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A meta-analysis of the prevalence of bovine trypanosomiasis in some African countries from 2000 to 2018

F. Ebhodaghe[a,b,*,1], C. Isaac[b], J.A. Ohiolei[c]

[a] African Regional Postgraduate Programme in Insect Science, West African Sub-Regional Centre, University of Ghana Legon, Accra, Ghana
[b] Department of Zoology, Ambrose Alli University, Ekpoma, Nigeria
[c] Lanzhou Veterinary Research Institute, Chinese Academy of Agricultural Sciences, Lanzhou, China

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ABSTRACT

Bovine trypanosomiasis is a disease of cattle. In sub-Saharan Africa, the disease mean prevalence estimates are unknown in most endemic countries. We therefore performed a meta-analysis with the aim of estimating national mean prevalence of bovine trypanosomiasis in endemic countries across sub-Saharan Africa. Relevant articles reporting bovine trypanosomiasis prevalence were retrieved through systematic literature search and scanning of articles reference-lists. Eligibility criteria included that articles reported sample size, prevalence, and diagnostic technique adopted. Overall, data from 180 eligible articles from 19 countries satisfied the inclusion criteria. Meta-analysis of prevalence data based on the random-effects model resulted in an overall mean prevalence of 15.10% (95% CI: 13.22–17.08). National prevalence estimates were generally high except those of Benin and Senegal where estimates ranked below 10.00%. Significant heterogeneity (I^2 = 98.75%. p = < 0.0001) was noted between studies, and univariate meta-regression analysis identified choice of diagnostic method being major contributor to observed heterogeneity (R^2 = 36.37%); while country of study (R^2 = 9.57%) and sample size (R^2 = 3.47%) had marginal effect on heterogeneity. In spite of past and ongoing control activities, bovine trypanosomiasis remains highly prevalent in most endemic sub-Saharan African countries. Nevertheless, dearth of epidemiological data in some countries and the use of less sensitive diagnostic tools limit reliable estimation of the disease prevalence. Therefore, there is the need to intensify efforts in aspects of surveillance and increased application of molecular diagnostic tool(s) across endemic locations as this would raise the chances of achieving a near-accurate estimate of the disease prevalence which is the first step to attempting eradication.

1. Introduction

Bovine trypanosomiasis, a vector-borne disease of cattle is caused by infection with trypanosomes. There are over 50 million cattle at risk of the disease in sub-Saharan Africa with potentially huge economic losses (Swallow, 1999; Leta et al., 2016; Holt et al., 2016). The determinants of trypanosomiasis prevalence in cattle hosts are varied and complex as population density of vectors, ecology of an area, livestock management system, and cattle trypanotolerance status could play some roles in influencing prevalence outcomes (Silbermayr et al., 2013; Sow et al., 2013; Lelisa et al., 2016). Also, the varied degree of sensitivity and the limitation(s) of respective diagnostic tools being used for epidemiological studies could distort true picture of prevalence of bovine trypanosomiasis (Miruk et al., 2008; Moti et al., 2014; Abdi et al., 2017). Furthermore, by cursory evaluation of bovine trypanosomiasis-prevalence data, heterogeneity has been observed in studies conducted in different locations (Adam et al., 2012; Michael et al., 2002; Pagabeleguem et al., 2012; Nakayima et al., 2012). Several factors and conditions may have underpinned these variations (Abdi et al., 2017) as meta-analysed data from Ethiopia indicated that the heterogeneity in the disease-prevalence data could have been influenced by location and year of study (Leta et al., 2016).

In countries endemic of bovine trypanosomiasis, there should be a surveillance system covering relatively large areas over a long period of time so as to establish a prevalence pattern before and after control activities; but this is rarely the case in Africa due to paucity of resources. Through synthesis of available data, meta-analyses provide an option to tackle this challenge such that mean-prevalence data within a time frame and in a given space are processed. This is useful in largely appraising the disease dynamics in Africa as well as guide on

* Corresponding author.
E-mail addresses: ebhodaghefaith@gmail.com (F. Ebhodaghe), cle21200@gmail.com (C. Isaac), asekhaenj@gmail.com (J.A. Ohiolei).
[1] Current address: International Centre of Insect Physiology and Ecology, P.O. Box 30772-00100, Nairobi, Kenya.

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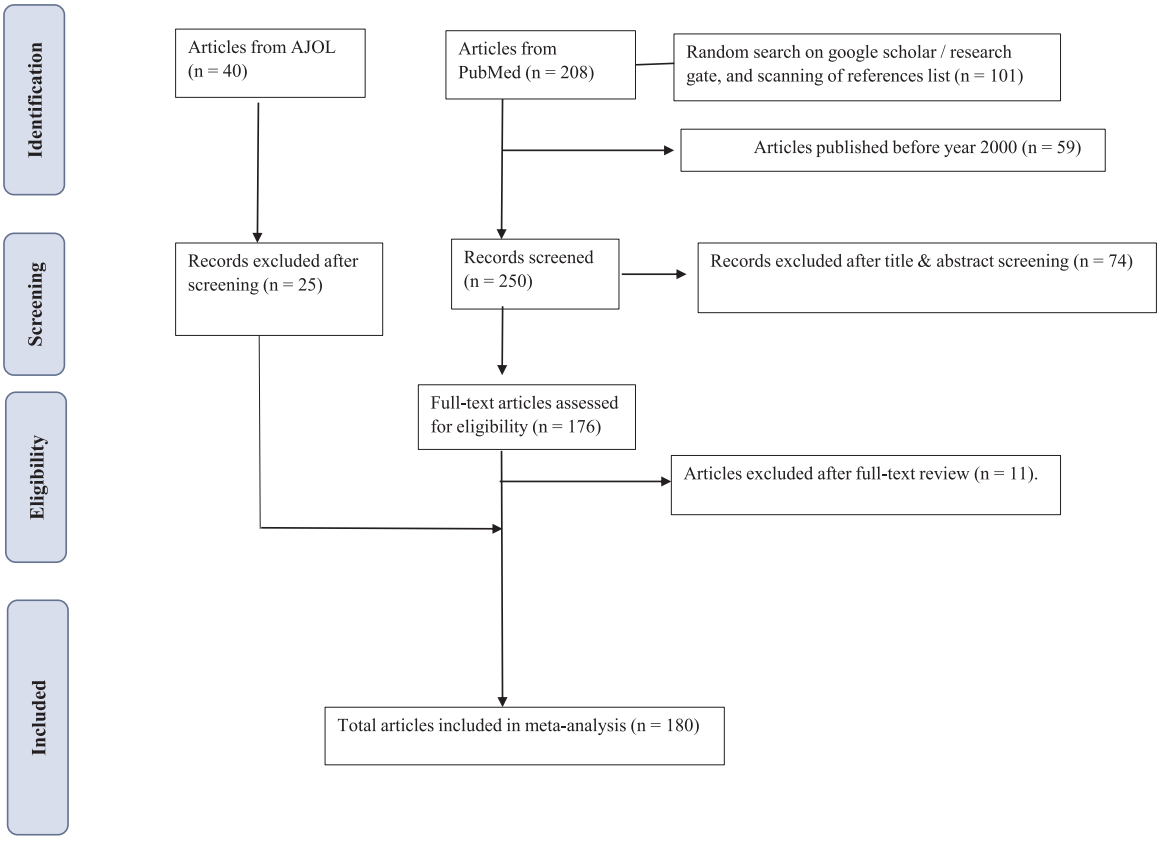

Fig. 1. A flowchart diagram showing paper selection and inclusion/exclusion process.

prioritizing control activities across endemic locations (Holt et al., 2016).

As bovine trypanosomiasis control programmes are mostly planned at country level, control efforts may not be substantially effective as a result of the trans-border nature of the disease (Tonah, 2000; Ahmed et al., 2016; Sigauque et al., 2000). Moving towards achieving the disease eradication in Africa, a collaborative control effort across national boundaries is a necessity (Mattioli et al., 2004; Adam et al., 2012). A basic step to possibly trigger the needed cooperation in the control efforts is by determining the disease prevalence by country as well as pooling all available and reliable published data from endemic countries with the aim of presenting a holistic prevalence picture for sub-Saharan Africa. These were carried out in this study including determining the possible factor(s) contributing to disease-prevalence heterogeneity across the endemic countries.

2. Methods

We followed the PRISMA guidelines (Preferred Reporting Items for Systematic Reviews and Meta-analyses) (Moher et al., 2009) in conducting and reporting results of the meta-analysis (Appendix A of Supplementary file).

2.1. Search strategy

We searched PubMed and African Journal Online (AJOL) for studies on bovine trypanosomiasis prevalence. In addition, search was conducted on Google Scholar and ResearchGate, while reference-lists on relevant papers were inspected for pertinent literature. In PubMed search, we used the search terms: “bovine OR cattle” and “trypanosomiasis OR trypanosomosis OR trypanosomes” and “prevalence” and “Country”. Article search was conducted in AJOL using the same search terms as in PubMed, but without addition of name of country. Search was conducted in July/August 2017 and repeated in March/April 2018. Finally, we screened titles and abstracts of articles, while the full-text (where possible) of articles were screened based on a set of inclusion/exclusion criteria and thereafter appraised for their quality.

2.2. Inclusion/exclusion criteria

Articles selected for the study must have reported field surveys on cattle. In addition, authors must have clearly stated study country, sample size, number of trypanosome-positive cattle, and diagnostic technique adopted. Articles reporting studies on other disease (s) and animal (s) aside trypanosomiasis and cattle, respectively were excluded. Also, articles were excluded if they reported studies outside sub-Saharan Africa and lacked clarity in results presentation. Articles published or reporting studies conducted before the year 2000 were excluded.

2.3. Study quality assessment

We adapted the tool developed by Munn et al. (2015) for the quality assessment of articles. Responses were either “yes”, “unclear” or “no” coded respectively as “2”, “1” and “0”. Also, individual and overall mean study quality was determined.

2.4. Data extraction

We extracted the following information from each study: study country, study period, cattle breed (trypanotolerance status), geographical location within country where study was conducted, sample size, diagnostic technique, and number of trypanosome-infected cattle. In studies where multiple diagnostic techniques were applied, the more or most sensitive technique was selected.

Table 1
Characteristics of studies derived from database search.

Country	Study Period	Breed	Location	Sample size	Diagnostic technique	No. infected	Apparent prevalence (%)	Reference
Benin	NA	T&S	W	134	Concentration	9	6.7	Farougou et al. (2012)
Botswana	2000	NA	NW	1809	Concentration	289	15.98	Sharma et al. (2001)
Burkina Faso	2003	T	SW	363	Concentration	27	7.54	Dayo et al. (2010)
Burkina Faso	NA	NA	SW	1784	ELISA	1309	73.37	Michael et al. (2002)
Burkina Faso	NA	T&S	S″,C,N	1041	ELISA	458	44	Pagabeleguem et al. (2012)
Burkina Faso	NA	T&S	SW	368	PCR	40	10.87	Silbermayr et al. (2013)
Burkina Faso	2007	T&S	NW	497	Concentration	25	5.03	Sow et al. (2012)
Burkina Faso	2007	T&S	NW	2002	ELISA	685	34.2	Sow et al. (2013)
Cameroon	NA	T&S	N	294	Concentration	42	14.3	Achukwi and Musongong (2009)
Cameroon	2004	S	N	170	Concentration	5	2.94	Mamoudou et al. (2006)
Cameroon	2005	NA	N	221	Concentration	46	20.81	Mamoudou et al. (2008)
Cameroon	2005	NA	N	334	Concentration	77	23	Mamoudou et al. (2009)
Cameroon	NA	S	N	504	Concentration	148	29.4	Mamoudou et al. (2015a)
Cameroon	2014	S	N	866	Concentration	78	9.01	Mamoudou et al. (2016b)
Cameroon	2013–2014	S	NW	301	Concentration	31	10.3	Mamoudou et al. (2016a)
Cameroon	2005	S	N	223	Concentration	22	9.86	Mamoudou et al. (2015b)
Cameroon	NA	NA	N	302	Concentration	44	14.6	Mbahin et al. (2008)
Cameroon	2008	S	N	330	ELISA	103	31.2	Mpouam et al. (2011)
Cameroon	2014	S	N	392	PCR	24	6	Ngomtcho et al. (2017)
Cameroon	2014	NA	N	635	Concentration	4	0.63	Suh et al. (2017)
Ethiopia	2010–2011	NA	C	177	Concentration	6	3.4	Sebele et al. (2015)
Ethiopia	2013–2014	S	S″	1508	Concentration	118	7.8	Abebe et al. (2017)
Ethiopia	2013–2014	S	W	384	Concentration	24	6.25	Abera et al. (2014)
Ethiopia	2010–2011	NA	S″	300	Concentration	64	21.33	Abera et al. (2016)
Ethiopia	2016	S	W	519	Concentration	29	5.58	Aki and Dinede (2016)
Ethiopia	2013	S	W	394	Concentration	22	5.6	Aki et al. (2016)
Ethiopia	2010–2011	S	W	385	Concentration	95	24.7	Ali and Bitew (2011
Ethiopia	2011–2012	S	NW	384	Concentration	8	2.1	Ayana et al. (2012)
Ethiopia	2010–2011	NA	SW	248	Concentration	57	23	Ayele et al. (2012)
Ethiopia	2009–2010	NA	W	384	Concentration	33	8.6	Bekele and Nasir (2011)
Ethiopia	2003	S	S″	323	Concentration	71	22	Bekele et al. (2010)
Ethiopia	2011–2012	S	SW	384	Concentration	21	5.47	Bekele et al. (2018)
Ethiopia	2013–2014	S	S″	384	Concentration	57	14.8	Bezabih et al. (2017)
Ethiopia	2013	NA	N	493	Concentration	36	7.3	Birhanu et al. (2015)
Ethiopia	NA	NA	NW	384	Concentration	30	7.81	Bishaw et al. (2012)
Ethiopia	2008–2009	NA	W	300	Concentration	35	11.7	Bitew et al. (2011)
Ethiopia	NA	S	W	384	Concentration	11	2.86	Biyazen et al. (2014)
Ethiopia	2011	S	W	384	Blood smear	38	9.89	Bogale et al. (2012)
Ethiopia	NA	NA	NW	240	ELISA	216	90	Cherenet et al. (2006)
Ethiopia	2008–2009	NA	W	202	Concentration	24	11.88	Dagnachew and Shibeshi (2011)
Ethiopia	2008–2009	NA	NW	300	Concentration	34	11.33	Dagnachew et al. (2011)
Ethiopia	2011–2012	S	NW	1435	Concentration	175	12.2	Dagnachew et al. (2017)
Ethiopia	2014–2015	S	S″	385	Concentration	14	3.7	Dawit et al. (2015)
Ethiopia	2015–2016	S	W	930	Concentration	131	14.1	Degneh et al. (2017)
Ethiopia	2007–2008	S	SW	1200	Concentration	307	25.66	Denu et al. (2012)
Ethiopia	2015	S	W	391	Concentration	52	13.3	Dinede and Aki (2016)
Ethiopia	2009–2012	NA	SW	7021	Concentration	675	9.61	Duguma et al. (2015)
Ethiopia	2006–2007	S	NW	568	Concentration	71	12.5	Efrem et al. (2010)
Ethiopia	2015–2016	NA	S″	384	Concentration	32	8.3	Eshetu et al. (2017)
Ethiopia	2011	NA	SW	212	Concentration	32	15.1	Fentahun et al. (2013)
Ethiopia	2011	S	SW	1524	PCR	472	31	Fikru et al. (2012)
Ethiopia	2011	S	NW	1260	Concentration	153	12.14	Girmay et al. (2016)
Ethiopia	2016	NA	W	395	Concentration	47	11.89	Golessa and Mekonnen (2017)
Ethiopia	2013–2014	S	S″	480	Concentration	32	6.67	Gona et al. (2016)
Ethiopia	2014–2015	NA	W	488	Concentration	19	3.9	Haile et al. (2016)
Ethiopia	2009–2008	NA	SW	780	Concentration	111	14.23	Kacho and Singh (2017)
Ethiopia	2015	S	S″	384	Concentration	101	26.3	Kassa and Megerssa (2017)
Ethiopia	2013	NA	SW	599	Concentration	101	16.9	Kassaye (2015)
Ethiopia	2015	NA	SW	862	Concentration	143	16.59	Kedir et al. (2016a)
Ethiopia	2014	NA	W	312	Concentration	41	13.14	Kedir et al. (2016b)
Ethiopia	2015	S	W	202	Concentration	46	22.8	Kenaw et al. (2015)
Ethiopia	NA	NA	S″	1008	Concentration	152	15	Kidanemariam et al. (2002)
Ethiopia	2015	NA	SW	408	Concentration	30	7.4	Kitila et al. (2017)
Ethiopia	2009–2010	NA	W	389	Concentration	42	10.8	Lelisa et al. (2014)
Ethiopia	2014	NA	NW	405	Concentration	22	5.43	Lelisa et al. (2015)
Ethiopia	2014–2015	NA	SW	566	Concentration	24	4.24	Lelisa et al. (2016)
Ethiopia	2009	S	NW	540	Concentration	67	12.41	Mekuria and Gadissa (2011)
Ethiopia	2015	S	S″	400	Concentration	21	5.25	Melese et al. (2017)
Ethiopia	2005–2006	S	NW	3360	Concentration	275	8.2	Mihret and Mamo (2007)
Ethiopia	2006	S	S″	152	Concentration	31	20.4	Miruk et al. (2008)
Ethiopia	NA	NA	SW	411	PCR	124	30.17	Moti et al. (2014)
Ethiopia	2012	S	SW	587	Concentration	106	18.1	Moti et al. (2015)
Ethiopia	2014–2015	S	S″	217	Concentration	64	29.5	Muktar et al. (2016)
Ethiopia	2011–2012	S	NW	543	Concentration	46	8.5	Mulatu et al. (2016)

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Table 1 (*continued*)

Country	Study Period	Breed	Location	Sample size	Diagnostic technique	No. infected	Apparent prevalence (%)	Reference
Ethiopia	2009–2010	NA	W	384	Concentration	108	28.1	Mulaw et al. (2011)
Ethiopia	2013–2014	NA	S″	1838	Concentration	133	7.2	Sheferaw et al. (2016)
Ethiopia	NA	NA	NW	1509	Concentration	92	6.1	Sinshaw et al. (2006)
Ethiopia	2008–2009	NA	SW	250	Concentration	11	4.4	Tadesse and Tsegaye (2010)
Ethiopia	2010–2011	S	W	386	Concentration	33	8.55	Tafese et al. (2012)
Ethiopia	2013–2014	S	SW	384	Concentration	30	7.81	Takile et al. (2014)
Ethiopia	2009–2010	NA	S″	384	Concentration	17	4.43	Teka et al. (2012)
Ethiopia	NA	S	SW	409	Concentration	25	6.1	Terefe et al. (2015)
Ethiopia	2013–2014	NA	W	310	Concentration	80	25.8	Tesfaye and Ibrahim (2017)
Ethiopia	2001	NA	W	904	Concentration	70	7.74	Tewelde et al. (2004)
Ethiopia	2013	NA	SW	384	Concentration	52	13.6	Tola et al. (2016)
Ethiopia	2007	NA	S″	399	Concentration	166	41.6	Wogayehu et al. (2017)
Ethiopia	2009–2010	NA	S″	400	Concentration	48	12	Wondimu et al. (2017)
Ethiopia	2014–2015	NA	W	400	Concentration	85	21.5	Yalew and Fantahun (2017)
Ethiopia	NA	S	W	360	ELISA	167	46.4	Yeshidinber and Eguale (2004)
Ethiopia	2015–2016	NA	SW	383	Concentration	8	2.1	Yigzaw et al. (2017)
Ethiopia	2011–2012	S	SW	500	Concentration	21	4.2	Yohannes et al. (2013)
Ethiopia	2010–2011	NA	S″	461	Concentration	127	27.55	Zeryehun and Abraham (2012)
Gabon	2014	S	S″	20	Concentration	13	65	Cossic et al. (2017)
Gabon	NA	T	SE	224	PCR	72	32.14	Maganga et al. (2017)
Ghana	2008–2009	T&S	N	1800	ELISA	342	19	Adam et al. (2012)
Ghana	2010	T&S	S″	40	PCR	20	50	Bakari et al. (2017)
Ghana	2001	T&S	N	1013	ELISA	390	38.5	Mahama et al. (2004)
Ghana	2010	NA	S″	146	PCR	84	57.5	Nakayima et al. (2012)
Ivory Coast	NA	T&S	NE	200	PCR	41	20.5	Koffi et al. (2014)
Ivory Coast	2013	S	WC	87	PCR	22	25.28	N'Djetchi et al. (2017)
Kenya	NA	NA	S″	358	PCR	70	19.55	Odongo et al. (2016)
Kenya	NA	NA	W	103	PCR	29	28.1	Thumbi et al. (2008)
Kenya	2004	NA	W	1260	PCR	253	20.1	von Wissmann et al. (2011)
Mali	2007	T&S	SE	796	Concentration	125	15.7	Mungube et al. (2012)
Mozambique	2014	T&S	C	467	Concentration	107	22.9	Mulandane et al. (2018)
Nigeria	2012	NA	NC	214	Concentration	28	13.08	Abenga (2015)
Nigeria	2001	S	NC	526	Concentration	48	9.13	Abenga et al. (2004)
Nigeria	2007	S	NC	300	Concentration	19	6.33	Adama et al. (2010)
Nigeria	2009	S	SW	200	Blood smear	12	6	Akande et al. (2011)
Nigeria	2006	NA	SW	305	Concentration	15	4.92	Ameen et al. (2008)
Nigeria	NA	NA	NW	96	Concentration	15	15.63	Andrew et al. (2014)
Nigeria	NA	S	NC	200	Concentration	76	38	Anosike et al. (2003)
Nigeria	NA	S	NW	32	Concentration	13	40	Danbirni et al. (2010)
Nigeria	2004–2005	S	NW	1293	Concentration	109	8.4	Enwezor et al. (2009)
Nigeria	2008	S	NC	395	Concentration	15	3.8	Enwezor et al. (2012)
Nigeria	2008	NA	NW	500	Concentration	9	1.8	Fajinmi et al. (2011)
Nigeria	2012	T&S	SW	320	Concentration	15	4.69	Fasanmi et al. (2014)
Nigeria	NA	NA	NW	40	Concentration	15	37.5	Haruna et al. (2017)
Nigeria	2016	S	NC	150	Concentration	80	53.33	Hassan et al. (2016)
Nigeria	NA	NA	NE	400	Concentration	28	7	Karshima and Bobbo (2011)
Nigeria	2016	S	NW	352	Concentration	14	3.98	Machina et al. (2017)
Nigeria	2012	NA	NC	2330	PCR	1046	44.89	Majekodunmi et al. (2013)
Nigeria	2008	S	NE	277	Concentration	20	7.22	Obaloto et al. (2015)
Nigeria	NA	T&S	NC	200	PCR	28	14	Ode et al. (2017)
Nigeria	2003–2004	NA	SE	405	Blood smear	15	3.7	Ohaeri (2010)
Nigeria	NA	S	NC	400	Concentration	39	9.75	Oluwafemi et al. (2007)
Nigeria	2014	S	NC	200	Concentration	9	4.5	Pam et al. (2016)
Nigeria	2014	S	NE	120	Blood smear	1	0.83	Paul et al. (2016)
Nigeria	2009	NA	NC	634	Concentration	14	2.2	Samdi et al. (2011)
Nigeria	2014	T&S	SW	162	Blood smear	3	1.85	Sam-Wobo et al. (2016)
Nigeria	NA	T&S	NW, SW	411	PCR	262	63.7	Takeet et al. (2013)
Nigeria	NA	NA	SE	115	Blood smear	30	26.09	Ukpai and Obasi (2017)
Nigeria	NA	S	NE	218	Concentration	2	0.92	Usman et al. (2008)
Nigeria	NA	NA	NW	94	Concentration	24	25.53	Wayo et al. (2017)
Nigeria	NA	NA	NW	118	PCR	11	12.98	Yusuf et al. (2015)
Nigeria	2002	S	NE	240	Concentration	32	13.33	Zubairu et al. (2013)
Senegal	2012	T&S	W	104	PCR	4	3.85	Ravel et al. (2015)
Senegal	2007	NA	W	1141	Concentration	23	2.02	Seck et al. (2010)
South Africa	NA	S	SE	473	PCR	236	50	Gillingwater et al. (2010)
South Africa	NA	S	SE	673	PCR	125	18.6	Mamabolo et al. (2009)
South Africa	NA	S	SE	76	PCR	46	60.5	Van Den Bossche et al. (2006)
South Africa	2006	S	SE	60	PCR	3	5	Yusufmia et al. (2010)
Sudan	2008	NA	E	1008	Blood smear	16	1.58	Gumaa et al. (2011)
Sudan	NA	NA	SE,C,W,E	97	PCR	56	57.73	Osman et al. (2016)
Sudan	2003	S	SE	46	Concentration	23	50	Rahman et al. (2008)
Sudan	2010	NA	SE	141	PCR	80	56.7	Salim et al. (2011)
Tanzania	2002	NA	E	970	Concentration	8	0.8	Goossens et al. (2006)
Tanzania	2013	S	N	295	Blood smear	7	2.4	Haji et al. (2014)
Tanzania	2013	S	N	295	LAMP	82	27.8	Haji et al. (2015)

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Table 1 (*continued*)

Country	Study Period	Breed	Location	Sample size	Diagnostic technique	No. infected	Apparent prevalence (%)	Reference
Tanzania	NA	S	E	171	PCR	40	23.4	Karimuribo et al. (2011)
Tanzania	NA	NA	S″	420	Blood smear	39	9.3	Kassian et al. (2017)
Tanzania	2008	NA	N	148	PCR	8	5.4	Laohasinnarong et al. (2011)
Tanzania	2015	NA	N	424	Concentration	10	2.36	Malulu et al. (2017)
Tanzania	2013	NA	W	229	Blood smear	6	2.6	Matogo et al. (2015)
Tanzania	NA	NA	E	390	Concentration	52	13	Mugittu et al. (2001)
Tanzania	NA	T&S	E	237	PCR	122	51.47	Nhamitambo et al. (2017)
Tanzania	NA	S	E	691	Concentration	16	2.3	Nonga and Kambarage (2009)
Tanzania	2013–2014	NA	N	117	PCR	55	47	Ruiz et al. (2015)
Tanzania	2015–2016	NA	N	1002	PCR	172	17.2	Simwango et al. (2017)
Tanzania	2006	S	N	239	Blood smear	12	5	Swai and Kaaya (2012)
Togo	2012–2013	T&S	N	1883	Concentration	203	10.8	Tchamdja et al. (2017)
Uganda	2006	NA	N,E	600	PCR	63	10.5	Ahmed et al. (2013)
Uganda	2012	T&S	SW	295	PCR	6	2.4	Alingu et al. (2014)
Uganda	2011–2012	S	N	816	PCR	338	41	Angwech et al. (2015)
Uganda	NA	NA	W,E,S	1891	Concentration	144	7.6	Biryomumaisho et al. (2013)
Uganda	NA	NA	E	203	ELISA	92	45.3	Jing et al. (2009)
Uganda	NA	S	E	250	PCR	96	38.4	Magona et al. (2003)
Uganda	2000	T&S	E	98	Concentration	7	7.1	Magona and Mayende (2001)
Uganda	NA	T&S	E	1475	Concentration	124	8.4	Magona et al. (2004)
Uganda	2002	S	SE	1992	Concentration	221	11.09	Magona et al. (2005)
Uganda	2005	NA	E	401	Concentration	49	12.22	Magona et al. (2008)
Uganda	2011	S	SE	6048	PCR	928	15.3	Muhanguzi et al. (2014)
Uganda	2016	S	NE	2030	PCR	331	16.3	Muhanguzi et al. (2017)
Uganda	NA	T&S	N,E	1428	PCR	221	15.5	von Wissmann et al. (2014)
Uganda	NA	T	SW	1309	Concentration	84	6.42	Waiswa and Katunguka-Rwakishaya (2004)
Uganda	2013	T	W	186	Blood smear	8	4.3	Weny et al. (2017)
Zambia	NA	S	E	734	PCR	149	20.3	Marcotty et al. (2008)
Zambia	2013	S	C	58	PCR	17	29.3	Mbewe et al. (2015)
Zambia	2010	NA	NE,C,S″	472	PCR	98	20.76	Musinguzi et al. (2016)
Zambia	2004–2005	S	E	734	PCR	246	33.5	Simukoko et al. (2007)

N. B.: C: Central. Concentration: Buffy Coat and/or Haematocrit Centrifugation Technique. E: East. ELISA: Enzyme Linked Immunosorbent Assay. LAMP: Loop-mediated isothermal Amplification. N: North. NA: Not Available. NC: North-Central. NE: North-East. NW: North-West. PCR: Polymerase Chain Reaction. S″: South. S: Susceptible. SE: South-East. SW: South-West. T&S: Tolerant and Susceptible. T: Tolerant. W: West. WC: West Central.

2.5. Data analysis

Mean prevalence estimates, between-study heterogeneity and meta-regression analyses were determined using the *Metafor* package in *R* (version 1.1.453.0). We employed the *MetaXL* add-in for Microsoft Excel (www.epigear.com) to construct forest plot and assess for publication bias.

2.5.1. Mean prevalence estimates

Transformation of proportions was by the double arcsine method (Miller, 1978), while the estimation of mean prevalence with their respective 95% Confidence Intervals was based on the random-effects model (Hedges and Vevea, 1998; DerSimonian and Kacker, 2007).

2.5.2. Heterogeneity

Between-study heterogeneity was investigated by the inverse variance statistic (I^2) and the Cochran Q test (Higgins and Thompson, 2002). The I^2 reports percentage of observed total variation between studies that are due to heterogeneity rather than by chance. Heterogeneity is described as low, moderate or high where the I^2 is '≤ 25%', '50%' or '≥ 75%', respectively (Higgins and Thompson, 2002; Leta et al., 2016). An I^2 of '0' indicates absence of heterogeneity. Only the *p*-values of the Cochran Q test were reported with significance at $p < 0.05$. Q is the weighted of squares on a standardized scale.

2.5.3. Meta-regression

To identify source(s) of heterogeneity, we conducted a univariate meta-regression analysis with 'country', 'sample size', 'diagnostic technique' and 'study year' as independent variables. Where study year was unavailable, we assumed study year to be that preceding publication year. We further conducted a multivariate meta-regression to ascertain combined effect of explanatory variables which had *p*-value of < 0.25 in the univariate meta-regression analysis.

2.5.4. Publication bias

Publication bias was inspected by the Luis Furuya-Kanamori (LFK) index (Barendregt and Doi, 2016). An LFK-index within the range of '± 1', '± 2', and outside '± 2' is interpreted respectively as symmetrical, slightly asymmetrical, and significantly asymmetrical. A symmetrical index signifies absence of publication bias.

3. Results

3.1. Literature search

Overall, 180 articles satisfied the general inclusion criteria (Fig. 1, Table 1). From these, we had a total sample size of 109,985 cattle with 17,808 cases of trypanosomes infection. Studies were conducted between the year 2000 and 2016 although, in some articles, study year was not indicated (Table 1).

3.2. Study quality assessment

Mean scores of individual articles ranged from 1.63 to 2.00, while for all articles, average score was 1.89 (Appendix A of Supplementary file). Clearly, articles were of acceptable quality, although some authors were unclear as to whether sample size was appropriate and what sampling method was adopted.

3.3. Mean prevalence estimates

Overall, mean prevalence was 15.10% (95% CI: 13.22–17.08) (Table 2). However, heterogeneity was substantial ($I^2 = 98.75\%$. $p < 0.0001$). By country, the least prevalent was Senegal with 2.27%

Table 2
Mean prevalence of bovine trypanosomiasis according to sub-groups.

Characteristics	Number of studies	Pooled bovine trypanosomiasis prevalence				Heterogeneity	
		Sample size	Cases	Prevalence	95%CI	I^2 (%)	*P*-value (Cochran's Q)
Overall	180	109,985	17,808	15.10	13.22–17.08	98.75	< 0.0001
Country							
Benin	1	134	9	6.72	3.01–11.66	–	1
Botswana	1	1,809	289	15.98	14.32–17.70	–	1
Burkina Faso	6	6055	2544	26.2	8.32–49.63	99.71	< 0.0001
Cameroon	12	4572	624	12.74	7.12–19.66	97.56	< 0.0001
Ethiopia	72	47,304	6061	13.02	11.02–15.16	97.75	< 0.0001
Gabon	2	244	85	46.38	16.63–77.55	87.54	0.0046
Ghana	4	2999	836	39.98	23.57–57.63	98.45	< 0.0001
Ivory Coast	2	287	63	21.87	17.24–26.88	–	0.3617
Kenya	3	1721	352	20.93	17.70–24.36	47.02	0.1514
Mali	1	796	125	15.7	13.26–18.32	–	1
Mozambique	1	467	107	22.91	19.21–26.84	–	1
Nigeria	31	11,247	2047	12.42	7.11–18.90	98.85	< 0.0001
Senegal	2	1245	27	2.27	0.87–4.22	36.79	0.2085
South Africa	4	1282	410	30.99	11.25–55.21	98.37	< 0.0001
Sudan	4	1292	175	37.04	2.68–82.37	99.34	< 0.0001
Tanzania	14	5628	629	11.63	6.87–17.41	98.34	< 0.0001
Togo	1	1883	203	10.78	9.42–12.22	–	1
Uganda	15	19,022	2712	14.28	10.39–18.67	98.36	< 0.0001
Zambia	4	1998	510	25.44	18.16–33.47	92.56	< 0.0001
Trypanotolerance status							
Susceptible	76	45,507	6785	14.5	12.28–16.87	97.86	< 0.0001
Tolerant	4	2082	191	10.84	3.57–21.31	96.95	< 0.0001
Diagnostic technique							
Blood smear	12	3763	187	4.99	2.77–7.79	91.36	< 0.0001
Concentration	119	72,218	7739	11.06	9.83–12.36	96.51	< 0.0001
ELISA	9	8773	3762	47.25	32.43–63.32	99.49	< 0.0001
LAMP	1	295	82	27.8	22.82–33.06	0	1
PCR	39	24,936	6038	26.22	21.71–30.90	98.45	< 0.0001
Sample size							
< 199	30	3258	758	24.88	16.52–34.27	97.07	< 0.0001
200–399	72	22,423	3382	13.94	11.12–17.00	97.59	< 0.0001
400–599	33	15,477	2147	12.16	8.56–16.27	98.21	< 0.0001
600 >	45	68,827	11,521	14.69	11.17–18.60	99.49	< 0.0001
Study year							
2000–2004	22	16,895	3519	17.66	10.21–26.60	99.49	< 0.0001
2005–2009	49	28,437	4331	14.77	11.21–18.71	98.73	< 0.0001
2010–2014	79	51,596	8049	14.17	11.73–16.79	98.48	< 0.0001
2015 >	30	13,057	1909	16.15	12.37–20.32	97.33	< 0.0001

(95% CI: 0.87–4.22. I^2 = 36.79%. p = 0.2085), while the highest was Gabon with 46.38% (95% CI: 16.63–77.55. I^2 = 87.54%. p = 0.0046) (Table 2). One hundred and thirty three (133) articles reportedly performed random sampling; while in a study (von Wissmann et al., 2011) diagnosis was conducted on all cattle available. Thus, a total of 134 studies were clear on sampling procedure adopted and had a mean prevalence of 14.62% (95% CI: 12.48–16.90). Similarly, 87 studies were reported to be adequate based on sample size estimation with mean prevalence of 14.38% (95% CI: 11.94–16.99).

Trypanotolerant cattle had lower prevalence in comparison to trypanosusceptibile cattle (Table 2). Expectedly, among diagnostic techniques, ELISA recorded highest prevalence outcomes with blood smear being the least (Table 2, Fig. 2). Results of mean prevalence according to sample size and study-year brackets are shown in Table 2.

3.4. Meta-regression

We could not include trypanotolerance status of cattle in the regression analysis because, in most studies, this was not reported. Where reported, cattle were mostly trypanosusceptible or a mix of tolerant and susceptible breeds. From univariate regression analysis, country and sample size significantly influenced heterogeneity respectively explaining 9.57% and 3.47% of total variation in prevalence. Diagnostic technique had the most contribution (36.37%) to variation (Table 3). The addition of the independent variables 'country' and 'sample size' to 'diagnostic technique' in a multivariate meta-regression did not improve rate of determination (25.25%) (Table 4).

3.5. Publication bias

The LFK index was 0.67 signifying absence of publication bias. See Appendix A of Supplementary file for funnel plot).

4. Discussion

This study reported high prevalence of bovine trypanosomiasis in most endemic countries in sub-Saharan Africa. Authors of some of the studies included in this meta-analysis were not clear on sampling method adopted and thus may have included samples by the convenience method with potential of introducing bias to the overall mean prevalence estimate in this study. However, the possibility of bias was somewhat tested and there was marginal variation between the overall mean prevalence from the 180 studies and the respective mean prevalence from studies that reportedly performed random sampling and used adequate sample-size. Higher prevalence of the disease in trypanosusceptible than trypanotolerant breeds of cattle were noted. Also, we noted significant between-study heterogeneity in prevalence estimates of bovine trypanosomiasis with choice of diagnostic method as a

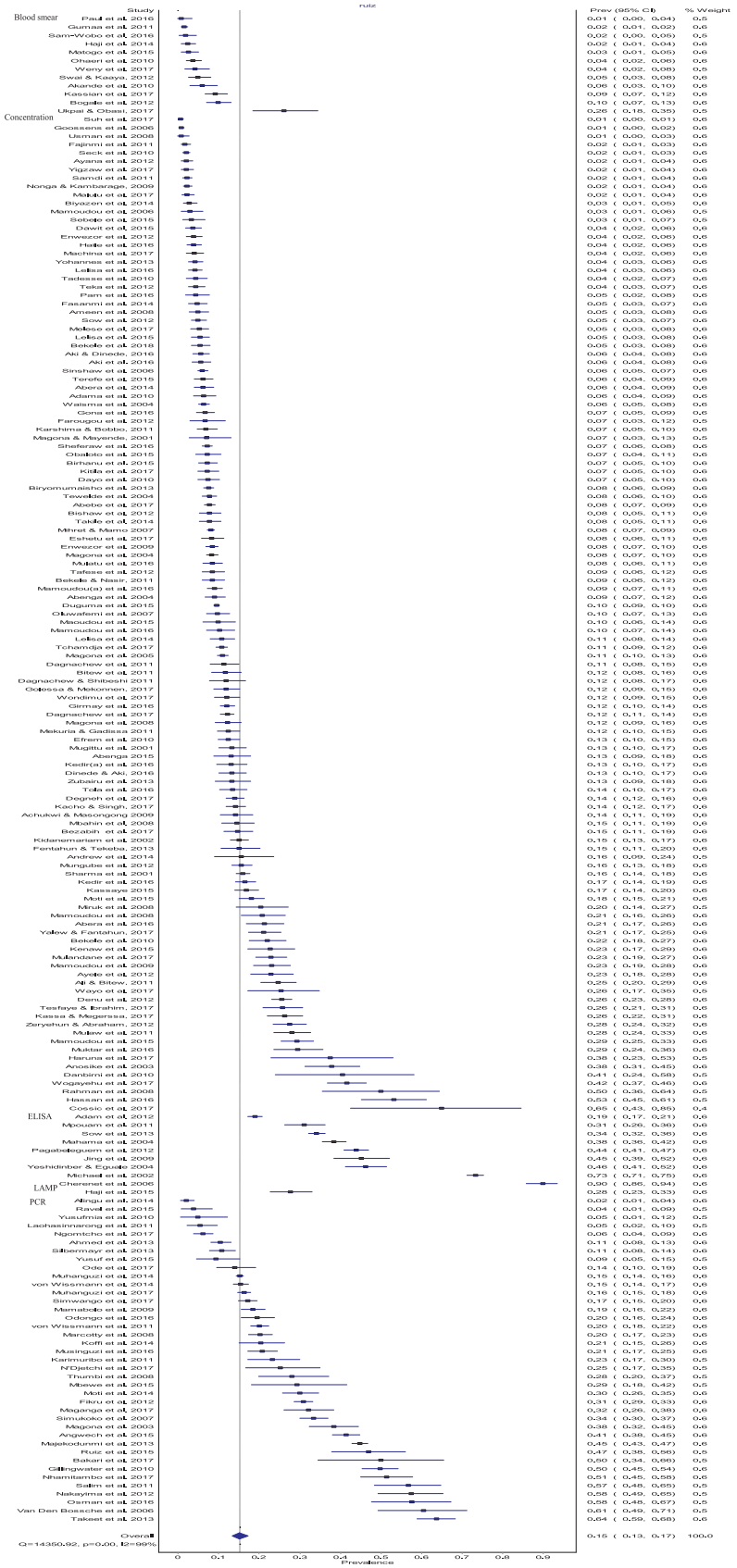

Fig. 2. Forest plot showing prevalence studies according to diagnostic technique in order of increasing prevalence.

Table 3
Results of univariate meta-regression analysis showing the coefficients, *p*-values and Cochran's Q statistics according to sub-groups.

Variable	Category	Sample size	Coefficient	*P*-value	Cochran's Q statistics (R^2 %)
Country	Benin	134	Reference		Q = 37.8735. df = 18. p = < 0.004 (9.57).
	Botswana	1809	0.143	0.6032	
	Burkina Faso	6055	0.2703	0.2022	
	Cameroon	4572	0.0983	0.6309	
	Ethiopia	47,304	0.1024	0.6053	
	Gabon	244	0.4778	0.0513	
	Ghana	2999	0.4180	0.0574	
	Ivory Coast	287	0.2319	0.3363	
	Kenya	1721	0.2257	0.3193	
	Mali	796	0.1396	0.6122	
	Mozambique	467	0.2314	0.4015	
	Nigeria	11,247	0.0939	0.6387	
	Senegal	1245	−0.0932	0.6981	
	South Africa	1282	0.3246	0.1403	
	Sudan	1292	0.3793	0.0851	
	Tanzania	5628	0.0829	0.6838	
	Togo	1883	0.0665	0.8091	
	Uganda	19,022	0.1205	0.5529	
	Zambia	1998	0.2645	0.2286	
Diagnostic technique	Blood smear	3763	Reference		Q = 98.5789. df = 4. p = < 0.0001 (36.37)
	Concentration	72,218	0.1132	0.0229	
	ELISA	8773	0.5264	< 0.0001	
	LAMP	295	0.3253	0.0563	
	PCR	24,936	0.3081	< 0.0001	
Sample size	< 199	3258	Reference	< 0.0001	Q = 10.2429. df = 3. p = 0.0166 (3.47).
	200–399	22,423	−0.1237	0.0053	
	400–599	15,477	−0.1506	0.0033	
	600 >	68,827	−0.1143	0.017	
Study year	2000–2004	16,895	Reference		Q = 1.0755. df = 3. p = 0.7830(0).
	2005–2009	28,437	−0.0381	0.4696	
	2010–2014	51,596	−0.0456	0.3569	
	2015 >	13,057	−0.017	0.7674	

Table 4
Results of multivariate meta-regression analysis.

Variable	Coefficient	*P*-value	95% confidence interval	
Country	0.0006	0.9734	−0.0327	0.0338
Sample size	−0.0707	0.3505	−0.2192	0.0778
Diagnostic technique	0.0007	0.9926	−0.1422	0.1436
Country * sample size	−0.0011	0.8576	−0.0131	0.0109
Country * diagnostic technique	0.0029	0.5978	−0.0080	0.0138
Sample size * diagnostic technique	0.0381	0.1728	−0.0167	0.0929
Country * sample size * diagnostic technique	−0.0016	0.4338	−0.0055	0.0024

major contributor.

Most of the reports considered for analysis showed high prevalence. Therefore, mean prevalence for each country was relatively high except for Benin and Senegal where prevalence estimates were below 10.00%. Several factors and conditions have been attributed to the high prevalence of bovine trypanosomiasis in sub-Saharan Africa; some of which are the presence of small ruminant-reservoirs of trypanosomes in cattle-rearing areas (Sinshaw et al., 2006), and high vector abundance with the vectors having preference for cattle over other livestock (Mulaw et al., 2011; Sinshaw et al., 2006; Terefe et al., 2015; Abebe et al., 2017). Others are close proximity of cattle populations to tsetse-belts (Bitew et al., 2011), compromised cattle-host immunity due to engagement in various strenuous activities (Ali and Bitew, 2011; Bitew et al., 2011; Denu et al., 2012; Kassaye, 2015; Muktar et al., 2016; Kitila et al., 2017; Melese et al., 2017; Tesfaye and Ibrahim, 2017) and emergence of drug-resistant strains of trypanosomes (Bitew et al., 2011; Kassaye, 2015; Melese et al., 2017). The low population of trypanotolerant breeds and high population of trypanosusceptible breeds of cattle may also have contributed to the results of high prevalence. Many farmers prefer trypanosusceptible breeds on account of their perceived higher productivity and traction power over their trypanotolerant counterparts.

Generally, ELISA and PCR are highly sensitive diagnostic techniques for epidemiological studies. However, ELISA is unable to distinguish cured from current infections, and so, could exaggerate prevalence estimates. Thus, a likely reason it recorded highest mean prevalence among diagnostic techniques. Moreover, the technique was scantily applied which limit our interpretation of its comparative performance. Similarly, PCR, though recorded in more studies than ELISA, was scantily used particularly in comparison to the concentration technique. The concentration technique was most commonly applied compared to the easy-to-use blood smear possibly for reason of higher sensitivity, but more importantly, its relatively low cost. In this study, diagnostic technique was a significant contributor to heterogeneity in prevalence which is not unconnected with the varying sensitivity of diagnostic tools utilized during epidemiological investigations.

Absence of heterogeneity between studies in some countries was the result of paucity of data. Sample size and country of study, had marginal effects on heterogeneity while prevalence over the years appeared not to have declined. By implication, control efforts in most locations may have had little or no meaningful effect on the disease burden possibly because most often the control strategies adopted are largely unstructured and non-systematic (Diall et al., 2017; Isaac et al., 2017). Another contributory factor might be the complete absence of control activities in some locations. Whatever the case, owing to tsetse and transhumance activity across national boundaries, there is the need for endemic countries to collaborate and intensify control efforts.

Results of the present study suggest high prevalence of bovine trypanosomiasis in most of the studied countries but identified poor epidemiological surveys as a major challenge towards achieving near-accurate disease burden estimations. To further enhance reliability of prevalence estimates, efforts should be made to avoid over

concentration of investigations in particular geographical locations at the neglect of other endemic areas albeit with very low infection burden (Leta et al., 2016).

The variation in prevalence data in this report is largely due to differences in the diagnostic tools used for epidemiological studies at various times and in sundry places. Unambiguously, the use of PCR tool should be highly encouraged for surveillance purpose albeit relatively expensive. As much as possible, it is expected that sponsoring bodies and relevant authorities should come to terms with the need to heavily support bovine-disease epidemiologists in the usage of molecular tools for epidemiological studies. We are also of the view that national authorities with the mandate of elimination/eradication of animal African trypanosomiasis should institute measures whereby disease epidemiologists are encouraged to constantly apply highly sensitive tools preferably PCR technique while other methods should only be complementary. Potentially, overtime, this could eliminate the ambiguity that fraught the prevalence data in the studied areas. This is highly necessary because a near-accurate estimate of the disease prevalence is the first step towards elimination/eradication of bovine trypanosomiasis in Africa. Additionally, control activities would need to be structured within the Progressive-Control-Pathway (PCP) model for any prospects of elimination/eradication to be in sight (Diall et al., 2017).

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Declaration of interest

The authors declare that they have no competing interests.

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Appendix A. Supplementary data

Supplementary material related to this article can be found, in the online version, at doi:https://doi.org/10.1016/j.prevetmed.2018.09.018.

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