Introduction

Pig rearing plays a vital role in alleviating poverty and development of socio-economic condition in rural farming community in the developing Asian countries including India. The pig population of India is around 10.29 million as per 19th Livestock census, which constitutes about 2% of the livestock population of India [1]. The development of a modern swine industry in India is indeed a need in recent years to negotiate the ever-increasing demand of animal protein but still majority of the pig reapers in the country do not have the sufficient knowledge about the pig production and their diseases. Piglet diarrhoea in neonatal and weaned piglets due to *Escherichia coli* is an economically important disease, affecting pigs during the first 2 weeks and post-weaning and is characterised by sudden death or diarrhoea, dehydration and growth retardation in surviving piglets [2, 3, 4].

Weaning is one of the important causes for piglet diarrhoea, which causes psychological, nutritional, environmental and physiological stress on piglets [5]. The other risk factors associated with piglet diarrhoea are pathogenic *E. coli*, stress, management factors and excessive feed intake [6, 7].

The enterotoxigenic *E. coli* (ETEC) colonises on intestinal epithelium by F4, F5, F6, F18 and F41 fimbriae attaching to specific receptors on the villous enterocytes and results in diarrhoea, dehydration, growth retardation and sometimes sudden death in piglets [3, 8–10].

In order to reduce the incidence of piglet diarrhoea, piglets are often treated with antibiotics. The indiscriminate and non-judicial use of antibiotics in piggery is also one of the causes for the emergence of resistant *E. coli* [11, 12]. Extended-spectrum β-lactamas (ESBLs) are a cluster of enzymes that exist in *Enterobacteriaceae* family members, especially in *E. coli* that facilitates the resistance to most β-lactams approved in human and veterinary medicine. In the recent times, the quick emergence and spreading of ESBL-positive *E. coli* isolates in...
food animals have been reported and gained huge attention globally due to their possible transmission through the food chain [13]. However, there are only limited reports stating the prevalence, pathotyping, virulence factors and risk factors for the occurrence of \(E.\ coli\) in neonatal and weaned piglets in India.

In this study, we assessed the risk factors of piglet diarrhoea, antimicrobial resistance pattern, pathotypes of \(E.\ coli\) associated with pre- and post-weaning diarrhoea in piglets from organised farms in India.

**Materials and methods**

**Sampling design**

From August 2014 to July 2017, a total of 909 faecal samples were aseptically collected from 13 organised swine farms located in three regions (Northern, North-Eastern and Southern) covering eight states namely Assam, Meghalaya, Nagaland (North-Eastern states), Uttar Pradesh and Uttarakhand (Northern states) and Karnataka, Tamil Nadu and Kerala (Southern states) of India (Fig. 1). The selected states represent the major pig rearing pockets of North, North-East and Southern India [1]. The North-Eastern states have hilly terrain and subtropical climate, whereas Southern states have tropical climate. The Northern states lie mainly in the north temperate zone of the Earth, with cold winters, hot summers and moderate monsoons. A semi-structured peer-evaluated questionnaire (Supplementary file) was used for the collection of information about the demography of swine farm and husbandry practices, etc. The details of farm and number of samples collected were shown in Table 1. For each farm, the sample size calculations were carried out using Epitools software (http://epitools.ausvet.com.au/content.php?page=home) with 10–20% prevalence of piglet diarrhoea based on our preliminary study, 95% confidence interval and 80% power. Simple random sampling procedure with random number table was used in each farm to collect the faecal samples from pre- and post-weaning piglets, with and without diarrhoea, and were not treated with any antibiotics at least 2 weeks preceding the date of sample collection. A diarrhoeic case was considered when the piglet voided watery faecal material more than thrice a day, for at least 1 day. The diarrhoea was categorised based on frequency of defecation (3–5, >5 times/day), consistency of faeces (soft, watery, bloody, with or without mucus), and status of dehydration (severe, moderate, mild). The point prevalence of diarrhoea for each farm was calculated as the total number of piglets with diarrhoea at the time of sampling (numerator) divided by the total number of piglets available for sampling during that particular time (denominator). The faecal samples were collected aseptically using sterile swabs (HiMedia, India) and transported to the laboratory under cold chain.

**Isolation and phenotypic characterisation of \(E.\ coli\)**

The samples were suspended in 10 ml buffered peptone water and incubated for 6 h at 37 °C for pre-enrichment. Subsequent to enrichment in MacConkey broth for overnight at 37 °C, it was streaked on MacConkey agar added with cefotaxime (1 mg/l) and incubated at 37 °C for 18–24 h. From each plate, four lactose-fermenting colonies were picked up and streaked on eosin methylene blue agar (EMB) medium and incubated at 37 °C overnight for preliminary characterisation, and the isolates with metallic sheen were biochemically characterised.

**Antimicrobial susceptibility assay of \(E.\ coli\) isolates**

The reference strains (Accession No: KT853018, KT867018, KT867020 and KT867021) were collected from the repository maintained at Division of Epidemiology, ICAR-Indian Veterinary Research Institute, Izatnagar to serve as control positive strains. The isolates were tested for antibiotic susceptibility pattern with amoxicillin (AMX, 10 µg), aztreonam (ATM, 30 µg), chloramphenicol (C, 30 µg), ceftriaxone (CRO, 30 µg), ceftizoxime (CPD, 10 µg), cefazidime (CAZ, 30 µg), cefazidime + clavulanic acid (CAZ-CLA, 30/10 µg), cefotaxime (CTX, 30 µg), cefepime (FEP, 30 µg), cefixime (CFM, 5 µg), cefotaxin (FOX, 30 µg), cefotaxime + clavulanic acid (CTX-CLA, 30/10 µg), cefoperazone (CFP, 75 µg), tetracycline (TE, 30 µg), nitrofurantoin (F/M, 300 µg), gentamicin (GM, 10 µg), cotrimoxazole (COT, 25 µg), ciprofloxacin (CIP, 5 µg) and norfloxacin (NOR,10 µg) by using disk diffusion test [14]. The Clinical and Laboratory Standards Institute (CLSI), 2014 breakpoints were used for the interpretation of susceptibility pattern [15]. The \(E.\ coli\) isolates were screened by combination disk method for phenotypic confirmation of ESBL production [14]. Multidrug-resistant (MDR) strains (i.e. strains showing resistance to at least two groups of antibiotics) were identified. Multiple antibiotic resistance (MAR) index was calculated using the formula as total number of antibiotics to which the organism was resistant divided by the total number of antibiotics to which the organism was tested [16].

**PCR targeting antimicrobial resistance and virulence genes of \(E.\ coli\)**

Genomic DNA was extracted from \(E.\ coli\) isolates by QIAamp DNA Mini Kit (Qiagen, Hilden, Germany) and PCR was performed for β-lactamase [17], sulphomamide resistance [18], plasmid-mediated quinolone resistance determinants [19], tetra-cycline resistance genes [20] and virulence markers for Shiga toxin [21]. The PCR was carried out in 25 μl reaction volume containing 2 μl of DNA template, 10 pmol/μl of each primer (1 μl), 2x DreamTaq PCR master mix (Thermo Fisher Scientific Baltics UAB, Lithuania, 12.5 μl) and nuclease-free water to make the volume of 25 μl. The PCR primers and cycle conditions were given in Supplementary Table S2. The amplified PCR products were resolved by electrophoresis on 1.5% agarose gel containing ethidium bromide (0.5 μg/l) (Molecular Bio Grade; Merck, Mumbai, India) with 100 bp ladder (Thermo Fisher Scientific®). The gels were run at 100 V for 1.5 h in 1X TBE buffer and documented by the gel documentation system (UVP, UK).

**Statistical analysis**

Information from the questionnaire were digitised into a Microsoft excel spreadsheet (Microsoft Corporation) and piglet diarrhoea results were coded as negative = 0 and positive = 1. The \(χ^2\) test or Fisher’s exact test with Yates correction was used to test the associations between the predictor variables and the outcome variable. Fisher’s exact test with Yates correction was used when expected cell frequencies were <5. In piglet diarrhoea model, the analysis of multiple predictors of pre- and post-wean diarrhoea was performed by multivariable logistic regression analysis using stepwise forward method considering only the factors.
with $P \leq 0.2$ in univariable analysis. In the final multivariable logistic regression model, only the factors significant at $P \leq 0.05$ level for Wald test were retained. The model fit was assessed by Hosmer and Lemeshow (HL) test. A mixed-effect model was created once the single-level model had been finalised in order to assess any impact of the region as a random effect [22].

**Results**

This study reveals the point prevalence of *E. coli*-associated piglet diarrhoea on 13 pig farms from different regions of India along with the risk factor analysis, pathotyping and antimicrobial resistance in pre- and post-weaning piglets. The information collected through questionnaire revealed that all farms were negative for gastrointestinal helminths and coccidian oocysts. Farms practised routine screening for gastrointestinal helminths and regular deworming. The farms were classified based on the information collected and presented in Supplementary Table S1. Based on the area or size of the landholding, the farms were classified as small, medium and large (<100 acres – small; 100–300 acres – medium; >300 acres – large). Based on the number of pigs reared, the farms were classified as small (<200), medium (200–500) and large (>500). Majority of the farms reared pure and cross breeds of Landrace, Large White Yorkshire and Duroc. Few farms also reared native and cross breeds. Except one pig farm (Guwahati, Assam), other farms reared farm animals such as cattle, sheep and goat. Many of the farms provided heaters or coolers for temperature control. Seven farms used commercial feed and six farms used own mill ground feed. All farms used β-lactam and cephalosporin antimicrobials for treating sick animals. In general, all the farms had cement floor with regular disinfectant cleaning and ventilated animal shed. In common, weaning was practiced between 35 and 45 days. No outbreak of any contagious disease was recorded over the last 12 months. There was no dedicated handler to take care of diseased and healthy animals in all the farms.

The point prevalence of piglet diarrhoea ranged from 3.57% to 14.29%, was lowest (3.57%) at pig farm from Jharnapani, Nagaland (North-East) whereas highest (14.29%) from Hassan, Karnataka (South). There was no significant difference in point prevalence of piglet diarrhoea ($P = 0.46$) across the three regions.

The data analysis of 13 farms showed that the risk factors for diarrhoea were weaning status, season, altitude, ventilation, use of heater/cooler for temperature control in the sheds, feed type, water source, and use of disinfectant, (Table 2). The crude, strata-specific and adjusted odds ratio revealed that there was no confounding effect of sex and weaning status, while effect modification was noticed for sex. The post-weaning piglets were 3.7 times more prone to diarrhoea than pre-wean. Compared with monsoon, in winter piglets had 2.8 times higher risk of diarrhoea. The piglets reared in plain or low altitude had 1.8 times more risk for diarrhoea than piglets in hilly or high altitude. Use of shallow well water, commercial feed, poor ventilation and absence of temperature control mechanism were positively

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**Fig. 1.** Sample collection locations for piglet diarrhoea ($N = 13$).
| Region                  | Location | Longitude | Latitude | No. of piglets available for sampling | No. of samples collected for isolation of E. coli | Sex | Weaning | Health status |
|-------------------------|----------|-----------|----------|--------------------------------------|-----------------------------------------------|-----|---------|---------------|
|                         |          |           |          | Pre-wean | Post-wean | M | F | Pre-wean | Post-wean | Non-diarrhoeic | Diarrhoeic |
| Southern India (n = 405) | Hassan   | 76.1279   | 13.0210  | 60       | 45       | 70 |    | 41       | 29       | 58            | 12        | 55 | 15 |
|                         | Mannuthy | 76.2589   | 10.5306  | 210      | 95       | 171 |    | 80       | 91       | 119           | 52        | 152 | 19 |
|                         | Pookode  | 76.0202   | 11.5412  | 121      | 45       | 88 |    | 42       | 46       | 71            | 17        | 78 | 10 |
|                         | Chennai farm1 | 80.2310 | 13.1478  | 92       | 31       | 53 |    | 31       | 22       | 42            | 11        | 42 | 11 |
|                         | Chennai farm2 | 80.04528 | 12.8231 | 58       | 18       | 23 |    | 14       | 9        | 18            | 5         | 19 | 4  |
| Northern India (n = 310) | Bareilly | 79.4320   | 28.3930  | 130      | 76       | 188 |    | 99       | 89       | 141           | 47        | 167 | 21 |
|                         | Pantnagar | 79.4760   | 29.0270  | 25       | 16       | 10 |    | 4        | 6        | 8             | 2         | 8  | 2  |
|                         | Sitapur  | 81.0550   | 27.3970  | 128      | 45       | 71 |    | 33       | 38       | 52            | 19        | 61 | 10 |
|                         | Aligarh  | 78.0880   | 27.8974  | 95       | 26       | 41 |    | 22       | 19       | 30            | 11        | 32 | 9  |
| North Eastern India (n = 194) | Guwahati | 91.6131   | 26.1017  | 95       | 35       | 53 |    | 24       | 29       | 43            | 10        | 43 | 10 |
|                         | Jharnapani | 93.8388 | 25.7585  | 70       | 42       | 48 |    | 26       | 22       | 27            | 21        | 44 | 4  |
|                         | Barapani | 91.9223   | 25.6906  | 115      | 36       | 62 |    | 30       | 32       | 46            | 16        | 48 | 14 |
|                         | Kohima   | 94.1139   | 25.6585  | 40       | 24       | 31 |    | 15       | 16       | 22            | 9         | 25 | 6  |
| Total                   |          |           |          | 1239     | 534      | 909 |    | 461      | 448      | 677           | 232       | 774 | 135 |

M, male; F, female
associated with piglet diarrhoea, while regular use of disinfectants reduced the piglet diarrhoeal cases. Logistic regression analysis of the factors having $P \leq 0.2$ showed a predictive model with weaning and water source as significant risk factors ($\chi^2$ test: $\chi^2 = 9.4; df = 8; P = 0.31; -2 \log$ likelihood = 660.703, Nagelkerke $R^2 = 0.183$) (Table 3). The inclusion of region as a random effect in the final model resulted in a minor (<10%) alteration to the coefficients associated with each of the variables retained within the model and all variables remained statistically significant.

In North-Eastern region, the only risk factor associated with piglet diarrhoea was weaning, while the Southern and Northern regions showed weaning, presence of other animals, altitude of the farm, use of disinfectant, ventilation, water source, presence of heater or cooler, type of feed and season as risk factors (Supplementary Table S3).

On bacterial isolation, 531 ESBL-E. coli were isolated from 909 samples on cefotaxime-added MacConkey plates. The isolation rate of E. coli was less since they were selected against cefotaxime. Of the 774 non-diarrhoeic and 135 diarrhoeic faecal samples, 438 and 93 E. coli, respectively, were isolated. The isolation rate of E. coli from diarrhoeic samples (17.51%) was significantly higher than non-diarrhoeic samples (11.11%, $P \leq 0.01$). The E. coli (n

### Table 2. Univariable analysis of statistically significant risk factors associated with piglet diarrhoea

| Variables          | Diarrhoeic | Non-diarrhoeic | $P$ value | OR (95% CI) |
|--------------------|------------|----------------|-----------|------------|
| Weaning            |            |                |           |            |
| Post-wean          | 67         | 67             | 0.00**    | 3.73(2.54–5.44) |
| Pre-wean           | 164        | 611            |           | 1 (Ref)    |
| Season             |            |                |           |            |
| Winter             | 51         | 147            | 0.00**    | 2.80 (1.83–4.26) |
| Summer             | 27         | 177            |           | 1.23 (0.75–2.0) |
| Monsoon            | 56         | 451            |           | 1 (Ref)    |
| Altitude           |            |                |           |            |
| Plain              | 254        | 521            | 0.00**    | 1.85 (1.19–2.86) |
| Bore well          | 28         | 106            |           | 1 (Ref)    |
| Shallow well       | 45         | 167            | 0.00**    | 1.84(1.24–2.74) |
| Water source       |            |                |           |            |
| Shallow well       | 22         | 49             | 0.00**    | 3.64 (2.0–6.6) |
| Bore well          | 2         | 86             |           | 0.19(0.045–0.79) |
| Both bore and shallow well | 67 | 291           | 1.87(1.24–2.83) |
| Ventilation        |            |                |           |            |
| Fair               | 45         | 167            | 0.00**    | 1.84(1.24–2.74) |
| Good               | 89         | 608            |           | 1 (Ref)    |
| Water source       |            |                |           |            |
| Shallow well       | 22         | 49             | 0.00**    | 3.64 (2.0–6.6) |
| Spring             | 2          | 86             |           | 0.19(0.045–0.79) |
| Bore and shallow well | 67   | 291           | 1.87(1.24–2.83) |
| Bore well          | 43         | 349            |           | 1 (Ref)    |
| Feed               |            |                |           |            |
| Commercial         | 473        | 302            | 0.00**    | 1.93 (1.34–2.79) |
| Own mill           | 60         | 74             |           | 1 (Ref)    |
| Presence of heater/cooler |      |                |           |            |
| No                 | 76         | 312            | 0.00**    | 1.95 (1.34–2.82) |
| Yes                | 58         | 463            |           | 1 (Ref)    |
| Disinfectant       |            |                |           |            |
| Weekly             | 56         | 242            | 0.00**    | 2.30 (1.5–3.52) |
| Occasional         | 35         | 106            |           | 3.28 (2.0–5.38) |
| Daily              | 43         | 427            |           | 1 (Ref)    |

Ref, reference category.

**$P \leq 0.01$.**

### Table 3. Risk factors associated with piglet diarrhoea in multivariable logistic regression model

| Factors                       | Coefficient ($\beta$) | s.e. | $P$ value | Exp ($\beta$)/odds ratio | Lower 95% CI | Upper 95% CI |
|-------------------------------|-----------------------|------|-----------|--------------------------|--------------|--------------|
| Weaning                       | Post-wean             | 0    | –         | –                        | –            | –            |
|                               | Pre-wean              | -1.517 | 0.222    | 0.00**                   | 0.219        | 0.142        | 0.339        |
| Water source                  | Spring                | 0    | –         | –                        | –            | –            |
|                               | Bore well             | 2.294 | 1.357    | 0.09                     | 9.915        | 0.694        | 141.68       |
|                               | Shallow well          | 4.418 | 1.451    | 0.00**                   | 82.89        | 4.824        | 1424.54      |
|                               | Both bore and shallow well | 3.301 | 1.398    | 0.00**                   | 27.135       | 1.750        | 420.625      |
|                               | Constant              | -3.157 | 1.066 | 0.00** | – | – | – |

Ref, reference category.

(Hosmer and Lemeshow Test: $\chi^2 = 9.4; df = 8; P = 0.31; -2 \log$ likelihood = 660.70, Nagelkerke $R^2 = 0.183$).

**$P \leq 0.01$.**
Discussion

Pig rearing plays a vital role in improving the livelihood of poor and marginal farmers of India. Production with minimum inputs and maximum output is the basis and requirement of the poor farmers. However, piglet diarrhea is of great economic challenge to intensive pig farming and cause substantial economic losses [23]. Pre- and post-weaning piglet diarrhea is a multi-factorial disease primarily attributed to E. coli [5, 23, 24]. It is commonly associated with the proliferation of β-haemolytic strains of ETEC in the small intestine [3] and frequently occurs within 2 weeks after weaning due to implications between the piglet, sow, environment and farm practices [25]. It also results into substantial economic losses in many swine herds due to 20–30% mortality in weaned piglets during acute outbreaks [2].

In the present study, point prevalence of piglet diarrhea varied from 3.57% to 14.29%, across the locations surveyed. The region-wise prevalence of piglet diarrhea was almost similar across the regions which indicates that piglet diarrhea is one of the commonest problems throughout India. The occurrence of diarrhea in post-weaned piglets was significantly higher than pre-weaned piglets. It may be due to the weaning stress, change in the physiological status and nutrition of the piglets during this period [5, 6]. The observations were in corroboration with

Table 4. Association of virulence factors with health and weaning status of piglets

| Piglet status | Diarrhea | Non-diarrhea |
|---------------|----------|--------------|
| Pre-wean | 79 | 1 (Ref) |
| Post-wean | 96 | 1 (Ref) |
| Health status | | |
| Diarrhoeic | 20.4 | 0.001*** | 7.5 | 2.29 (1.43–3.43) |
| Non-diarrhoeic | 1 (Ref) | 1 (Ref) |

| Ref | Reference category | P-value | OR (95%CI) |
|-----|--------------------|----------|------------|
| Pre-wean | 1 (Ref) | 1 (Ref) |
| Post-wean | 1 (Ref) | 1 (Ref) |

*P < 0.05; **P < 0.001.

Ref, reference category.
Australian pig farms finding published recently [25]. Reports also state that this might be associated with the weaning stress, dietary changes and lack of antibodies due to withdrawal of sow’s milk, which makes the piglets susceptible to commensal E. coli [3, 26]. The rate of isolation of E. coli from post-weaned diarrhoeic faecal samples was significantly higher than pre-weaned diarrhoeic faecal samples; the findings are in corroboration with Dutta et al. [27] from North-Eastern region. The higher rate of isolation of E. coli in post-weaning piglets might be due to stress, decrease in maternal antibody and lack of self-immunity [28]. In this study, a higher prevalence of E. coli in diarrhoeic piglets was observed (68.87%, 93/135) than non-diarrhoeic piglets (56.88%, 438/774). In piglets, diarrhoea is mainly associated with E. coli [4, 10] in pre- and post-weaning stages [29].

In the present study, the risk factors associated with piglet diarrhoea were weaning, season, ventilation, altitude, water source, feed, presence of heater/cooler and use of disinfectants. Poor ventilation, harsh climatic conditions, absence of temperature control devices in the piglet sheds cause stress and may predispose the piglets to diarrhoea. The pig farms using shallow well have more diarrhoea cases. Since shallow well has more chances for faecal contamination compared with deep bore wells [30]. Van Breda et al. [31] reported that bedding, temperature control in piglet pen and recent disease events were the risk factors associated with piglet diarrhoea on Australian pig farms. Weaning is a stressful phase in piglets, after weaning feed intake get reduced initially and the piglets may develop anorexia of variable duration and the extent varies between farms, depending on livestock management and the nature of the feed [32]. Hence investigating management practices to minimise the risk factors of pathogenic E. coli may help to cost reduction in the veterinary and medical care.

In the study, the occurrence of 64% (345/531) of ESBL-producing E. coli isolates might be associated with the selection of E. coli in cefotaxime-added media. The common use of β-lactam and cephalosporin antibiotics on the farms investigated may also contribute for ESBL-producing E. coli. In another study, the ESBL-producing E. coli was detected in 34 (56.7%) of 60 pigs, and 20.0% (eight of 40) of the pig farm worker’s rectal swabs in China [33]. Our observations for isolation of higher proportion of ESBL-positive E. coli among piglets might be due to the fact that in earlier studies, selective β-lactam antibiotic(s) were not used in the isolation procedures. From India, ESBL-producing E. coli were reported in healthy piglets under organised and backyard piggery [34]. The carbapenem-resistant E. coli were reported in piglets of India [11]. Mandakini et al. [35] reported ESBL-producing Shiga toxigenic E. coli in piglet diarrhoea. The E. coli isolated from diarrhoeic piglets were comparatively more ESBL-positive than non-diarrhoeic piglets. Our results were in harmonious with the findings of Xu et al. [4], they reported high occurrence of ESBLs in sick animals. In the present study, virulent E. coli had lesser resistance for co-trimoxazole, nitrofurantoin, tetracycline and chloramphenicol compared with other antibiotics. However, earlier studies reported higher level of resistance to gentamicin, neomycin and sulphonamides among various virulent isolates of E. coli from diarrhoeic and non-diarrhoeic piglets [36]. This discrepancy might be associated with the overall decline in the use of these antibiotics in India since 2000 [37]. The antibiotic resistance pattern and MAR indices of our study were in concurrence with the earlier findings [4, 38]. Akwar et al. [39] reported MDR E. coli in weaner and finisher pigs.

In this study, out of the 531 E. coli, 174 isolates harboured any one of the virulence genes screened and the E. coli isolates from diarrhoeic piglets harbourd significantly higher number of virulence genes in E. coli isolates than non-diarrhoeic piglets. The post-wean piglets harboured significantly higher number of virulence genes positive for E. coli compared with pre-wean piglets which was in corroboration with Van Breda et al. [31]. The distribution of virulence genes did not show any significant difference across the regions, this may be due to the ubiquitous nature of the E. coli in the environment. Pruthvishree et al. [11] reported carbapenem-resistant isolates harbouring Stx1, Stx2, eaeA and hlyA virulence genes. Furthermore, a significant statistical association between antimicrobial resistance and presence of virulence genes (P ≤ 0.05) was seen. Association of antimicrobial resistance and virulence genes of E. coli from swine in Ontario, Canada has been reported previously [40]. Toledo et al. [41] hypothesised that the pathogenic E. coli presence in intestinal tract of healthy piglets may cause the disease due to the consequence of immune response induced by stress, temperature changes and diet. Besides, continuous shedding of pathogenic E. coli into the environment through faeces might be responsible for the maintenance of a stable bacterial population, which contributes to the re-occurrence of disease in herds as well as potential public health threat due to possible transfer of ESBL organism to humans [42].

Even though this study describes the potential risk factors associated with piglet diarrhoea across India, it has certain limitations such as difference in agro climatic region, local management practices, feed ingredients used for feeding and viral agents associated with diarrhoea which were not taken in to consideration in this study.

Conclusion

Piglet diarrhoea is one of the major causes of economic loss in pig farming. Tackling the risk factors associated with piglet diarrhoea may help in reducing the incidence. High ESBL-positive E. coli in faecal samples of diarrhoeic piglets with virulence genes warrants the establishment of antibiotics resistance surveillance programmes along with intensive research to develop alternatives to antimicrobials to ensure the high-level food safety standards to improve human and animal health.

Supplementary material. The supplementary material for this article can be found at https://doi.org/10.1017/S0950268819000591.

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References

1. Basic Animal Husbandry Survey (BAHS) (2015) Available at https://data.gov.in/catalog/basic-animal-husbandry-survey-2015 (Accessed July 2018).
2. Amezua R et al. (2002) Presentation of postweaning Escherichia coli diarrhoea in southern Ontario, prevalence of hemolytic E. coli serogroups involved, and their antimicrobial resistance patterns. Canadian Journal of Veterinary Research 66, 73.
3. Fairbrother JM, Nadeau E and Gyles CL (2005) Escherichia coli in post-weaning diarrhoea in pigs: an update on bacterial types, pathogenesis, and prevention strategies. Animal Health Research Reviews 6, 17–39.
4. Xu G et al. (2015) Prevalence and characteristics of extended-spectrum beta-lactamase genes in Escherichia coli isolated from piglets with post-weaning diarrhoea in Heilongjiang province, China. Frontiers in Microbiology 6, 1103.
5. Hampson D (1994) Postweaning Escherichia coli Diarrhoea in Pigs. Wallingford, UK: CAB International. pp. 171–191.
6. Laine TM et al. (2008) Risk factors for post-weaning diarrhoea on piglet producing farms in Finland. Acta Veterinaria Scandinavica 50, 21.
