Abstract

Background: Clostridium perfringens is a key pathogen in poultry-associated necrotic enteritis (NE). To date there are limited Whole Genome Sequencing based studies describing broiler-associated C. perfringens in healthy and diseased birds. Moreover, changes in the caecal microbiome during NE is currently not well characterised. Thus, the aim of this present study was to investigate C. perfringens virulence factors linked to health and diseased chickens, including identifying putative caecal microbiota signatures associated with NE.

Results: We analysed 88 broiler chicken C. perfringens genomes (representing 66 publicly available genomes and 22 newly sequenced genomes) using different phylogenomics approaches and identified a potential hypervirulent and globally-distributed clone spanning 20-year time-frame (1993–2013). These isolates harbored a greater number of virulence genes (including toxin and collagen adhesin genes) when compared to other isolates. Further genomic analysis indicated exclusive and overabundant presence of important NE-linked toxin genes including netB and tpeL in NE-associated broiler isolates. Secondary virulence genes including pfoA, cpb2, and collagen adhesin genes cna, cnaA and cnaD were also enriched in the NE-linked C. perfringens genomes. Moreover, an environmental isolate obtained from farm animal feeds was found to encode netB, suggesting potential reservoirs of NetB-positive C. perfringens strains (toxinotype G). We also analysed caecal samples from a small sub-set of 11 diseased and healthy broilers for exploratory microbiome investigation using 16S rRNA amplicon sequencing, which indicated a significant and positive correlation in genus Clostridium within the wider microbiota of those broilers diagnosed with NE, alongside reductions in beneficial microbiota members.

Conclusions: These data indicate a positive association of virulence genes including netB, pfoA, cpb2, tpeL and cna variants linked to NE-linked isolates. Potential global dissemination of specific hypervirulent lineage, coupled with distinctive microbiome profiles, highlights the need for further investigations, which will require a large worldwide sample collection from healthy and NE-associated birds.

Keywords: Clostridium perfringens, Toxin, Phylogenomics, Necrotic enteritis, Poultry, Caecal microbiome, 16S rRNA analysis
**Background**

Broiler chickens are solely bred for meat production, and represent a key global livestock asset; with an estimated annual production of 50 billion birds worldwide [1]. As broilers reach slaughter weight at a young age (4–7 weeks) they are susceptible to several welfare and infection issues. Importantly, poultry Necrotic Enteritis (NE), an inflammatory gut infection in chickens, is responsible for a loss of US$6 billion per annum in the poultry industry, with *C. perfringens* reported to be the main causative agent [2–5].

NE-associated pathologies are mainly characterised by gaseous lesions and mucosa necrosis in gas-filled distended small intestines [6]. Proposed key *C. perfringens*-associated factors linked to NE include α-toxin, and more recently NetB and TpeL (both pore-forming toxins) [7]. Other aetiological factors that have been shown to increase risk of NE include high-protein diets and environmental stressors, which may alter gut-associated microbial communities (i.e. the microbiota), host immunity, and co-infection with the poultry parasite *Eimeria* [8–10]. In addition, sub-clinical NE (SNE), which is a mild form of NE, is represented by poor growth and small intestinal ulcerative lesions and has also been associated with *C. perfringens* colonisation [7, 11].

*C. perfringens*, a ultra-rapid-growing anaerobic Gram positive pathogen, is known to harbour an arsenal of >20 toxins and has been associated with a wide range of gut diseases in animals, including poultry NE [5]. Specifically, toxin NetB is considered to be an essential *C. perfringens* virulence factor in NE pathogenesis, as determined in animal studies [2]. Expression of this pore-forming toxin has previously been reported to be higher (92%) in NE chicken *C. perfringens* isolates, as compared to healthy chickens (29%), thus supporting its role in disease progression [12]. This toxin is known to be encoded exclusively on conjugative plasmids, indicating horizontal gene transfer may play a role in dissemination to NetB-negative strains [13]. Collagen adhesin (encoded by gene *cna* and its variants) is another candidate disease determinant, which has been associated with chicken NE isolates in a recent bacterial genomic study [14].

The caecum represents the primary site for *C. perfringens* colonisation, which also contains the highest density of the chicken gut microbiota, therefore NE-induced alterations of this GI site are likely to reflect disease changes [15]. Moreover, the chicken caecal microbiome is known to play a protective role in pathogen resistance to other enteric pathogens, including *Campylobacter jejuni*, and as such intestinal microbiota disruption may impact development of *C. perfringens*-associated NE in broiler chickens, although direct biological impact is yet to be confirmed [9, 16, 17].

At present there are only two smaller scale Whole Genome Sequencing (WGS) based studies on broiler-associated *C. perfringens* [14, 18]. Thus, to further our understanding on *C. perfringens* dissemination and virulence profiles in the context of broiler-NE, we performed phylogenetics and in-depth comparative genomics on 88 chicken-associated *C. perfringens* isolates, (strains from public genome databases, alongside 22 newly isolated and sequenced strains). Moreover, it is unclear if and how the chicken caecal microbiome changes during NE development, therefore a small-scale microbiota profiling study was carried out to understand if there are any disease-specific disturbances induced after *C. perfringens* infection.

**Results**

**Phylogenetic analysis reveals a potentially important intercontinental lineage**

We investigated 88 broiler-associated *C. perfringens* genomes (including 62 from NE-linked birds, 20 from healthy birds and 6 environmental isolates from broiler farms), spanning a 23-year period from 1993 to 2016 from 8 countries across European, Australasian and North American continents (Additional file 1: Table S1). Twenty-two *C. perfringens* genomes were sequenced and assembled specific to this study and the remaining isolates were publicly available. Broiler isolates Del1 and LLY_N11 were publicly available complete genomes sequenced using long-read sequencing and were included in analyses [4, 19]. A Maximum Likelihood (ML) phylogenetic tree was assembled using 88 isolates from 20,194 SNPs identified from the alignment of 1810 core genes in analyses [4, 19]. A Maximum Likelihood (ML) phylogenetic tree was assembled using 88 isolates from 20,194 SNPs identified from the alignment of 1810 core genes (Fig. 1). Clustering was assigned to define population structure via hierBAPS analysis; with the 88 isolates clustering into 5 major lineages.

The core gene alignment of 20,194 SNPs was subjected to SNP distance analysis. Phylogenetic clustering and pairwise SNP analysis suggested several sub-lineages that comprised multiple highly-similar strains including lineages IVa, IVb, Va, Vc, Vd and Vf (Fig. 1). Importantly, lineage Vf that consisted of 14 broiler isolates obtained from 4 different countries namely Australia, Canada, Denmark and USA (in between 1993 and 2013) displayed evident clonality; 65.0 ± 52.8 SNPs between strains, which was in contrast to the closest sub-lineage Ve, with pairwise SNP distance of 1474.0 ± 162.6 SNPs (P < 0.0001; Fig. 2a–c). Average Nucleotide Identity (ANI) analysis also supported the apparent clonality in sub-lineage Vf (n = 14), with isolates demonstrating a pair-wise mean genome-wide ANI of 99.81 ± 0.08%, compared to closest sub-lineage pairwise ANI of 98.77 ± 1.04% (P < 0.0001; Fig. 2d). Delving further into this interesting cluster of multi-continental isolates, sub-lineage Vf3 displayed the highest genetic similarity of
Fig. 1 Mid-point rooted maximum-likelihood tree based on 20,194 SNPs in 1810 core genes labelled by hierarchical Bayesian clusters (1–5), health states of hosts, country of isolates, poultry host species, sample origin and year of isolation. Scale bar, ~ 2000 SNPs.
pairwise SNP distance of 11.4 ± 6.7 SNPs; 7 isolates originated from Denmark, USA and Canada, spanning a period of 16 years (Fig. 2a). Sub-lineage Vf2 displayed a similar trend of low overall pairwise SNP distance of 19.1 ± 10.6 SNPs with these 6 isolates sourced from Australia, USA and Denmark. Australian isolate NAG-NE31 was shown to be distant at 171 SNPs (Fig. 2b). This analysis suggests a potential widespread reservoir of this C. perfringens lineage given they are genetically highly-similar, and previous studies have indicated this species has a highly divergent genome [20–22].

Lineages IVa and IVb exclusively comprised newly-sequenced C. perfringens isolates from English farms. Lineage IVb encompassed 4 isolates from 4 individual birds (J36, I060, G049 and I058), which were identical at strain level (0 SNPs), revealing potential inter-transmission of C. perfringens strains among poultry farms in the same region. Interestingly, in lineage Va,
Danish isolate C48 was shown to be highly similar to Australian isolates EHE-NE18 and EUR-NE15 at 7 SNPs difference, with all these isolates obtained in the same year 2002 (Additional file 2: Figure S2). Isolates in lineages Vd and Vc exhibited geographical similarity by country at minimal SNP counts.

**Virulence association analysis supports a hypervirulent *C. perfringens* lineage**

*C. perfringens* encodes an arsenal of virulence-related genes including toxin, antimicrobial resistance (AMR), and collagen adhesin genes, which are linked with gut colonisation and pathogenesis [5]. Virulence plasmids are known to encode for NE-associated toxin genes *netB* and *tpeL*. We therefore carried out a comprehensive search on all the known virulence genes, AMR determinants and virulence plasmids encoded in each *C. perfringens* genome using both assembly-based approaches (as most public genomes were only available in assemblies) and read-mapping methods for plasmid searches (if sequencing reads available) (Fig. 3).

Initial analysis indicated that isolates in intercontinental lineage Vf consistently encoded more virulence genes, including *netB* and *tpeL*, thus a further comparative virulence gene analysis was performed (Additional file 2: Figure S3). Isolates within lineage Vf

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**Fig. 3** Mid-point rooted maximum-likelihood tree based on 20,194 SNPs from 1810 core genes aligned with key virulence and resistance determinants, and predicted plasmids present in each genome for 88 broiler-associated *C. perfringens*. Coloured cells indicate predicted presence of genes/plasmids. AMR: Anti-Microbial Resistance. Scale bar, ~ 2000 SNPs
encoded significantly more toxin genes (9.5 ± 0.6 toxin genes vs 8.2 ± 1.3 toxin genes; P < 0.0001) and collagen adhesin genes (2.4 ± 0.6 vs 1.4 ± 1.0; P = 0.0005) when compared to the remaining isolates, suggesting this is potentially a ‘hypervirulent’ sub-lineage. This was supported by further analysis comparing virulence gene counts between sub-lineage Vf, and remaining NE-linked isolates (Additional file 2: Figure S3). Vf isolates encoded more toxin (9.5 ± 0.6 vs 8.2 ± 1.1) and collagen adhesin genes (2.4 ± 0.6 vs 1.7 ± 0.9), when compared to the remaining NE-associated C. perfringens strains.

Comparative analysis was also performed to define differences between NE-linked (n = 62) isolates and healthy-broiler isolates (n = 20; Additional file 2: Figure S4). Both toxin genes (8.8 ± 1.1 vs 7.2 ± 1.0) and collagen adhesin genes (1.9 ± 0.9 vs 0.8 ± 1.0) were significantly elevated in NE-related isolates (P < 0.0001). Considering overall virulence (toxin + adhesin genes), NE-linked isolates encoded significantly more virulence genes (10.8 ± 1.7) than healthy-broiler isolates (8.0 ± 1.6; P < 0.0001; Fig. 4). Notably, isolates in lineage Vf encode the most virulence genes (12.0 ± 1.0 genes).

To explore potential enrichment and correlation of NE-related toxin genes including netB, tpeL, and other secondary toxin genes pfoA and cpb2, an association statistical analysis (Chi-square test) was performed (Additional file 2: Figure S5). Toxin gene netB was exclusively encoded in NE-linked isolates (31/62; 50%) compared to healthy-broiler isolates (0/20; P < 0.0001). Moreover, tpeL (12/50; 19.3%; P = 0.0332), pfoA (59/62; 95.1%; P = 0.0017) and cpb2 (49/62; 79.0%; P < 0.0001) were all shown to be enriched in NE-linked isolates. Most isolates in lineage Vf encoded these 4 toxin genes including netB (12/14; 85.7%), tpeL (10/14; 71.4%), pfoA (14/14; 100%) and cpb2 (14/14; 100%), supporting the hypothesis of a hypervirulent clone.

Genome-wide association analysis highlighted additional factors that may correlate with widespread nature of lineage Vf isolates. Aside from the associations of toxin genes tpeL (sensitivity: 64.2%; specificity: 97.3%; 9/14 isolates) and netB (sensitivity: 85.7%; specificity: 72.9%; 12/14 isolates) as described above, collagen adhesin cnaA (sensitivity: 100%; specificity: 85.1%; 14/14 isolates) and a pilin-associated gene (group_5443; sensitivity: 100%; specificity: 86.5%; all 14/14 isolates) were specifically associated with this lineage of isolates (Additional file 1: Table S10). When we further compared the representative pilin-associated gene group_5443 using NCBI non-redundant (nr) nucleotide database via BLASTn, this gene was detected in both reference chicken isolates EHE-NE18 and Del1 complete genomes at 100% identity, which was suggested as a hypothetical protein in the annotated file (Additional file 1: Table S10). Other lineage Vf-associated genes including ABC transporter-related genes (n = 4; group_1636, group_3194, group_2785, group_3195; sensitivity: 100%; specificity: 82.4%) and phage-associated genes including capsid protein (group_1646), phage-regulatory protein (group_6371) and endolysin (group_4126) were also identified.

Adhesin is an important virulence factor in broiler-linked NE [14, 18], and in this study we found that adhesin genes (at least one variant) were overall enriched (P < 0.0001) in NE-linked isolates (58/62; 93.5%) vs healthy isolates (9/20; 45%). Among all related adhesin variants, cna, cnaA and cnaD genes were significantly enriched in NE-associated C. perfringens isolates (P < 0.05), linking these genes to NE-disease development (Additional file 2: Figure S6). Importantly, environmental isolates encoded comparable virulence gene profiles, suggesting potential reservoir including soil and feeds. Indeed, environmental isolate C. perfringens FR063 was found to encode the NE-linked netB.

Previous studies [20, 23] have indicated that acquired AMR genes are not widespread, and a total of 7 AMR genes were detected across 88 isolates (Fig. 3). Tetracycline resistance genes tetA(P) and tetB(P) were encoded in the greatest number of genomes (44 and 32 isolates respectively), with erythromycin-resistance genes ermB and ermQ encoded in 2 and 4 isolates respectively. Macrolide-resistant efflux-pump gene mefA was detected in two sub-lineage Vf isolates, while multidrug-resistant gene emeA was detected in one isolate SYD-NE41 [24]. Notably, approximately half (47.7%) of healthy-broiler and NE-linked isolates (n = 42) did not carry any acquired AMR genes.

The presence of plasmid(s) was predicted in all genomes using a reference-based sequence-search approach. Overall, 43 out of 88 (~ 48.8%) isolates carried at least 1 plasmid (18 isolates carried 1 plasmid, 15 isolates harboured 2 plasmids, 4 isolates harboured 3 plasmids, 6 isolates carried 4 plasmids; detailed in Additional file 1: Table S11). Geographical association analysis indicated that two specific plasmids were present in birds from Europe, Australia and North America - plasmids pCP15_1 and pCP15_2 which were first identified in isolate CP15 from an NE-linked chicken in USA (Additional file 2: Figure S7). These two reference plasmids did not carry any well-studied virulence-related genes, nevertheless, the re-annotation of plasmid genes using genus-specific database indicated that this small 14-kb plasmid pCP15_2 encoded a number of genes associated with sugar metabolism including phosphotransferase system (PTS), and sugar transporters sub-units (n = 5; Additional file 1: Table S12). In terms of plasmid types, European isolates carried 13 different types of isolates, Australian 5 types and USA 6 types. Australian isolates were not found to encode a ‘continent-specific’, plasmid type, while Europe had 9 unique plasmid types. Plasmids
Fig. 4 Virulence profiles of toxin genes and collagen adhesin genes categorised by host health states of bacterial isolates. Coloured cells indicate presence of gene. Data: Mean ± S.D. in virulence gene count include toxin (red) and adhesin (light blue) genes.
pDel1_4 and pCW3 were the common plasmids detected in isolates from England, Finland and Denmark (Additional file 2: Figure S8). Importantly, both plasmids pDel1_4 (Additional file 1: Table S13) and pCW3 (Additional file 1: Table S14) belonged to conjugative plasmid pCW3 family, carrying AMR genes tetA(P) and tetB(P) and adhesin gene cnaC; sharing highly similar genomic characteristics including plasmid size (47–49 kb) and CDS number (50–55; Additional file 1: Table S15) [25].

**Specific microbiota signatures identified in broiler caecal contents**

We next performed a small exploratory/pilot study to profile poultry gut microbiota bacterial members using caecal content samples obtained from 11 individual broilers representing 3 NE birds, 3 healthy birds and 5 sub-clinical NE birds (Fig. 5 a-d).

**Principle Component Analysis (PCA)** did not indicate distinct clustering of samples; suggesting a lack of distinctive microbiota signatures between diseased and healthy broilers; however healthy caecal samples appeared to have an inverse relationship with Enterococcus (Additional file 2: Figure S9). Notably, disease-specific profiles might be masked by the fact that a probiotic (Additional file 2: Figure S10). Relative bacterial genus abundance in each caecal sample was constructed to visualise microbiota profiles (Fig. 5). Thirty-seven genera were represented, with Bifidobacterium and Lactobacillus most abundant, which likely reflected the probiotic supplementation in the chicken feed. A number of secondary genera, which are usual intestinal microbiota members, were detected in these samples (relative abundance < 10% in each sample) including Blautia, Coprococcus, Dorea and Oscillospira. Blautia was more abundant in health-associated caecal microbiomes (mean abundance: 3.06 ± 2.84%) compared to diseased-associated caecal microbiomes NE (0.72 ± 0.5%) and SNE (0.14 ± 0.89%). The microbiota member Enterococcus, which is widely used as veterinary probiotic (especially Enterococcus faecium), was found at high levels in broilers NE2 (50.3%) and SNE5 (31.0%). Certain genera appeared to be more abundant in disease-linked NE and SNE samples including Enterococcus and Bacteroides (Additional file 2: Figure S11).

An additional paired-end BLASTn approach, to assign species level 16S rRNA sequences, indicated several important genera were present (Additional file 2: Figure S12) [26]. Lactobacillus reuteri (common broiler gut member, also widely used as probiotic supplement), Lactobacillus salivarius (common swine gut microbiota member used as broiler probiotic that improves production and general health) and Lactobacillus vaginatus (frequently found in broiler gut and a persistent gut coloniser) were the main species within the Lactobacillus genus [27–30]. Enterococcus genus primarily consisted of species Enterococcus faecium, a widely-used probiotic reported to promote broiler growth and suppress C. jejuni and C. perfringens infections, while stimulating the growth of Lactobacillus and Bifidobacterium [31, 32]. Importantly, Clostridium genus was mainly assigned to C. perfringens sequences, denoting the potential NE-link of C. perfringens origins in NE-broilers particularly NE3, where C. perfringens strains C036 and J36 were isolated from the same NE bird.

**Discussion**

Clostridium, particularly C. perfringens, is consistently described as the primary infectious agent to cause chicken NE. As C. perfringens thrives at ambient bird body temperature (i.e. 40–42 °C), with a doubling time <8 mins in vitro (the shortest generation time known for a microorganism), this may link to its ability to rapidly overgrow and cause disease pathology [5, 33]. In this study, we profiled the genomes of C. perfringens isolates, including newly sequenced strains, across a geographically diverse and varied health status sample collection. Genome-wide analysis revealed positive associations of important toxin genes with broiler-NE, and we identified a globally-disseminated potentially hypervirulent lineage Vf, which comprised isolates encoding important toxin genes netB and tpeL [13, 34].

In silico toxin profiling indicated that the NetB toxin, which has been identified as an essential toxin in NE development, [13, 34], was present in ∼50% of the NE isolates, with environmental samples also encoding this toxin, which may act as potential reservoirs, linked to NE outbreaks [35]. The fact that netB gene was exclusively encoded in NE-linked broiler isolates, when compared to healthy isolates, further supported the strong association of this toxin and NE pathogenesis.

Other virulence factors have also been implicated in NE pathogenesis. Several studies have indicated that collagen adhesin (encoded by cna) [14, 18, 36, 37] may facilitate bacterial colonisation within the chicken gut.
Fig. 5  

(a) Relative abundance of Operational Taxonomical Units (OTUs) based on 16S rRNA amplicon sequencing in 11 individual caecal samples on genus level, with classified comparisons on healthy, NE and SNE (sub-clinical NE) samples.  

(b-d) Comparison of taxa reads in 3 groups of samples.  

(e) Linear Discriminant Analysis (LDA) indicating significantly enriched taxa.
Our analysis indicated this gene (including its variants *cnaA* and *cnaC*) was overabundant in NE-associated isolates when compared to healthy-broiler isolates (*P < 0.05*), which also suggests a positive association with NE outcomes [37].

*C. perfringens* encodes a diverse array of toxins, and interestingly we also observed that several other accessory toxins were enriched in NE isolates, indicating these may also play an underrated role in broiler NE [38]; PFO, a pore-forming toxin which has been linked with bovine haemorrhagic enteritis [39], and CPB2, or beta2-toxin, another pore-forming cytolytic toxin associated with NE in piglets and enterocolitis in foals [40].

This genomic study indicates a potentially prevalent hypervirulent lineage Vf (comprising 14 isogenic strains; pairwise mean SNPs: 65 in 1810 core genes), with strains obtained from Australia, Canada, Denmark and USA, spanning a period of 20 years (1993–2013). Previous analysis with 9 isolates (out of 14) also indicated these (isogenic) strains grouped within the same lineage [18]. Notably, lineage Vf isolates carried significantly more virulence genes (toxins, including *netB* and *tpeL* and collagen adhesin) than isolates in other NE-linked isolates, toxin genes, supports that this lineage may be hypervirulent. TpeL toxin is not typically considered essential for pathogenesis due to its low carriage rate among NE-associated *C. perfringens* isolates (in this study *tpeL* was exclusively detected in lineage Vf) [41]. Nevertheless, in a broiler-NE infection model, infection with *tpeL*-positive (also *netB*-positive) strains induced disease symptoms more rapidly, and with a higher fatality rate, in contrast to *tpeL*-negative strains encoding only *netB*, highlighting a role for TpeL in more severe chicken-NE pathogenesis [42]. These data also indicate a potential global dissemination of NE-associated virulent genotypes, which is in agreement with a previous study that indicated clonal expansion of *C. perfringens* via multiple-locus variable-number tandem repeat analysis (*n = 328*) [43]. However, significantly larger sample sizes from various geographical origins will be required for in-depth WGS population structure analysis, if we are to understand the spread of *C. perfringens* in chicken farms worldwide, which will be vital in the context of disease control.

Key *C. perfringens* virulence factors including toxin and AMR genes are known to be carried on plasmids [44], including the poultry-NE-related toxin *netB* [13, 34]. The universal tcp conjugative system in majority of plasmids may facilitate horizontal gene transfer and enhance the virulence of *C. perfringens* strains [45, 46]. As almost half of the genomes carried plasmids (~48.8%) this implies widespread plasmid transfer within broiler-associated *C. perfringens* strains. However, as our analysis was carried out using reference-based approaches, in some cases, fragmented short-read sequenced genome assemblies from public databases this may not readily identify plasmid sequences. Indeed, within lineage Vf we did not observe the expected high carriage rates of plasmids encoding *netB* [47]. The availability of long-read sequencing (e.g. PacBio and Nanopore) will improve investigations into *C. perfringens*, as plasmids can be sequenced and predicted more accurately despite encoding numerous tandem repeats [48, 49].

In this study, we also analysed *C. perfringens* isolates obtained from healthy or asymptomatic birds, with several isolates (LLY_N11 and T18) encoding comparable numbers of virulence genes when compared to broiler-NE isolates (*n > 10*). Importantly, healthy-broiler isolate LLY_N11 (*netB*-negative strain, encoded *pfoA* and *cpb2*) has previously been shown to successfully induce NE in an experimental model [4, 50]. These data highlight the important role other host factors may play in prevention of overt disease e.g. the chicken gut microbiota. Gut-associated microbial ecosystems are known to play a key colonisation resistance role, preventing overgrowth of so-called pathobionts, or infection by known enteric pathogens (e.g. *Salmonella*).

In this exploratory/pilot broiler microbiome study, healthy broiler caecal microbiomes appeared to have enhanced abundance of the genera *Blaautia*. Members of the *Blaautia* genus are known to be butyrate producers, and reductions in this genus have previously been associated with a *C. jejuni* infection model [51]. As butyrate is an important energy source for intestinal cells, these *Blaautia* spp. may act as key beneficial microbiota members, serving to enhance intestinal health of chickens by strengthening the epithelial barrier, thus preventing pathogenic microbes successfully colonising and initiating disease. In NE caecal samples we observed appearance of the *Clostridium* genus, which was significantly enriched, albeit at low reads in NE individuals. Further species-level assignment analysis indicated that most *Clostridium* sequences mapped to *C. perfringens*, indicating that even a small proportion (mean relative abundance: 0.44%) of *C. perfringens* could potentially be lethal to broiler hosts. Therefore, microbiota profiling may be useful as a potential biomarker for NE-onset, however larger studies, with healthy and diseased birds from different flocks, would be required to verify these findings.

Probiotics, including *Bifidobacterium* and *Lactobacillus*, and also *Enterococcus*, have been frequently used in broiler farming primarily for growth-promotion and prevention of bacterial infections [29, 52, 53]. These taxa of beneficial bacteria have been reflected in caecal microbiome analysis, with predominant OTU proportions associated with *Bifidobacterium* and *Lactobacillus* across all samples. A previous study identified specific antibacterial peptides produced by *Bifidobacterium*.
*longum* that may correlate with the proposed probiotic/pathogen-inhibitory effect against *C. perfringens* [54]. However, several birds did present with SNE and NE suggesting the strains supplemented to these birds may not be effective in reducing the disease burden associated with *C. perfringens*. Further large scale-controlled supplementation trials are required to provide robust evidence for health promotion using probiotics in poultry.

**Conclusions**

In conclusion, genomic analysis of 88 broiler-associated *C. perfringens* isolates indicates positive correlations relating to virulence genes including *netB, pfo, cpb2, tpeL*, and *cna* variants linked to NE-linked isolates. Furthermore, potential global dissemination of hypervirulent lineage Vf *C. perfringens* strains highlights the need for further investigations, which will require a large worldwide dataset on NE-related *C. perfringens* isolates.

**Methods**

**Sample collection and bacterial isolation**

Birds (Ross 308 broilers; culled as part of routine farm surveillance) were collected from four external sites (Oxford, UK) reporting both healthy flocks and flocks that had been diagnosed with NE (Additional file 1: Table S8). All samples were collected within 36 h after culling. All birds were vaccinated using PARACOX®-5 (MSD, UK), and prior to euthanisation were aged between 19 to 25 days of age. Culled birds were necropsied and putative disease identification performed, followed by caecum content collection. A representative sub-set of caecal content samples were selected and processed to be sequenced (16S rRNA amplicon sequencing) as part of the pilot caecal microbiome study. Isolation of *C. perfringens* was carried out by isolating organs and submerging 0.1% peptone water (Oxoid, UK) in a 1:10 ratio of organ to peptone. Samples were streaked onto egg yolk agar supplemented with cycloserine (Oxoid, UK) and incubated overnight anaerobically at 37 °C [55]. Single black colonies were re-streaked on brain heart infusion agar (Oxoid, UK) and incubated anaerobically at 37 °C overnight. Several colonies were collected and subjected to identification of the *plc* gene by PCR, followed by 16S rRNA full-length amplicon sequencing as described previously for species verification [56, 57].

**Bacterial isolates and DNA sequencing**

We isolated 22 novel *C. perfringens* strains from broilers and environmental samples from farms in Oxford, UK. Genomic DNA of these bacterial isolates was extracted using phenol-chloroform method as described previously [57]. Details of these isolates are given in Additional file 1: Table S1. Sequencing was performed at the Wellcome Trust Sanger Institute using Illumina HiSeq 2500 to generate 125 bp paired-end reads. Illumina reads are available in the European Nucleotide Archive under project PRJEB32760.

**Genome assembly and annotation**

Broiler-related *C. perfringens* genome assemblies (RefSeq) and quality-trimmed sequencing reads (SRA) were retrieved from NCBI databases in May 2019 including available metadata (*n* = 68). A total of 22 newly sequenced genomes were assembled in-house. All adapter-trimmed sequencing reads were used as input for MEGAHIT v1.1.1 [58]. Genome assembly was carried out using MEGAHIT options --k-min 27 --k-max 247 (for paired-end reads 2 × 250 bp), --k-min 27 --k-max 97 (for paired-end reads 2 × 125 bp), --no-mercy (specifically for generic assembly) and --min-contig-len 300. Over-fragmented draft genome assemblies were excluded from further computational analysis if > 500 contigs (*n* = 2). Assembly statistics were calculated using custom Perl script and all sequences were checked to have ANI > 95% with respect to type strain ATCC13124 genome (Additional file 1: Table S2). All genomes were annotated using Prokka v1.13 with specific *Clostridium* genus (35 *Clostridium* species from NCBI RefSeq annotations) database with parameters --usegenus --mincontiglen 300 (Additional file 1: Table S3).

**Phylogenetic analysis, SNP detection, in silico virulence gene and plasmid detection**

Annotated gff files were used as input for Roary v3.12.0 to construct pangenome with option -e -n to generate a core gene alignment via MAFFT, -s do not split paralogs, -i to define a gene at BLASTp 90% identity and -y to obtain gene inference [59]. A total of 20,194 single nucleotide variants (315,715 site alignment from 1810 core genes) were called using snp-sites v2.3.3 [60]. We used the 20,194 site-alignment to infer a ML phylogeny using RAxML v8.2.10 with GTR+ nucleotide substitution model at 100 permutations conducted for bootstrap convergence test [61]. The ML tree constructed was with the highest likelihood out of 5 independent runs (option -N 5). Pairwise SNP distances were calculated using snp-dists v0.2 [62]. ANI was computed using module pyani v0.2.7 [63]. R package rhierBAPS was used for phylogenetic clustering analysis to identify population structure [64].

Nucleotide sequence search was performed using ABIRicate v0.8.11 on genome assemblies with coverage ≥90% and sequence identity ≥90% [65]. Toxin database was constructed as previously described [20] and collagen adhesin genes was detailed in Additional file 1: Table S4. Plasmids were predicted computationally using PlasmidSeeker v1.0 where sequence reads are available...
(k-mer coverage > 80%), and ABRiccate on all genome assemblies, with best-hit approach at query coverage threshold ≥70% and nucleotide identity ≥90% via custom database as detailed in Additional file 1: Table S5.

**Genome-wide gene association analysis**

Scoary v1.6.11 was run to draw gene associations at default parameters [66]. Specificity cutoff was set at 80%, sensitivity at 100% to obtain 63 genes specifically associated with sub-lineage Vf isolates (Additional file 1: Table S6).

**16S rRNA amplicon sequencing and analysis**

Genomic DNA extraction of caecal samples was performed with FastDNA Spin Kit for Soil following manufacturer’s instructions and extending the bead-beating step to 3 min as described previously [26]. Extracted DNA was quantified and normalised to 5 ng/μl for all samples before subject to 16S rRNA Illumina MiSeq sequencing library preparation, amplifying V1 + V2 regions of the 16S rRNA gene as detailed in additional file 1: Table S7 for the primer sequences. PCR amplification conditions were: 1 cycle of 94°C for 3 min, followed by 25 cycles of 94°C for 45 s, 55°C for 15 s and 72°C for 30 s. Libraries were sequenced on the Illumina MiSeq platform using a read length up to 2 × 300 bp.

Sequencing reads were analysed using OTU clustering methods via QIIME v1.9.1 using SILVA_132 as reference database to assign OTU by clustering at 97% similarity [67, 68]. Briefly, paired-end sequences were merged using PEAR, followed by quality filtering using split_libraries_fastq.py, chimera identification using identify_chimeric_seqs.py and chimera removal using filter_fasta.py [69]. OTU picking step was run using open reference approach pick_open_reference_otus.py which does not discard unassigned reads in the final output. BIOM output file was visualised on MEGAN6 [70]. Paired-end approach of taxa assignment using BLASTn as described previously [26].

Caecal contents were processed to generate an average of 116,967 (range: 80426–1152,763) raw sequence reads per sample, with an average of 606 (range: 364–1559) OTUs assigned in each sample, clustering at 97% similarity (Additional file 1: Table S8). Rarefaction analysis supports the availability of sufficient sequence reads to achieve asymptotic based on rarefied reads (normalized to the lowest reads of all samples), i.e. optimal diversity of richness (range: 15–23 genera, 15–25 families) in each individual sample to represent each member of the microbiota (Additional file 2: Figure S1).

LDA was performed using LEfSe via Galaxy server to identify significantly enriched taxa in the dataset. Alpha value for non-parametric Kruskal-Wallis test was set at 0.05 and threshold on LDA score at 2.0 for statistical significance. Graph was illustrated using the LEfSe plotting module [71].

R package vegan function rarecurve was used to draw rarefaction curves using rarefied reads (normalised to the lowest-read sample as implemented in MEGAN6). Diversity indices including Inverse Simpson index, Shannon index and Fisher index were computed using R package vegan function diversity [72].

**Statistical analysis and graphing**

Venni 2.1 was used to analyse plasmid data [73]. Graphpad PRISM v6.0 was used for various statistical analyses, R package ggplot2 was used for various plotting.

**Supplementary information**

Supplementary information accompanies this paper at https://doi.org/10.1186/s42523-019-0015-1.

Additional file 1. Supplementary tables.

Additional file 2. Supplementary figures.
3. Phylogenetic tree aligned with metadata and virulence profiles is available in iTOL: https://itol.embl.de/tree/14915519625227531559222489

Consent for publication
Not applicable.

Competing interests
The authors declare that they have no competing interests.

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Received: 8 July 2019 Accepted: 23 September 2019
Published online: 18 October 2019

References
1. About chickens [https://www.ciwf.org.uk/farm-animals/chickens/]. Accessed 9 May 2019.
2. Keyburn AL, Boyce JD, Vaz P, Bannam TL, Ford ME, Parker D, Di Rubbo A, Rood J, Moore RJ. NetB, a new toxin that is associated with avian necrotic enteritis caused by Clostridium perfringens. PLoS Pathog. 2008;4(2):e26.
3. Lepp D, Rosas B, Pareira VR, Mani PR, Rosey EL, Gong J, Songer JG, Vedantam G, Prescott JF. Identification of novel pathogenicity loci in Clostridium perfringens strains that cause avian necrotic enteritis. PLoS One. 2010;5(5):e10795.
4. Li C, Yan X, Lillehoj HS. Complete Genome Sequence of Clostridium perfringens LLY_N11, a Necrotic Enteritis-Inducing Strain Isolated from a Healthy Chicken Intestine. Genome Announc. 2017;5(4):e01225–17.
5. Rood JI, Keyburn AL, Moore RJ. NetB and necrotic enteritis: the hole story. Vet Microbiol. 2012;159(1–2):213–5.
6. Abildgaard L, Sondergaard TE, Engberg RM, Schramm A, Hojberg O. In vitro evaluation of the probiotic potential of Lactobacillus salivarius MTC 1026 as a potential probiotic. J Gen Appl Microbiol. 2009;55(1):103–7.
7. Drew MD, Syed NA, Goldabe BG, Laarveld B, Savicki G. Sub-clinical necrotic enteritis in broiler chickens: novel etiological consideration based on ultra-structural and molecular changes in the intestinal tissue. Res Vet Sci. 2008;85(3):543–53.
8. Keyburn AL, Boyce JD, Vaz P, Bannam TL, Ford ME, Parker D, Di Rubbo A, Rood J, Moore RJ. NetB, a new toxin that is associated with avian necrotic enteritis caused by Clostridium perfringens. PLoS Pathog. 2008;4(2):e26.
9. Li C, Yan X, Lillehoj HS. Complete Genome Sequence of Clostridium perfringens LLY_N11, a Necrotic Enteritis-Inducing Strain Isolated from a Healthy Chicken Intestine. Genome Announc. 2017;5(4):e01225–17.
10. Rood JI, Keyburn AL, Moore RJ. NetB and necrotic enteritis: the hole story. Vet Microbiol. 2012;159(1–2):213–5.
11. Drew MD, Syed NA, Goldabe BG, Laarveld B, Savicki G. Sub-clinical necrotic enteritis in broiler chickens: novel etiological consideration based on ultra-structural and molecular changes in the intestinal tissue. Res Vet Sci. 2008;85(3):543–53.
12. Abildgaard L, Sondergaard TE, Engberg RM, Schramm A, Hojberg O. In vitro evaluation of the probiotic potential of Lactobacillus salivarius MTC 1026 as a potential probiotic. J Gen Appl Microbiol. 2009;55(1):103–7.
13. Drew MD, Syed NA, Goldabe BG, Laarveld B, Savicki G. Sub-clinical necrotic enteritis in broiler chickens: novel etiological consideration based on ultra-structural and molecular changes in the intestinal tissue. Res Vet Sci. 2008;85(3):543–53.
14. Stankey D, Wu SB, Rodgers N, Swick RA, Moore RJ. Differential responses of Campylobacter microbiome of broiler chickens and shifts associated with clinical necrotic enteritis in broiler chickens. Poult Sci. 2011;90(12):2753–65.
15. Tintin S, Saraya S, Traidej Chomnawang M. Isolation and characterization of Lactobacillus salivarius MTC 1026 as a potential probiotic. J Gen Appl Microbiol. 2011;57(9):365–78.
16. Messaoudi S, Madf Madi A, Prevost H, Feuilloley M, Manai M, Dousset X, Connil N. Diverse antimicrobial killing by Enterococcus faecium—SMXD51. Anaerobe. 2012;18(6):584–9.
17. Wang L, Lilburn M, Yu Z. Intestinal microbiota of broiler chickens as affected by litter management regimens. Front Microbiol. 2016;7:593.
18. Lacey JA, Allnutt TR, Vezina B, Van TTH, Stent T, Han X, Rood JI, Wade B, Keyburn AL, Seemann T, et al. Whole genome analysis reveals the diversity and evolutionary relationships between necrotic enteritis-causing strains of Clostridium perfringens. BMC Genomics. 2018;19(1):379.
19. Li C, Yan X, Lillehoj HS. Complete genome sequences of Clostridium perfringens Del1 strain isolated from chickens affected by necrotic enteritis. Gut Pathog. 2017;9:69.
20. Kiur, Caim S, Alexander S, Pachori P, Hall LJ. Probing genomic aspects of Clostridium perfringens isolates from healthy broiler chickens at a commercial farm. Vet Microbiol. 2008;127(1–2):116–27.
21. Nauery B, Pedersen K, Madsen M. Analysis by pulsed-field gel electrophoresis of the genetic diversity among Clostridium perfringens isolates from chickens. Vet Microbiol. 2003;94(3):257–66.
22. Ghelamandehkordi A, Eeckhaut V, Lanckaert L, Timmermont L, Bjerum L, Ducatelle R, Haesebroeck F, Van Immerseel F. Antimicrobial resistance in Clostridium perfringens isolates from broilers in Belgium. Vet Res Commun. 2009;33(8):1031–7.
23. Ja B, Raphehna AR, Alcock B, Waglechner N, Guo P, Tsang KK, Lago BA, Dave BM, Pereira S, Sharma AN, et al. CARD 2017: expansion and model-centric curation of the comprehensive antibiotic resistance database. Nucleic Acids Res. 2017;45(D1):D566–73.
24. Wheals TD, Vidal CJ, Awad MM, Lyra D, Rood JI, Adams V, PCP13, a representative of a new family of conjugative toxin plasmids in Clostridium perfringens. Plasmid. 2019;102:37–45.
25. Alcon-Giner C, Caim S, Mitra T, Selskemety J, Wegmann U, Wain J, Belteki G, Clarke P, Hall LJ. Optimisation of 16S rRNA gut microbiota profiling of extremely low birth weight infants. BMC Genomics. 2017;18(1):841.
26. Wang L, Lilburn M, Yu Z. Intestinal microbiota of broiler chickens as affected by litter management regimens. Front Microbiol. 2016;7:593.
27. Go T, Zeng XF, Chen AG, Zhou L, Zhang L, Xiao VP, Yang CM. Effects of a probiotic, Enterococcus faecium, on growth performance, intestinal morphology, immune response, and cecal microflora in broiler challenged with Escherichia coli K88. Poult Sci. 2013;92(11):2949–55.
28. Vechoth EA, Ersulanov BV, Perelygin WW, Mitsevich EV, Mitsevich IP, Bozarzkon VN, Levchuk VP, Vechoth OE, Kovalen EV, Stepanshin YG, et al. Diverse antimicrobial killing by Enterococcus faecium E 50-52 bacteriocin. J Agric Food Chem. 2008;56(19):4924–8.
29. Li J, McClane BA. Further comparison of temperature effects on growth and survival of Clostridium perfringens type a isolates carrying a chromosomal or plasmid-borne enterotoxin gene. Appl Environ Microbiol. 2006;72(7):4561–8.
30. Keyburn AL, Bannam TL, Moore RJ, Rood JI. NetB, a pore-forming toxin from necrotic enteritis strains of Clostridium perfringens. Toxins (Basel). 2010;2(7):1913–27.
31. Torok VA, Hughes RJ, Ophel-Keller K, Ali M, Macalpine R. Influence of different litter materials on cecal microbiota colonization in broiler chickens. Poul Sci. 2009;88(12):2474–81.
32. Wade B, Keyburn AL, Haring V, Ford M, Rood JI, Moore RJ. The adherent abilities of Clostridium perfringens strains are critical for the pathogenesis of avian necrotic enteritis. Vet Microbiol. 2016;197:53–61.
33. Wade B, Keyburn AL, Seemann T, Rood JI, Moore RJ. Binding of Clostridium perfringens to collagen correlates with the ability to cause necrotic enteritis in chickens. Vet Microbiol. 2015;180(1–2):299–303.
34. Fisher DJ, Miyamoto K, Harrison B, Akimoto S, Sarker MR, McClane BA. Association of beta2 toxin production with Clostridium perfringens type a human gastrointestinal disease isolates carrying a plasmid enterotoxin gene. Mol Microbiol. 2005;56(3):747–62.
43. Sawires YS, Songer JG. Clostridium perfringens

44. Freedman JC, Theoret JR, Wisniewski JA, Uzal FA, Rood JI, McClane BA.

45. Gervasi T, Curto RL, Minniti E, Narbad A, Mayer MJ. Application of

46. Mountzouris KC, Tsirtsikos P, Kalamara E, Nitsch S, Schatzmayr G, Fegeros K.

47. Arredondo-Alonso S, Willems RJ, van Schaik W, Schurch AC. On the (im)

48. Gonzalez-Escalona N, Allard MA, Brown EW, Sharma S, Hoffmann M.

49. Margos G, Hepner S, Mang C, Marosevic D, Reynolds SE, Krebs S, Sing A,

50. Li C, Lillehoj HS, Gadde UD, Ritter D, Oh S. Characterization of

51. Thibodeau A, Fravalo P, Yergeau E, Arsenault J, Lahaye L, Letellier A. Chicken

52. Lee JH, Li X, O’Sullivan DJ. Transcription analysis of a lantibiotic gene cluster

53. Kiu R, Caim S, Alcon-Giner C, Beltgeki G, Clarke P, Pickard D, Dougan G, Hall LJ. Preterm infant-associated Clostridium tertium, Clostridium cadaveris, and Clostridium paraputrificum strains: genomic and evolutionary insights. Genome Biol Evol. 2017(9)(10):2707–14.

54. Li D, Liu, CM, Luo R, Sadakane K, Larm T.W. MEGAHIT: an ultra-fast single-node solution for large and complex metagenomics assembly via succinct Bruin graph algorithms. Bioinformatics. 2015;31(10):1674–6.

55. Page AJ, Cummins CA, Hunt M, Hong WK, Reuter S, Holden MT, Fookes M, Falush D, Keane JA, Parkhill J. Roary: rapid large-scale prokaryote pan genome analysis. Bioinformatics. 2015;31(22):3691–3.

56. Page AJ, Taylor B, Delaney AJ, Soares J, Seemann T, Keane JA, Harris SR. SNP-sites: rapid efficient extraction of SNPs from multi-FASTA alignments. Microb Genom. 2016(2)(4):e000056.

57. Stamatakis A. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics. 2014;30(9):1312–3.

58. Seemann T, Krozil F. Page A.J. snp-dists. In., 0.2; 2018: Convert a FASTA alignment to SNP distance matrix.

59. Pritchard L, Glover RH, Humphris S, Elphinstone JG, Toth IK. Genomics and taxonomy in diagnostics for food security: soft-rotting enterobacterial plant pathogens. Anal Methods. 2016(8)(1):12–24.

60. Tonkin-Hill G, John AL, Stephen DB, Simon DW, Jukka C. EBI: An R Implementation of the Population Clustering Algorithm hierBAPS. Wellcome Open Research. 2013;3:July.93.

61. Seemann T. ABRicate. In., 0.5; 2018: Mass screening of contigs for antimicrobial resistance or virulence genes.

62. Brynildsrud O, Bohlin J, Scheffer L, Eldholm V. Rapid scoring of genes in microbial pan-genome-wide association studies with Scoary. Genome Biol. 2016;17:238.

63. Caporaso JG, Kuczynski J, Stombaugh J, Bittinger K, Bushman FD, Costello EK, Fierer N, Pena AG, Goodrich JK, Gordon JJ, et al. QIIME allows analysis of high-throughput community sequencing data. Nat Methods. 2010;7(5):335–6.

64. Quast C, Pruesse E, Yilmaz P, Gerken J, Schweer T, Yarza P, Peplies J, Glöcker ND. The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. Nucleic Acids Res. 2013;41(Database issue):D590–6.

65. Zhang J, Kobert K, Flouri E, Stamatakis A. PEAR: a fast and accurate illumina paired-end reAd mergeR. Bioinformatics. 2014;30(5):5614–20.

66. Huson DH, Beier S, Flade I, Gorschka A, El-Hadidi M, Mitra S, Ruscheweyh HJ, Tappu R. MEGAN Community edition - interactive exploration and analysis of large-scale microbiome sequencing data. PLoS Comput Biol. 2016;12(6):e1004957.

67. Segata N, Izard J, Waldron L, Gevers D, Miropolsky L, Garrett WS, Huttenhower C. Metagenomic biomarker discovery and explanation. Genome Biol. 2011;12(6):R60.

68. R Development Core Team. R: A language and environment for statistical computing. Vienna: R Foundation for Statistical Computing; 2010.

69. Venn diagram vectoR: an interactive tool for comparing lists with Venn’s diagrams. [http://bioinfogp.cnb.csic.es/tools/venny/index.html]. Accessed 16 May 2019.

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