, using logistic proportional hazards models, found that isolates from C were significantly associated with higher MIC for only two out of nine antimicrobials (streptomycin and sulfamethoxazole). Moreover, *Salmonella* isolates resistant to five or more antimicrobial agents were found on both FMS.
Two studies on AMR/AMS conducted on *Campylobacter* strains (Sn115, Sn116) [111,71] (both conducted in the USA). Sn115 found that resistance to one out of four antimicrobial molecules tested was more prevalent in C, while Sn116, did not find any difference.
Similar results came from the only recovered study focused on *Listeria monocytogenes* (Sn126) [83], conducted in USA.

AMR/AMS in IvsE comparisons. Three studies on IvsE (Sn103-Sn105) [112,113].
An Indian study (Sn105) [113], comparing intensive farms vs. farms were animal had access to grazing, found that fecal bacteria from intensive farms were characterized by higher prevalence of AMR, which was also affected by feeding practices and nutrient concentration. Two studies, conducted by the same research group in Belgium (Sn103-Sn104) [112], focused on AMR profiles of both *E. coli*, (retrieved from the rectum) and *Pasteurellaceae* bacteria (retrieved from the nasal cavity) found a strong relationship between antimicrobial treatment and resistance profiles of bacterial isolates, in particular on intensive farms.

4. CONCLUSIONS

This systematic review has not specifically been focused on the issues of zoonoses, EID of human relevance, and spillover phenomena. Rather, we developed search strings with the objective of a wide-spectrum retrieval of research publications, dealing with the general issue of the circulation of infections and AMR in dairy farms in relation with the type of management system. However, results are relevant to the scenarios associated with zoonotic spillover events, an issue that has attracted a great deal of attention following the COVID19 pandemics [114]. Indeed, the risks associated with intensive and extensive breeding systems are still debated (e.g., [114]), and the present systematic review would suggest that the circulation of infectious agents is not significantly influenced by the type of management system in dairy farms, whether it is conventional or organic, intensive or extensive. Indeed, only a few studies reported significant differences, but with contrasting results regarding the higher or lower circulation of different pathogens under the different types of management. As anticipated in the introduction, the overall interpretation of our results suggest that CvsO and IvsE comparisons can be regarded as partially equivalent in some respects, for example in relation to the consumers' perception of issues such as animal welfare and sustainability (e.g., [115] [116] [117]). Therefore, the main outcome of our study, in relation to the public debate on the "pros" and "cons" of the different types of animal management, would suggest that organic and extensive farming is not correlated with a decrease of circulation of infectious agents compared to conventional and intensive dairy FMS.

Despite consumer perception that organic and extensive production are the same thing, the present study used two separate strings for literature search, in order to separate the two comparisons, CvsO and IvsE. In-depth examination of the retrieved publications highlight that: 1) the definitions of intensive and extensive farming differ among studies, making the comparison of studies that are apparently similar difficult; 2) the definitions of conventional and organic farming are often not stated in the publications, even if part of the studies refer to the national transposition of the general FAO guidelines on organic farming (which may differ from country to country) [13]. Furthermore, different studies evaluated other risk factors, not necessarily associated with a given FMS.

Comparison between CvsO showed greater prevalence of antibiotic resistances in conventional farms. This is consistent with the minimal of antibiotics expected on organic farms, and the absence of selective pressure favoring the emergence of resistant strains. However, AMR was in general uncommon in both farming systems. Moreover, many confounding factors suggest that different bacterial species may behave differently depending on a variety of management and environmental variables in different environmental contexts and in different countries. For instance, age distribution, time of the year at sampling, an early or extended period of cow-calf contact, diagnostic methodology, type of drugs used, environmental context, etc. are quite different across the sampled farms, affecting interpretation of the significance. Herd size is particularly important because conventional herds maybe larger than organic ones or *vice-versa* and a reliable comparison is virtually impossible. As for the comparison IvsE, AMR was more prevalent in intensive farming, but results are to be interpreted with caution, since only three studies were retrieved for this comparison.

As already emphasized, the reading of the publications listed in Tables 1-3 revealed that terms like C, O, I, E are often defined differently. Furthermore, the results of the statistical tests in some of the examined studies might have been flawed by confounding factors, thus reducing the power of statistical analysis, which may have detected false significant correlations or not detected significant ones. For this reason, future studies on the impact of the management system on the circulation of infectious agents and AMR should apply statistical approaches exploiting generalized linear models (GLM) or similar statistical tools, instead of tests which only consider the variable of interest. Since GLMs account for additional factors, they can correctly identify the effect of confounding factors to highlight if significant differences really exist.

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REFERENCES

1. Bartlett, H. *et al.* Understanding the relative risks of zoonosis emergence under contrasting approaches to meeting livestock product demand. *R. Soc. Open Sci.* **9**, 211573 (2022).
2. Bellet, C., Hamilton, L. & Rushton, J. Re-thinking public health: Towards a new scientific logic of routine animal health care in European industrial farming. *Palgrave Commun.* **8**, 1–11 (2021).
3. Temple, D. & Manteca, X. Animal Welfare in Extensive Production Systems Is Still an Area of Concern. *Front. Sustain. Food Syst.* **4**, (2020).
4. Gilbert, W., Thomas, L. F., Coyne, L. & Rushton, J. Review: Mitigating the risks posed by intensification in livestock production: the examples of antimicrobial resistance and zoonoses. *Anim. Int. J. Anim. Biosci.* **15**, 100123 (2021).
5. Wagner, K., Brinkmann, J., Bergschmidt, A., Renziehausen, C. & March, S. The effects of farming systems (organic vs. conventional) on dairy cow welfare, based on the Welfare Quality® protocol. *Animal* **15**, 100301 (2021).
6. Hemsworth, P. H., Barnett, J. L., Beveridge, L. & Matthews, L. R. The welfare of extensively managed dairy cattle: A review. *Appl. Anim. Behav. Sci.* **42**, 161–182 (1995).
7. von Keyserlingk, M. a. G., Rushen, J., de Passillé, A. M. & Weary, D. M. Invited review: The welfare of dairy cattle--key concepts and the role of science. *J. Dairy Sci.* **92**, 4101–4111 (2009).
8. Page, M. J. *et al.* The PRISMA 2020 statement: an updated guideline for reporting systematic reviews. *BMJ* **372**, n71 (2021).
9. *Contribution of Terrestrial Animal Source Food to Healthy Diets for Improved Nutrition and Health Outcomes*. (FAO, 2023). doi:10.4060/cc3912en.
10. EPRS_STU(2016)581922_EN.pdf.
11. Ferma gli Allevamenti Intensivi. *Greenpeace Italia* https://www.greenpeace.org/italy/attivati/ferma-gli-allevamenti-intensivi/.
12. Chang, K. Organic Food vs. Conventional Food. *Well* https://archive.nytimes.com/well.blogs.nytimes.com/2012/09/04/organic-food-vs-conventional-food/ (1346795625).
13. Organically Produced Foods | FAO. https://www.fao.org/family-farming/detail/en/c/288137/.

14. Chincarini, M. *et al.* Animal Welfare and Parasite Infections in Organic and Conventional Dairy Farms: A Comparative Pilot Study in Central Italy. *Animals* **12**, (2022).
15. Olmos Antillón, G., Sjöström, K., Fall, N., Sternberg Lewerin, S. & Emanuelson, U. Antibiotic Use in Organic and Non-organic Swedish Dairy Farms: A Comparison of Three Recording Methods. *Front. Vet. Sci.* **7**, (2020).
16. Firth, C. L. *et al.* Relationship between the probability of veterinary-diagnosed bovine mastitis occurring and farm management risk factors on small dairy farms in Austria. *J. Dairy Sci.* **102**, 4452–4463 (2019).
17. Roberts, M. C. *et al.* Distribution of Staphylococcus species in dairy cows, workers and shared farm environments. *FEMS Microbiol. Lett.* **365**, (2018).
18. May, K. *et al.* Genetic line comparisons and genetic parameters for endoparasite infections and test-day milk production traits. *J. Dairy Sci.* **100**, 7330–7344 (2017).
19. Schmidt, J. W. *et al.* Antimicrobial resistance at two U.S. Cull cow processing establishments. *J. Food Prot.* **83**, 2216–2228 (2020).
20. Taponen, S., Liski, E., Heikkilä, A.-M. & Pyörälä, S. Factors associated with intramammary infection in dairy cows caused by coagulase-negative staphylococci, Staphylococcus aureus, Streptococcus uberis, Streptococcus dysgalactiae, Corynebacterium bovis, or Escherichia coli. *J. Dairy Sci.* **100**, 493–503 (2017).
21. Levison, L. J. *et al.* Incidence rate of pathogen-specific clinical mastitis on conventional and organic Canadian dairy farms. *J. Dairy Sci.* **99**, 1341–1350 (2016).
22. Kuhnen, S., Stibuski, R. B., Honorato, L. A. & Filho, L. C. P. M. Farm management in organic and conventional dairy production systems based on pasture in southern brazil and its consequences on production and milk quality. *Animals* **5**, 479–494 (2015).
23. Kouřimská, L., Legarová, V., Panovská, Z. & Pánek, J. Quality of cows' milk from organic and conventional farming. *Czech J. Food Sci.* **32**, 398–405 (2014).
24. Honorato, L. A., Machado Filho, L. C. P., Barbosa Silveira, I. D. & Hötzel, M. J. Strategies used by dairy family farmers in the south of Brazil to comply with organic regulations. *J. Dairy Sci.* **97**, 1319–1327 (2014).

25. Silva, J. B., Fagundes, G. M., Soares, J. P. G., Fonseca, A. H. & Muir, J. P. A comparative study of production performance and animal health practices in organic and conventional dairy systems. *Trop. Anim. Health Prod.* **46**, 1287–1295 (2014).
26. Cicconi-Hogan, K. M. *et al.* Associations of risk factors with somatic cell count in bulk tank milk on organic and conventional dairy farms in the United States. *J. Dairy Sci.* **96**, 3689–3702 (2013).
27. Cicconi-Hogan, K. M. *et al.* Risk factors associated with bulk tank standard plate count, bulk tank coliform count, and the presence of Staphylococcus aureus on organic and conventional dairy farms in the United States. *J. Dairy Sci.* **96**, 7578–7590 (2013).
28. Mullen, K. A. E., Sparks, L. G., Lyman, R. L., Washburn, S. P. & Anderson, K. L. Comparisons of milk quality on north carolina organic and conventional dairies. *J. Dairy Sci.* **96**, 6753–6762 (2013).
29. Richert, R. M. *et al.* Risk factors for clinical mastitis, ketosis, and pneumonia in dairy cattle on organic and small conventional farms in the United States. *J. Dairy Sci.* **96**, 4269–4285 (2013).
30. Park, Y. K., Fox, L. K., Hancock, D. D., McMahan, W. & Park, Y. H. Prevalence and antibiotic resistance of mastitis pathogens isolated from dairy herds transitioning to organic management. *J. Vet. Sci.* **13**, 103–105 (2012).
31. D'Amico, D. J. & Donnelly, C. W. Microbiological quality of raw milk used for small-scale artisan cheese production in Vermont: Effect of farm characteristics and practices. *J. Dairy Sci.* **93**, 134–147 (2010).
32. Garmo, R. T. *et al.* Reproductive Performance, Udder Health, and Antibiotic Resistance in Mastitis Bacteria isolated from Norwegian Red cows in Conventional and Organic Farming. *Acta Vet. Scand.* **52**, (2010).
33. Müller, U. & Sauerwein, H. A comparison of somatic cell count between organic and conventional dairy cow herds in West Germany stressing dry period related changes. *Livest. Sci.* **127**, 30–37 (2010).
34. Pol, M. & Ruegg, P. L. Treatment practices and quantification of antimicrobial drug usage in conventional and organic dairy farms in Wisconsin. *J. Dairy Sci.* **90**, 249–261 (2007).
35. Doherr, M. G., Roesch, M., Schaeren, W., Schallibaum, M. & Blum, J. W. Risk factors associated with subclinical mastitis in dairy cows on Swiss organic and conventional production system farms. *Vet. Med. (Praha)* **52**, 487–495 (2007).

36. Ellis, K. A. *et al.* Dairy cow cleanliness and milk quality on organic and conventional farms in the UK. *J. Dairy Res.* **74**, 302–310 (2007).

37. Roesch, M., Doherr, M. G., Schären, W., Schällibaum, M. & Blum, J. W. Subclinical mastitis in dairy cows in Swiss organic and conventional production systems. *J. Dairy Res.* **74**, 86–92 (2007).

38. Bennedsgaard, T. W. *et al.* Resistance to penicillin of Staphylococcus aureus isolates from cows with high somatic cell counts in organic and conventional dairy herds in Denmark. *Acta Vet. Scand.* **48**, (2006).

39. Boutet, P. *et al.* A comparison of somatic cell count and antimicrobial susceptibility of subclinical mastitis pathogens in organic and conventional dairy herds. *Ann. Med. Veterinaire* **149**, 173–182 (2005).

40. Sato, K., Bartlett, P. C., Erskine, R. J. & Kaneene, J. B. A comparison of production and management between Wisconsin organic and conventional dairy herds. *Livest. Prod. Sci.* **93**, 105–115 (2005).

41. Tikofsky, L. L., Barlow, J. W., Santisteban, C. & Schukken, Y. H. A comparison of antimicrobial susceptibility patterns for Staphylococcus aureus in organic and conventional dairy herds. *Microb. Drug Resist. Larchmt. N* **9 Suppl 1**, S39-45 (2003).

42. Suvajdžić, B. *et al.* Detection of ICAA and ICAD genes of staphylococcus aureus isolated in cases of bovine mastitis in the Republic of Serbia. *Acta Vet. (Beogr.)* **67**, 168–177 (2017).

43. Zhou, Y. *et al.* Survey of mycotic mastitis in dairy cows from Heilongjiang Province, China. *Trop. Anim. Health Prod.* **45**, 1709–1714 (2013).

44. Goldberg, J. J. *et al.* The Influence of Intensively Managed Rotational Grazing, Traditional Continuous Grazing, and Confinement Housing on Bulk Tank Milk Quality and Udder Health. *J. Dairy Sci.* **75**, 96–104 (1992).

45. Takeuchi-Storm, N. *et al.* Patterns of Fasciola hepatica infection in Danish dairy cattle: Implications for on-farm control of the parasite based on different diagnostic methods. *Parasit. Vectors* **11**, (2018).

46. El-Tahawy, A. S., Bazh, E. K. & Khalafalla, R. E. Epidemiology of bovine fascioliasis in the Nile Delta region of Egypt: Its prevalence, evaluation of risk factors, and its economic significance. *Vet. World* **10**, 1241–1249 (2017).

47. May, K., Brügemann, K., König, S. & Strube, C. Patent gastrointestinal nematode infections in organically and conventionally pastured dairy cows and their impact on individual milk and fertility parameters. *Vet. Parasitol.* **245**, 119–127 (2017).

48. Novobilský, A., Sollenberg, S. & Höglund, J. Distribution of Fasciola hepatica in Swedish dairy cattle and associations with pasture management factors. *Geospatial Health* **9**, 293–300 (2015).

49. Sorge, U. S. *et al.* Parasites and parasite management practices of organic and conventional dairy herds in Minnesota. *J. Dairy Sci.* **98**, 3143–3151 (2015).

50. Silverlås, C. & Blanco-Penedo, I. Cryptosporidium spp. in calves and cows from organic and conventional dairy herds. *Epidemiol. Infect.* **141**, 529–539 (2013).

51. Blanco-Penedo, I., Höglund, J., Fall, N. & Emanuelson, U. Exposure to pasture borne nematodes affects individual milk yield in Swedish dairy herds. *Vet. Parasitol.* **188**, 93–98 (2012).

52. Da Silva, J. B., Soares, J. P. G. & Da Fonseca, A. H. Gastrointestinal parasites occurrence in dairy cows kept in organic and conventional production system. *Semin. Agrar.* **33**, 2375–2382 (2012).

53. Höglund, J. *et al.* Antibodies to major pasture borne helminth infections in bulk-tank milk samples from organic and nearby conventional dairy herds in south-central Sweden. *Vet. Parasitol.* **171**, 293–299 (2010).

54. Silverlås, C., Emanuelson, U., de Verdier, K. & Björkman, C. Prevalence and associated management factors of Cryptosporidium shedding in 50 Swedish dairy herds. *Prev. Vet. Med.* **90**, 242–253 (2009).

55. Höglund, J., Viring, S. & Törnqvist, M. Seroprevalence of Dictyocaulus viviparus in first grazing season calves in Sweden. *Vet. Parasitol.* **125**, 343–352 (2004).

56. Svensson, C., Hessle, A. & Höglund, J. Parasite control methods in organic and conventional dairy herds in Sweden. *Livest. Prod. Sci.* **66**, 57–69 (2000).

57. Manyazewal, A. *et al.* Prevalence, risk factors and molecular characterization of Cryptosporidium infection in cattle in Addis Ababa and its environs, Ethiopia. *Vet. Parasitol. Reg. Stud. Rep.* **13**, 79–84 (2018).

58. Almería, S., Adelantado, C., Charlier, J., Claerebout, E. & Bach, A. Ostertagia ostertagi antibodies in milk samples: Relationships with herd management and milk production parameters in two Mediterranean production systems of Spain. *Res. Vet. Sci.* **87**, 416–420 (2009).

59. Keyyu, J. D., Kassuku, A. A., Msalilwa, L. P., Monrad, J. & Kyvsgaard, N. C. Cross-sectional prevalence of helminth infections in cattle on traditional, small-scale and large-scale dairy farms in Iringa district, Tanzania. *Vet. Res. Commun.* **30**, 45–55 (2006).

60. Genchi, C., Madonna, M. & Traldi, G. Epidemiology of Ostertagia ostertagi in dairy cow from different breeding systems. *Parassitologia* **31**, 123–132 (1989).

61. Beaver, A., Ruegg, P. L., Gröhn, Y. T. & Schukken, Y. H. Comparative risk assessment for new cow-level Mycobacterium avium ssp. paratuberculosis infections between 3 dairy production types: Organic, conventional, and conventional-grazing systems. *J. Dairy Sci.* **99**, 9885–9899 (2016).

62. Pieper, L. *et al.* Comparing ELISA test-positive prevalence, risk factors and management recommendations for Johne's disease prevention between organic and conventional dairy farms in Ontario, Canada. *Prev. Vet. Med.* **122**, 83–91 (2015).

63. Cazer, C. L. *et al.* Associations between Mycobacterium avium subsp. paratuberculosis antibodies in bulk tank milk, season of sampling and protocols for managing infected cows. *BMC Vet. Res.* **9**, (2013).

64. Licitra, F. *et al.* Management factors influence animal welfare and the correlation to infectious diseases in dairy cows. *Animals* **11**, (2021).

65. Liu, X. *et al.* The seroprevalence of Mycobacterium avium subspecies paratuberculosis in dairy cattle in Xinjiang, Northwest China. *Ir. Vet. J.* **70**, (2017).

66. Wolff, C., Emanuelson, U., Ohlson, A., Alenius, S. & Fall, N. Bovine respiratory syncytial virus and bovine coronavirus in Swedish organic and conventional dairy herds. *Acta Vet. Scand.* **57**, (2015).

67. Bidokhti, M. R. M., Tråvén, M., Fall, N., Emanuelson, U. & Alenius, S. Reduced likelihood of bovine coronavirus and bovine respiratory syncytial virus infection on organic compared to conventional dairy farms. *Vet. J.* **182**, 436–440 (2009).

68. Akagami, M. *et al.* Risk factors associated with the within-farm transmission of bovine viral diarrhea virus and the incidence of persistently infected cattle on dairy farms from Ibaraki prefecture of Japan. *Res. Vet. Sci.* **129**, 187–192 (2020).

69. Macêdo, A. A. M. *et al.* Occurrence of Mycoplasma bovigenitalium and Ureaplasma diversum in dairy cattle from to Pernambuco state, Brazil. *Arq. Bras. Med. Vet. E Zootec.* **70**, 1798–1806 (2018).

70. Klein-Jöbstl, D., Sofka, D., Iwersen, M., Drillich, M. & Hilbert, F. Multilocus sequence typing and antimicrobial resistance of Campylobacter jejuni isolated from dairy calves in Austria. *Front. Microbiol.* **7**, (2016).

71. Sato, K., Bartlett, P. C., Kaneene, J. B. & Downes, F. P. Comparison of Prevalence and Antimicrobial Susceptibilities of Campylobacter spp. Isolates from Organic and Conventional Dairy Herds in Wisconsin. *Appl. Environ. Microbiol.* **70**, 1442–1447 (2004).

72. Rapp, D., Ross, C. M., Cave, V. & Muirhead, R. W. Prevalence, concentration and genotypes of Campylobacter jejuni in faeces from dairy herds managed in farm systems with or without housing. *J. Appl. Microbiol.* **116**, 1035–1043 (2014).

73. Raquel Salazar, B., Rolando Barahona, R., Julián Chará, O. & María Solange Sánchez, P. Productivity and tick load in Bos Indicus X B. taurus cattle in a tropical dry forest silvopastoral system. *Trop. Subtrop. Agroecosystems* **18**, 103–112 (2015).

74. Papini, R., Nardoni, S., Fanelli, A. & Mancianti, F. High infection rate of Trichophyton verrucosum in calves from Central Italy. *Zoonoses Public Health* **56**, 59–64 (2009).

75. Cho, S. *et al.* Cattle-level risk factors associated with fecal shedding of Shiga toxin-encoding bacteria on dairy farms, Minnesota, USA. *Can. J. Vet. Res.* **73**, 151–156 (2009).

76. Cho, S. *et al.* Prevalence and characterization of Escherichia coli O157 isolates from Minnesota dairy farms and county fairs. *J. Food Prot.* **69**, 252–259 (2006).

77. Cho, S. *et al.* Prevalence of shiga toxin-encoding bacteria and shiga toxin-producing Escherichia coli isolates from dairy farms and county fairs. *Vet. Microbiol.* **118**, 289–298 (2006).

78. Kuhnert, P. *et al.* Prevalence and risk-factor analysis of Shiga toxigenic Escherichia coli in faecal samples of organically and conventionally farmed dairy cattle. *Vet. Microbiol.* **109**, 37–45 (2005).

79. Fossler, C. P. *et al.* Herd-level factors associated with isolation of Salmonella in a multi-state study of conventional and organic dairy farms. II. Salmonella shedding in calves. *Prev. Vet. Med.* **70**, 279–291 (2005).

80. Fossler, C. P. *et al.* Herd-level factors associated with isolation of Salmonella in a multi-state study of conventional and organic dairy farms: I. Salmonella shedding in cows. *Prev. Vet. Med.* **70**, 257–277 (2005).

81. Fossler, C. P. *et al.* Cattle and environmental sample-level factors associated with the presence of Salmonella in a multi-state study of conventional and organic dairy farms. *Prev. Vet. Med.* **67**, 39–53 (2005).

82. Fossler, C. P. *et al.* Prevalence of Salmonella spp on conventional and organic dairy farms. *J. Am. Vet. Med. Assoc.* **225**, 567–573 (2004).

83. Varsaki, A. *et al.* Prevalence and Population Diversity of Listeria monocytogenes Isolated from Dairy Cattle Farms in the Cantabria Region of Spain. *Animals* **12**, (2022).

84. Coorevits, A. *et al.* Comparative analysis of the diversity of aerobic spore-forming bacteria in raw milk from organic and conventional dairy farms. *Syst. Appl. Microbiol.* **31**, 126–140 (2008).

85. Swai, E. S. & Schoonman, L. Differences in prevalence of tuberculosis in indigenous and crossbred cattle under extensive and intensive management systems in Tanga Region of Tanzania. *Trop. Anim. Health Prod.* **44**, 459–465 (2012).

86. Durnez, L. *et al.* The prevalence of Mycobacterium bovis-infection and atypical mycobacterioses in cattle in and around Morogoro, Tanzania. *Trop. Anim. Health Prod.* **41**, 1653–1659 (2009).

87. Fetene, T. & Kebede, N. Bovine tuberculosis of cattle in three districts of northwestern Ethiopia. *Trop. Anim. Health Prod.* **41**, 273–277 (2009).

88. Shirima, G. M., Kazwala, R. R. & Kambarage, D. M. Prevalence of bovine tuberculosis in cattle in different farming systems in the eastern zone of Tanzania. *Prev. Vet. Med.* **57**, 167–172 (2003).

89. Terefe, Y., Girma, S., Mekonnen, N. & Asrade, B. Brucellosis and associated risk factors in dairy cattle of eastern Ethiopia. *Trop. Anim. Health Prod.* **49**, 599–606 (2017).

90. de Alencar Mota, A. L. A. *et al.* Large-scale study of herd-level risk factors for bovine brucellosis in Brazil. *Acta Trop.* **164**, 226–232 (2016).

91. da Silva Neto, A. L., Pajeú e Silva, B., Lúcio, É. C., do Nascimento, S. A. & Pinheiro Júnior, J. W. Soroepidemiological survey of chlamydia abortus infection in bovine in the State of Pernambuco, Brazil. *Semin. Agrar.* **42**, 229–240 (2021).

92. Adesiyun, A. A., Jagun, A. G. & Tekdek, L. B. Coxiella burnetii antibodies in some Nigerian dairy cows and their suckling calves. *Int. J. Zoonoses* **11**, 155–160 (1984).

93. Aktas, M. & Ozubek, S. Genetic diversity of major surface protein 1a of Anaplasma marginale in dairy cattle. *Infect. Genet. Evol.* **89**, (2021).

94. Nüesch-Inderbinen, M., Hänni, C., Zurfluh, K., Hartnack, S. & Stephan, R. Antimicrobial resistance profiles of Escherichia coli and prevalence of extended-spectrum beta-lactamase-producing Enterobacteriaceae in calves from organic and conventional dairy farms in Switzerland. *MicrobiologyOpen* **11**, (2022).

95. Sjöström, K. *et al.* Antimicrobial resistance patterns in organic and conventional dairy herds in sweden. *Antibiotics* **9**, 1–17 (2020).

96. Bok, E., Mazurek, J., Stosik, M., Wojciech, M. & Baldy-Chudzik, K. Prevalence of virulence determinants and antimicrobial resistance among commensal Escherichia coli derived from dairy and beef cattle. *Int. J. Environ. Res. Public. Health* **12**, 970–985 (2015).

97. Dolejska, M. *et al.* IncN plasmids carrying blaCTX-M-1 in Escherichia coli isolates on a dairy farm. *Vet. Microbiol.* **149**, 513–516 (2011).

98. Berge, A. C., Hancock, D. D., Sischo, W. M. & Besser, T. E. Geographic, farm, and animal factors associated with multiple antimicrobial resistance in fecal Escherichia coli isolates from cattle in the western United States. *J. Am. Vet. Med. Assoc.* **236**, 1338–1344 (2010).

99. Walk, S. T. *et al.* Influence of antibiotic selection on genetic composition of Escherichia coli populations from conventional and organic dairy farms. *Appl. Environ. Microbiol.* **73**, 5982–5989 (2007).

100. Sato, K., Bartlett, P. C. & Saeed, M. A. Antimicrobial susceptibility of Escherichia coli isolates from dairy farms using organic versus conventional production methods. *J. Am. Vet. Med. Assoc.* **226**, 589–594 (2005).

101. Cho, S. *et al.* Antimicrobial susceptibility of shiga toxin-producing Escherichia coli isolated from organic dairy farms, conventional dairy farms, and county fairs in Minnesota. *Foodborne Pathog. Dis.* **4**, 178–186 (2007).

102. da Silva Abreu, A. C. *et al.* Antimicrobial resistance of Staphylococcus spp. isolated from organic and conventional Minas Frescal cheese producers in São Paulo, Brazil. *J. Dairy Sci.* **104**, 4012–4022 (2021).

103. Tenhagen, B.-A. *et al.* Short communication: Methicillin-resistant Staphylococcus aureus in conventional and organic dairy herds in Germany. *J. Dairy Sci.* **101**, 3380–3386 (2018).

104. Bombyk, R. A. M. *et al.* Comparison of types and antimicrobial susceptibility of Staphylococcus from conventional and organic dairies in west-central Minnesota, USA. *J. Appl. Microbiol.* **104**, 1726–1731 (2008).

105. Pol, M. & Ruegg, P. L. Relationship between antimicrobial drug usage and antimicrobial susceptibility of gram-positive mastitis pathogens. *J. Dairy Sci.* **90**, 262–273 (2007).

106. Roesch, M. *et al.* Comparison of antibiotic resistance of udder pathogens in dairy cows kept on organic and on conventional farms. *J. Dairy Sci.* **89**, 989–997 (2006).

107. Galiot, L., Monger, X. C. & Vincent, A. T. Studying the Association between Antibiotic Resistance Genes and Insertion Sequences in Metagenomes: Challenges and Pitfalls. *Antibiotics* **12**, (2023).

108. Jauregi, L., Epelde, L., Alkorta, I. & Garbisu, C. Antibiotic Resistance in Agricultural Soil and Crops Associated to the Application of Cow Manure-Derived Amendments From Conventional and Organic Livestock Farms. *Front. Vet. Sci.* **8**, (2021).

109. Pitta, D. W. *et al.* The distribution of microbiomes and resistomes across farm environments in conventional and organic dairy herds in Pennsylvania. *Environ. Microbiomes* **15**, (2020).

110. Ray, K. A. *et al.* Antimicrobial susceptibility of Salmonella from organic and conventional dairy farms. *J. Dairy Sci.* **89**, 2038–2050 (2006).

111. Halbert, L. W. *et al.* Evaluation of antimicrobial susceptibility patterns in Campylobacter spp isolated from dairy cattle and farms managed organically and conventionally in the midwestern and northeastern United States. *J. Am. Vet. Med. Assoc.* **228**, 1074–1081 (2006).

112. Catry, B. *et al.* Effect of antimicrobial consumption and production type on antibacterial resistance in the bovine respiratory and digestive tract. *PLoS ONE* **11**, (2016).

113. Shrivas, V. L., Choudhary, A. K., Hariprasad, P. & Sharma, S. Nutrient concentrations affect the antimicrobial resistance profiles of cattle manures. *Environ. Sci. Pollut. Res.* **30**, 25141–25147 (2023).

114. Shepon, A. *et al.* Exploring scenarios for the food system-zoonotic risk interface. *Lancet Planet. Health* **7**, e329–e335 (2023).

115. Anders, S., Malzoni, M. & An, H. Altruism and anti-anthropocentrism shape individual choice intentions for pro-environmental and ethical meat credence attributes. *PloS One* **18**, e0294531 (2023).

116. Harper, G. C. & Makatouni, A. Consumer perception of organic food production and farm animal welfare. *Br. Food J.* **104**, 287–299 (2002).

117. Consumer attitudes towards production diseases in intensive production systems | PLOS ONE. https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0210432.

SUPPLEMENTARY MATERIAL

Tab. 1S: comparative studies on ID/IA presents in both comparations (CvsO, right) and (IvsE, on the left)

IvsE					CvsO				
Sn	**ID/IA**	**ref**	**year**	**A-2**	**ID/IA**	**ref**	**year**	**A-2**	**Sn**
Sn1	GIPs**	[57]	2018	ET	GIPs**	[14] [A, C]	2022	IT	**Sn16**
Sn2		[58] [C]	2009	ES		[45] [C]	2018	DK	**Sn17**
Sn3		[59] [C]	2006	TZ		[46]	2017	EG	**Sn18**
Sn4		[60]	1989	IT		[47]	2017	DE	**Sn19**
						[18] [A]	2017	DE	**Sn20**
						[48]	2015	SE	**Sn21**
						[49] [A]	2015	US	**Sn22**
						[25] [A, C]	2014	BR	**Sn23**
						[50]	2013	SE	**Sn24**
						[51]	2012	SE	**Sn25**
						[52]	2012	BR	**Sn26**
						[53]	2010	SE	**Sn27**
						[54]	2009	SE	**Sn28**
						[40] [B]	2005	US	**Sn29**
						[55]	2004	SE	**Sn30**
						[56] [C]	2000	SE	**Sn31**
Sn5	IMIs*	[42]	2017	RS	IMIs*	[14] [A, C]	2022	IT	**Sn32**
Sn6		[43]	2013	CN		[15] [A, C]	2020	SE	**Sn33**
Sn7		[44] [C]	1992	US		[16]	2019	AT	**Sn34**
						[17]	2018	US	**Sn35**
						[18] [A]	2017	DE	**Sn36**
						[19]	2017	US	**Sn37**
						[20]	2017	FI	**Sn38**
						[21]	2016	CA	**Sn39**
						[22]	2015	BR	**Sn40**
						[23]	2014	CZ	**Sn41**
						[24] [A, C]	2014	BR	**Sn42**
						[25] [A, C]	2014	BR	**Sn43**
						[26]	2013	US	**Sn44**
						[27]	2013	US	**Sn45**
						[28]	2013	US	**Sn46**
						[29] [A]	2013	US	**Sn47**
						[30] [B]	2012	US	**Sn48**
						[31] [A]	2010	US	**Sn49**
						[32] [B]	2010	NO	**Sn50**
						[33]	2010	DE	**Sn51**
						[34] [A, C]	2007	US	**Sn52**
						[35]	2007	CH	**Sn53**
						[36]	2007	UK	**Sn54**
						[37]	2007	CH	**Sn55**
						[38] [C]	2006	DK	**Sn56**
						[39] [B]	2005	BE	**Sn57**
						[40] [B]	2005	US	**Sn58**
						[41] [B]	2003	US	**Sn59**
Sn8	*Campylobacter*	[72]	2014	NZ	*Campylobacter*	[70]	2016	AT	**Sn60**
						[71] [B]	2004	US	**Sn61**
Sn9	Ectoparasite	[73]	2015	CO	Ectoparasite	[49] [C]	2015	US	**Sn62**
						[24] [A, C]	2014	BR	**Sn63**
						[25] [A, C]	2014	BR	**Sn64**
Sn10	MAP***	[64] [A]	2021	IT	MAP***	[61]	2016	US	**Sn65**
Sn11		[65]	2017	CN		[62]	2015	CA	**Sn66**
						[63]	2013	US	**Sn67**
Sn12	Mycosis	[74]	2009	IT	Mycosis	[74]	2009	IT	**Sn68**
Sn13	Urog. Reprod. Inf.	[69]	2018	BR	Urog. Reprod. Inf.	[29] [A]	2013	US	**Sn69**
						[34] [A, C]	2007	US	**Sn70**
Sn14	Viruses	[64] [A]	2021	IT	Viruses	[66]	2015	SE	**Sn71**
Sn15		[68]	2020	JP		[67]	2009	SE	**Sn72**

A: Comparative studies on IvsE or CvsO investigating more than one ID/IA (contextually reported for each investigated ID/IA)

B: Comparative studies on IvsE or CvsO investigating the targeted ID/IA in terms of both presence/prevalence and AMR/AMS

C: Comparative studies on IvsE or CvsO investigating the targeted ID/IA it terms of both presence/prevalence and AMU/DRU

*IMIs Intra Mammary Infections; **GIPs Gastro Intestinal Parasite Infectious; ***MAP *Mycobacterium avium subspecies paratuberculosis*, Sn (study number), ID/IA (infectious disease/infectious agent); ref (reference); year (year of publication); A-2 International acronym (ISO 3166-1 alpha-2)

Tab. 2S: comparative studies on the presence of infectious diseases or infectious agents (ID/IA), in intensive versus extensive management (IvsE, on the left) and conventional versus organic management (CvsO, right), in which the investigated ID/IA do not coincide

IvsE					**CvsO**				
Sn	**ID/IA**	**ref**	**year**	**A-2**	**ID/IA**	**ref**	**year**	**A-2**	**Sn**
Sn73	*Anaplasma*	[93]	2021	TR	Aero. Spor. Bact.**	[84]	2008	BE	**Sn84**
Sn74	*Brucella*	[89]	2017	ET	Lameness	[15] A, C	2020	SE	**Sn85**
Sn75		[90]	2016	BR		[25] A, C	2014	BR	**Sn86**
Sn76	*Chlamidia*	[64] A	2021	IT		[29] A	2013	US	**Sn87**
Sn77		[91]	2021	BR		[34] A, C	2007	US	**Sn88**
Sn78	*Coxiella*	[92]	1984	NG	*Listeria* sp.	[83] B	2022	ES	**Sn89**
Sn79	*Neospora*	[64] A	2021	IT		[31] A	2010	US	**Sn90**
Sn80	Tuberculosis	[85]	2012	TZ	Pneumonia	[29] A	2013	US	**Sn91**
Sn81		[86]	2009	TZ		[34] A, C	2007	US	**Sn92**
Sn82		[87]	2009	ET	*Salmonella* sp.	[31] A	2010	US	**Sn93**
Sn83		[88]	2003	ET		[79]	2005	US	**Sn94**
						[80]	2005	US	**Sn95**
						[81]	2005	US	**Sn96**
						[82]	2004	US	**Sn97**
					STEC*/ STEB*	[31] A	2010	US	**Sn98**
						[75]	2009	US	**Sn99**
						[76] B	2006	US	**Sn100**
						[77]	2006	US	**Sn101**
						[78]	2005	CH	**Sn102**

A: Comparative studies on IvsE or CvsO investigating more than one ID/IA (contextually reported for each investigated ID/IA)
B: Comparative studies on IvsE or CvsO investigating the targeted ID/IA in terms of both presence/prevalence and AMR/AMS
C: Comparative studies on IvsE or CvsO investigating the targeted ID/IA it terms of both presence/prevalence and AMU/DRU
*STEC (Shiga Toxigenic *Escherichia coli*), *STEB (Shiga Toxigenic Encoding Bacteria); **Aero. Spor. Bact. (Aerobically Spore-forming Bacteria), Sn (study number); ID/IA (infectious disease/infectious agent); ref. (reference); year (year of publication), A-2 International acronym (ISO 3166-1 alpha-2)

Tab. 3S: comparative studies of antimicrobial resistance/antimicrobial susceptibility (AMR/AMS) in infectious diseases or infectious agents (ID/IA) in intensive versus extensive management (IvsE, on the left) and conventional versus organic management (CvsO, right)

IvsE					**CvsO**				
Sn	**ID/IA**	**ref.**	**year**	**A-2**	**ID/IA**	**ref.**	**year**	**A-2**	**Sn**
Sn103	*E. coli*	[94] A	2016	BE	*E. coli*	[96]	2022	CH	**Sn106**
Sn104	*Pasteurellaceae*	[94] A	2016	BE		[19] A	2020	US	**Sn107**
Sn105	MCGT**	[95]	2023	IN		[97] C	2020	SE	**Sn108**
						[98]	2015	PL	**Sn109**
						[99]	2011	CZ	**Sn110**
						[100]	2010	US	**Sn111**
						[101]	2007	US	**Sn112**
						[76] B	2006	US	**Sn113**
						[102]	2005	US	**Sn114**
					Campylobacter	[113] B	2006	US	**Sn115**
						[71] B	2004	US	**Sn116**
					IMIs***	[104]	2021	BR	**Sn117**
						[105]	2018	DE	**Sn118**
						[30] B	2012	US	**Sn119**
						[32] B	2010	NO	**Sn120**
						[106]	2008	US	**Sn121**
						[107] C	2007	US	**Sn122**
						[108]	2006	CH	**Sn123**
						[39] B	2005	BE	**Sn124**
						[41] B	2003	US	**Sn125**
					Listeria spp.	[83] B	2022	ES	**Sn126**
					MCGT**	[109]	2023	CA	**Sn127**
						[110]	2021	ES	**Sn128**
						[111]	2020	US	**Sn129**
					Salmonella spp.	[19] A	2020	US	**Sn130**
						[112]	2006	US	**Sn131**
					STEC*	[103]	2007	US	**Sn132**

A: Comparative studies on IvsE or CvsO investigating more than one ID/IA (contextually reported for each targeted ID/IA)
B: Comparative studies on IvsE or CvsO investigating the targeted ID/IA it terms of both, presence/prevalence and AMR/AMS
C: Comparative studies on IvsE or CvsO investigating the targeted ID/IA it terms of both, presence/prevalence and AMU/DRU
*STEC (Shiga Toxigenic *Escherichia coli*); **MCGT (Microbial Community Gene Transfer); ***IMIs Intra Mammary Infections, Sn (study number), ID/IA (infectious disease/infectious agent); ref (reference); year (year of publication); A-2 International acronym (ISO 3166-1 alpha-2)

Tab.4S: Results and comments for the IDs/IAs with limited number of comparative studies

ID/IA	**CvsO**	**IvsE**	**Synthesis of results**
MAP	Sn65-Sn67	Sn10 Sn11	In Sn65, and Sn66 (US), risk factors for MAP infection more prevalent in O, especially in calving and pre-weaned calf areas. In Sn66, O and C farms did not present appreciable differences in positivity of the herd, but O had higher prevalence when at least one animal tested positive. In Sn67 (US) no correlation between farming management and MAP circulation; however, MAP presence influenced by calving practice, seasonal bulk milk sampling and the protocols adopted to manage positive cows. In IvsE, results of study Sn10 (IT) and Sn11 (CH) are not congruent: no significant differences in Sn10; higher prevalence in Sn1, in I.
Viral inf.	Sn71 Sn72	Sn14 Sn15	Sn71 (SE) didn’t find difference between C and O, while Sn72 (SE) found a significantly prevalence of anti-viral antibody in the C farms. The two studies on IvsE classified farms as I or E based on the access of animals to the environment outside the stable. Sn14 (IT) found that the bovine herpesvirus is significantly more present in cows with no access to the outside, while the bovine viral diarrhea virus (BVDV) presents a similar circulation in the two types of farms. Finally, Sn15 (JP) focused on BVDV did not provide a list of risk factors not strictly related I. and E.
Urogen/Re-product. Inf.	Sn69 Sn70	Sn13	Both, Sn69 and Sn70 (US) highlighted a higher prevalence and incidence of metritis in C farms. Sn13 (BR), comparing the infection rate by *Mycoplasma bovigenitlium* and *Ureoplasma diversum* in semi-intensive and intensive breeding systems highlighted a higher infection risk associated with semi-intensive ones.
Campylobacter	Sn60 Sn61	Sn8	Three studies focused on *Campylobacter* spp. were retrieved. Two of these (Sn60, Sn61) deal with CvsO, and one (Sn8) with IvsE. In **CvsO** studies, Sn60 (AT), identified the practice of housing calves in groups together with cows as a specific risk factor associated with OFM Sn61 (US) did not refer significant differences, but found risk factors associated with the seasonality (higher in March than in September), age (higher in calves than in cows), and farming dimension (higher in small farms). Sn8 (NZ), comparing different housing systems, including farms characterized by outdoor grazing, did not found significant differences among different FMs, even though the confinement of animals in stables after the grazing season resulted as a risk factor for the circulation of the infection.
Ectoparasite	Sn62-Sn64	Sn9	Sn64 (BR) reported a higher ectoparasite load in C farms, while Sn63 (BR), found more infestation in O farms, in March, but not in September. Sn62 (US) didn’t found differences. Sn9 (Colombia), was only loosely related with IvsE: the two groups of farms under comparison were defined as follows: group 1 “intensive silvopastoral system”; group 2 “traditional farms located on the Valley of Ibague”. It found a higher rate of ticks parasitization in group 1.
Mycotic inf.	Sn68	Sn12	Both Sn68 and Sn12 focusing on the prevalence of *Trichophyton verrucosum* didn’t find any difference both in CvsO and in IvsE as well.
STEC and STEB	Sn98-Sn102		Sn99-Sn101 (US) highlighted a higher prevalences in O farms, while Sn98 (US) didn’t detect *E. coli* O157:H7 in raw milk samples. Sn102 (CH) didn’t find significant differences between FMs, but using multivariate statistical analyses, highlighted the most significant risk factors, mainly related to the potential of cross-contamination of feeds, cross-infection of cows, and age of the animals.
lameness	Sn85-Sn88		Sn86 (BR) and Sn87 (US) didn’t detect any difference in the prevalence of lameness, while Sn85 (SE), and Sn88 (US) detected a lower prevalence but higher incidence of foot infection cases per year in O farms (Sn88).
Salmonella	Sn93-Sn97		No significant difference in the prevalence was detected in all the five retrieved studies from USA (Sn93-Sn97), but risk factors were suggested, such as lack of routine feeding of milk replacer containing antimicrobials to pre-weaned calves, and the use of maternity housing as a hospital area for sick cows more than once a month.
Pneumonia	Sn91 Sn92		Both the two retrieved studies conducted in USA (Sn91-Sn92), found a higher prevalence and incidence of cases in C farms highlighting a direct correlation with the lack of grazing.
Listeria	Sn89 Sn90		Both Sn89 (ES) and Sn90 (US) didn’t report significant difference highlighting that a good practice of herd and manure management are needed.
Aerobic-Sporef.Bact.	Sn84		Sn84 (BE), focalized on raw milk samples found a higher presence of *Bacillus cereus* in O milk and a higher number of thermotolerant organisms in particular *Ureibacillus thermosphaericus* in raw C milk.
Tuberculosis		Sn80-Sn83	Sn 80 (TZ), found a higher prevalence in smallholder I. farms rather than in traditionally E. managed herds, while the second one Sn81 (TZ) referred opposite evidence. Both Sn82 (ET) and Sn83 (ET) highlighted a higher tuberculosis prevalence in I. farms.

Brucellosis		Sn74 Sn75	Sn74 (ET), found a higher prevalence in I. herds, while Sn75 (BR), highlighted the higher presence of risk factors for brucellosis in E farms. Both studies, furthermore, highlighted a number of risk factors related to the specific peculiarities of the analyzed farms.
Chlamydia		Sn76 Sn77	Sn76 (IT), comparing herds with access to outdoor grazing and herds keeps indoor fulltime, did not find any difference in terms of prevalence of pathogens, while Sn77 (BR), comparing “intensive”, “semi-intensive” and “extensive” breeding systems (no clear definition), found out a linear increasing prevalence and a higher risk factor from I. to E farms
Coxiella burnetii		Sn78	Sn78 (NG), compared institutional and governmental farms under semi-intensive husbandry with Fulani nomadic herds under extensive management system. It found higher prevalence in semi-intensive rather than extensive breeding. Risk factors and peculiarity associated to both FMs were discussed.
Neospora		Sn79	Sn79 (IT), compared herds with access to outdoor grazing and herds keeps indoor fulltime. It found a higher prevalence in herds with access to outdoor.
Anaplasma marginale		Sn73	Sn73 (TR) was focused on genome characterization of *A. marginale*. Authors were able to discriminate different genotyping across IvsE farming managements.