Table S1 Summary of 43 studies focused on cryptosporidiosis in Australia; study focus, location and design and main findings

| **Study Design** | **Setting****Year (Reference)** | **Location** | **Main findings, including risk factors for epidemiological studies** |
| --- | --- | --- | --- |
| **Case-Control**  | Outbreak 2008 ([1](#_ENREF_1)) | Urban New South Wales | Single point source swimming pool identified as cause of outbreak (31 confirmed cases). Risk factors identified included swimming at facility A and household member with diarrhoea. Animal contact reduced odds of illness. |
| Outbreak1997-1998 ([2](#_ENREF_2)) | State-wide New South Wales | Multiple swimming pool sources identified. Younger mean age of cases (n=100) at 4.2 years versus 7.1 years for controls (n=200). Risk factors identified included swimming at a public pool, swimming in a dam, river or lake, and cases were less likely to drink bottled water. *Cryptosporidium* oocysts detected more commonly in water from case pools (n=6) than control pools (n=2). |
| Outbreak2001 ([3](#_ENREF_3)) | UrbanQueensland | Unpasteurized milk identified as the cause of the outbreak (8 confirmed cases). Six of 10 unpasteurised milk samples positive for *Cryptosporidium* antigen. |
| Outbreak1998 ([4](#_ENREF_4)) | UrbanVictoria  | Swimming at pool “X” associated with illness (7 confirmed cases in analysis). Cryptosporidium not detected in any of the four pools at implicated facility sampled.  |
| Outbreak1998 ([5](#_ENREF_5)) | UrbanQueensland | Swimming pool complex identified as cause of outbreak (31 confirmed cases in analysis).Three of four pools at Complex A positive for *Cryptosporidium* oocysts. |
| Outbreak1994-1995 ([6](#_ENREF_6)) | Urban New South Wales  | Swimming in a particular indoor swimming pool associated with illness (43 confirmed cases in analysis). Oocysts were also detected in water from the swimming pool. |
| Sporadic 1998-2001([7](#_ENREF_7), [8](#_ENREF_8)) | Urban Victoria & South Australia | Significant risk factors identified by region as: Victoria, Melbourne (201 cases): swimming in public pools, contact with a child with diarrhoea, household member with diarrhoea and calf contact.South Australia, Adelaide (134 cases): contact with a child with diarrhoea, household member with diarrhoea, calf contact and drinking unboiled water from a river, lake or dam. |
| Sporadic cases1990-1991([9](#_ENREF_9)) | UrbanSouth Australia | No significant risk factors identified (51 confirmed cases in analysis), but cases tended more than controls to have consumed only spring water, or only mains water; controls more likely to have consumed only rainwater than cases. |
| **Ecological study** | Sporadic 2001 ([10](#_ENREF_10)) | State-wide Queensland | Temperature and SEIFA were statistically associated with the probability of occurrence of cryptosporidiosis across Queensland |
| Sporadic 1996-2004 ([11](#_ENREF_11)) | UrbanQueensland | Infection associated with warmer, drier conditions. |
| Sporadic 1996-2004 ([12](#_ENREF_12)) | Urban Queensland | Cryptosporidiosis risk was best explained by an interaction between SEIFA and the proportion of residents with low educational attainment at an SLA level |
| Serological survey1998 ([13](#_ENREF_13)) | UrbanNew South Wales & Victoria | No serological evidence to suggest increased risk of infection in Sydney residents (Sydney drinking water contaminated with high levels of *Cryptosporidium)* when compared to Melbourne residents (Melbourne drinking water supply infrequent detections of Cryptosporidium). |
| Survey2010 ([14](#_ENREF_14)) | RuralNew South Wales | Prevalence in calves: 73.5% (144/196), identified *C. parvum, C. bovis* and *C. ryanae.*Prevalence in humans: 23.8% (15/63), identified *C. parvum* and *C. bovis.* |
| **Descriptive epidemiology: Case series** | Outbreak2005 ([15](#_ENREF_15)) | UrbanNew South Wales | 38% (11/29) of cases interviewed swam at the same indoor heated pool. Swimming pool water detected *Cryptosporidium* oocysts.  |
| Outbreak2005 ([16](#_ENREF_16)) | UrbanNew South Wales | 53% (89/178) reported swimming in a public pool in 12 days before onset of symptoms. Four of five pools tested were positive for *Cryptosporidium* oocysts. |
| Outbreak 2001-2002([17](#_ENREF_17), [18](#_ENREF_18)) | Urban Northern Territory | Cases reported attending childcare centres (36/57, 63%) and swimming pools (18/57, 32%), with some of the cases clustered in one childcare centre (7 cases) and one public pool (7 cases). |
| Outbreak2001 ([19](#_ENREF_19)) | State-wideTasmania | 81% (29/36) had attended the same agricultural show, and 75% (27/36) reported contact with animals in the animal nursery. |
| Surveillance data analysis1990-2000([20](#_ENREF_20)) | State-wide New South Wales | Average yearly notification rates were highest in the 0–4 year age group (43.4/100,000 population), followed by 5–9 years (14.8/100,000), geographical and seasonal variation in disease rates, including peak rates in summer.  |
| Outbreak2001([21](#_ENREF_21)) | UrbanNorthern Territory | Cases clustered in multiple child care centres, no source identified (43 cases investigated). |
| Outbreak 1999([22](#_ENREF_22)) | RuralNorthern Territory | Human to human transmission implicated in younger age groups |
| Outbreak1998([23](#_ENREF_23)) | UrbanVictoria | Seven clusters associated with public swimming pools (53 cases across these pools) and one cluster associated with a childcare centre (4 cases). |
| Surveillance data analysis2001-2009([24](#_ENREF_24)) | State-wideVictoria | Annual notification rates increased in two outbreak years (2006 and 2009) at 20/100 000, compared to 4-12/100 000 in other years; rates highest in children (40.7/100 000 for children less than 10 compared with 6.5/100 000 for those aged 10 years and older); peak of cases in warmer months (February-April); and two-thirds of cases reported form metropolitan regions. |
| Hospital data2007-2010 ([25](#_ENREF_25)) | UrbanNew South Wales | *Cryptosporidium* was identified as the causative agent in 7% (18/910) of people hospitalized for enteric protozoan infections in four Sydney hospitals.  |
| Prevalence survey1988\*([26](#_ENREF_26)) | Urban and remoteQueensland | 36 (4.6%) faecal samples from 780 patients from the Townsville and remote Palm Island region were positive for *Cryptosporidium*. |
| Clinical treatment assessment2007-2012([27](#_ENREF_27)) | Urban and remoteNorthern Territory | Nitazoxanide may be an effective treatment for cryptosporidiosis in Indigenous children (n=28). |
| Serological survey1989-1991([28](#_ENREF_28)) | UrbanVictoria | Indication of recent infection in 8% (29/369) of children and 5 % (5/79) of adults. |
| **Descriptive epidemiology:****Case report** | Case report2013\*([29](#_ENREF_29)) | Urban and travelWestern Australia | Mixed infection in one person with three species of *Cryptosporidium*; two wildlife associated (*C.* *meleagridis* and *C. mink* genotype) and one unknown species. Case reported interstate (Queensland) and overseas (Papua New Guinea) travel in incubation period, drank untreated water and swam in public swimming pools. (*16 Ng-Hublin 2013)* |
|  | Surveillance report 2007 ([30](#_ENREF_30)) | Urban South West,Western Australia | Clusters of reported disease associated with animal petting farms and domestic swimming pool. |
|  | Surveillance report2003([31](#_ENREF_31)) | Northern Territory | Quarterly surveillance report, July – September 2003, reported 1 case in the quarter, considerably below mean (14) for quarter in previous four years  |
| **Molecular analysis**  | Outbreak2009([32](#_ENREF_32)) | State-wideNew South Wales | Public swimming pool use contributing factor to outbreak. Anthroponotic *C*. *hominis* IbA10G2 subtype (449 confirmed cases) identified as the causative parasite.Spatiotemporal analysis identified outbreak confined to densely populated coastal cities of Sydney and Newcastle. |
| Outbreaks2007 ([33](#_ENREF_33)) | Urban (majority)South Australia & Western Australia | Western Australia (n=48): all isolates were *C. hominis* South Australia (n=24): 21 *C. hominis* isolates two C*. parvum* isolates and 1 was mixed with both (*C*. *parvum* and *C.* *hominis*) . |
| Sporadic2008-2011([34](#_ENREF_34)) | State-wideNew South Wales | Human infections (n=261) were mixed: with predominantly human and cattle subtypes (*C. hominis 66%, C. parvum 33%, C. andersoni 0.5%* and *C. fayeri 0.5%*.Cattle samples (n=205) identified as *C. hominis, C. parvum, C. bovis* and *C. ryanae.*  |
| Sporadic2008([35](#_ENREF_35)) | RuralNew South Wales | Cattle samples identified *C. parvum* (14) and *C. bovis* (1).Human infections were mixed with cattle and human subtypes (4 *C. parvum*, 3 *C. hominis*). |
| Sporadic2005-2008([36](#_ENREF_36)) | State-wideWestern Australia | Majority of illnesses due to *C. hominis*  at 78.6%, 19.8% due to *C. parvum* and 1.6% with *C. meleagridis* (of 248 tested). |
| Sporadic2006-2007([37](#_ENREF_37)) | UrbanNew South Wales | 58% of cases (19/33) identified as *C. parvum*.Molecular evidence that human infections were of anthroponotic and zoonotic transmission. |
| Sporadic 2009\*([38](#_ENREF_38)) | State-wideNew South Wales | Report on genotypes (subtypes) of a selection on human cases (n=69).Extensive variation was observed within the GP 60 locus for genotyping of human samples (*C. parvum* and *C. hominis*). |
| Sporadic2008\*([39](#_ENREF_39)) | State-wideSouth Australia | Report on typing of a selection of human cases. *C. hominis* (n= 38) and *C. parvum* (n= 24) were identified. Sequences and subtypes identified.  |
| Sporadic2014\*([40](#_ENREF_40)) | State-wideTasmania | Report on typing of a selection of human cases. *C. hominis* (n=66), *C. parvum* (n=15) and an unidentified genotype (n=1) from traveller to Indonesia identified. |
| Sporadic2008\*([41](#_ENREF_41)) | Australia | Report on speciation of a selection of human and cattle cases. 82% of human cases (41/50) infected with *C. hominis* and 18% with *C. parvum*. All cattle samples (n=7) were *C. parvum*. |
| Case report2009 ([42](#_ENREF_42)) | RuralNew South Wales | *C. fayeri* identified in human case with same subtype as previously identified in a kangaroo. |
| Case report2014\*([43](#_ENREF_43)) | UnspecifiedVictoria | Genetic analysis of human isolate. New *C. cuniculus* genotype identified in human, similar to genotype identified in a kangaroo. |

\*Indicates publication date as no study period dates provided in publication.

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