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# *Candida albicans* in Faeces of Migratory Geese Can Persist in Agricultural Soils: One-Health Implications for Grazing Livestock

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## ABSTRACT

The World Health Organization has classified five species of *Candida* as pathogens of critical concern on its recent 'Fungal Pathogen Priority List'. *Candida albicans* is the most common species aetiologically associated with human and animal mucosa; however, we know almost nothing about the environmental survival and the transfer pathways of *C. albicans* in natural environments. Here, we have isolated *C. albicans* from the faeces of newly arrived migratory geese in two agricultural fields in Scotland (the United Kingdom). All 14 confirmed isolates were characterised in terms of their pathogenicity (in a *Galleria* larval infection model) and resistance to four classes of antifungal drugs. Multilocus sequence typing (MLST) was used to assess the relatedness of these isolates with *C. albicans* isolated from the faeces of sheep grazing in the same field. Finally, mesocosms were used to test whether *C. albicans* in geese faeces could persist and remain viable when incorporated into agricultural soils. All *C. albicans* isolates were virulent, and exhibited resistance to at least one of the four classes of antifungal drugs against which they were screened. Maximum likelihood phylogenetic analysis of MLST sequences revealed that *C. albicans* isolated from goose and sheep faeces were relatively conserved, although they did cluster independently on separate clades. *C. albicans* remained viable in common agricultural soils, and after 60 days, the concentrations of all three representative *C. albicans* isolates had only declined by one log. The unrestricted movement of migratory birds provides a significant opportunity for the widespread dissemination of pathogens. Although *C. albicans* is not generally considered to be zoonotic, its introduction into new environments and subsequent persistence in agricultural systems has the potential to facilitate transmission between animal species or humans. Therefore, it is critical that more emphasis be put on monitoring animal migration and the potential for cross-boundary movement of pathogens, particularly with climate change widening the geographic range for pathogen persistence.

## 1 | Introduction

Several species of the yeast *Candida* are well-characterised opportunistic fungal pathogens of humans and animals [1, 2] and cause an estimated 700,000 annual cases of human candidiasis [3]. *Candida albicans* is the most common species aetiologically associated with human and animal mucosa, although it is typically not pathogenic when in its yeast form; however, in response to certain environmental cues, it can enter its hyphal state, where it can then cause candidiasis or, in some cases, lead to invasive candidiasis and candidemia [4]. Globally, cases of *Candida* infections are rising concomitantly with reports of increased virulence [5] and antifungal drug resistance [6, 7]. This has led to *C. albicans*, together

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with *C. auris* (*Candidozyma auris*), *Nakaseomyces glabratus* (*C. glabrata*), *C. tropicalis*, *C. parapsilosis* and *Pichia kudriavzevii* (*C. krusei*) being placed on the WHO Priority Fungal Pathogen list [8], which was generated as a global effort to prioritise the research of high-priority pathogens, including preventing the development of antifungal resistance.

Although the majority of research on human pathogenic *Candida* has been conducted in a clinical context, there are several reports of *Candida* being able to persist in the natural environment [9–12]. In a mesocosm study, *C. albicans* persisted in a range of agricultural soil types for up to 30 days [13], although persistence was determined by PCR, so it is unclear whether these particular strains of *C. albicans* were still viable by the end. Similarly, molecular sequencing data have been used to identify *Candida* in a range of other environmental matrices [14, 15]. Recently, viable multidrug-resistant pathogenic strains of *C. tropicalis* and *C. glabrata* have been isolated from the surfaces of plastic pollution in both freshwater and marine environments, whilst the persistence and virulence of *C. auris* have been demonstrated in mesocosms simulating coastal and marine environments [16–18].

*Candida* is not generally considered to be a zoonotic pathogen [1]; however, there are concerns about the genetic relatedness of *Candida* isolates from animals and humans and the potential for the evolution and transmission of new variants in shared ecosystems and under climate change conditions [19, 20]. Little is known about the potential for *Candida* transmission, or spillover, from wild animals to livestock or humans and the risks associated with this [21]. Infections by strains of antifungal-resistant *C. albicans* have been reported in both livestock [22, 23] and wild birds [24–27], including migratory birds that often land and roost in agricultural fields during migratory flights. Therefore, grazing livestock could be exposed to faeces or soil contaminated with *Candida* shed from migratory birds, with evidence suggesting that *Candida* in bird faeces can express virulence factors in similar ways to known clinical isolates, highlighting the pathogenic potential of these isolates [28].

Despite the potential for species of *Candida* to infect domestic animals and migratory birds and enter the environment in animal faeces, there is a lack of recognition of the one-health potential of *Candida* persisting in agricultural systems. Therefore, the aim of this study was to determine whether fresh faeces of the migratory pink-footed goose (*Anser brachyrhynchus*) were a source of drug-resistant pathogenic species of *Candida* and the potential for these strains to subsequently persist in two different types of agricultural soil. We have quantified the resistance profiles of *Candida* isolated from goose faeces to four commonly used antifungal drugs, fluconazole, caspofungin, amphotericin B and voriconazole, and tested for pathogenicity in a *Galleria mellonella* model of infection. Finally, we have used multilocus sequence typing (MLST) to determine the genetic relatedness of *Candida* isolates from goose faces, with isolates of *Candida* recovered from sheep faeces collected in the same fields after the geese had left.

## 2 | Methods

### 2.1 | Field Sites and Faeces Collection

Two field sites in central Scotland (the United Kingdom) were identified as areas where large numbers of pink-footed geese (*A. brachyrhynchus*) landed during migratory flights during September/October (Figure 1). At both sites, large flocks of geese (>500 birds) were observed resting in agricultural fields containing crop stubble following the recent harvest of the cereal crop.

At 25 points across each site, four freshly deposited goose faecal pellets within a $3 \times 3\,m^2$ area (and the specific GPS location recorded) were collected as a composite sample and added to sterile 50 mL falcon tubes, giving a total of 100 faecal pellets at each of the two sites (Figure 1); there was no contact with any animals during any of the fieldwork. In addition, 20 soil samples and four stover samples were taken randomly at both sites. All faeces, soil and stover samples were processed on the day of collection.

A second visit to site A was carried out approximately 3 weeks after the first collection date, referred to herein as site AA. At this second visit, a flock of sheep had been moved into the field and were grazing on the stubble, but no geese were observed. Eight sheep faecal pellets were collected in individual sterile Falcon tubes and screened for *Candida* species on the day of collection. Additionally, any remaining goose faecal pellets were collected ad hoc to be used in subsequent mesocosm experiments (Section 2.4).

### 2.2 | Isolation and Identification of *Candida* Species in Faeces

Replicate faecal samples (1 g) were homogenised in 10 mL phosphate-buffered saline (PBS) by vortexing for 30 s in a sterile glass 30 mL universal vial. From this resuspension, 1 mL was added to 5 mL of yeast extract peptone dextrose (YPD) broth supplemented with antibiotics (gentamicin 50 mg/L, chloramphenicol 50 mg/L; Sigma-Aldrich, USA) for pre-enrichment. Replicate soil samples were processed in the same way; stover was added directly to 5 mL of YPD. All pre-enrichment broths were incubated at 37°C for 48 h at 120 rpm in a shaking incubator (SciQuip, UK). Following incubation, serial dilutions were performed using PBS, and $10^0$, $10^{-2}$ and $10^{-4}$ dilutions were streaked onto CHROMagar *Candida* Plus agar (CHROMagar, France) and incubated at 37°C for 48 h. Positive colonies were putatively identified based on colony morphology and colour on CHROMagar. Stocks of each colony type were made by adding a single colony to a 1:1 (v:v) YPD and 80% glycerol solution and storing them at −80°C.

Single colonies from all *Candida*-positive cultures were picked and added to 50 μL nuclease-free water, and heat-shocked at 95°C for 5 min to lyse the cells. PCR was performed using primers targeting the ITS region [29]. Briefly, 5 μL of the heat-shocked solution was added to a PCR reaction made up as follows: 2x master mix (Qiagen, Germany), 0.4 μM forward and reverse primer (forward primer—5′ GTCAAACTTGGTCATTTA 3′ and reverse primer—5′ TTCTTTTCCTCCGCTTATTG 3′), and made up to 25 μL using molecular grade water. Cyclic conditions of 94°C for 30 s, 50°C for 30 s and 72°C for 2 min were run for 34 cycles, with an initial 3 min denaturation step at 94°C and a final extension step for 10 min at 72°C. Amplification was confirmed on a 1% agarose gel, and each PCR product was purified using a Promega Wizard PCR Purification Kit (Promega, UK). PCR products were Sanger sequenced using the ITS forward primer, and NCBI BLAST was used to confirm species ID (Table 1).



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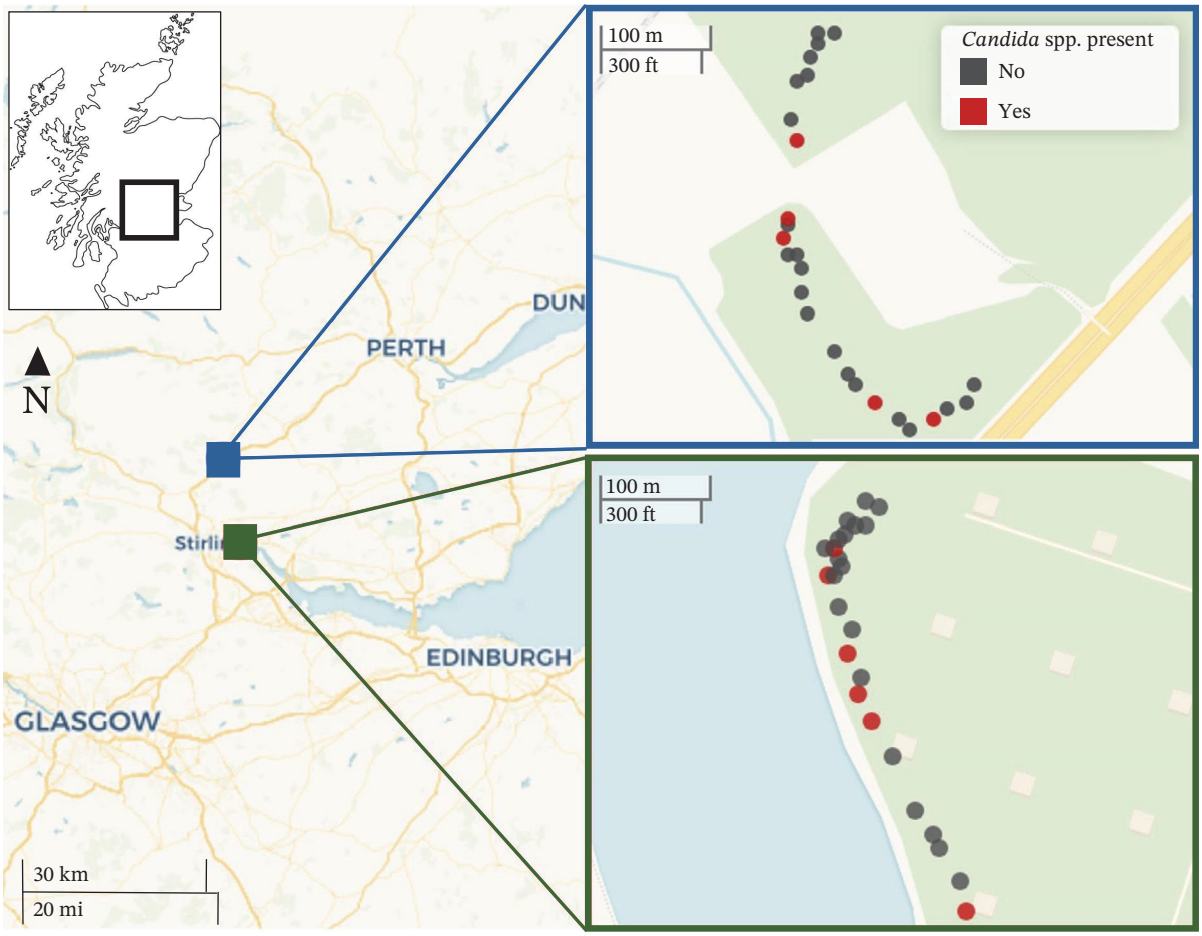


**FIGURE 1** | Locations of two flocks of migratory pink-footed geese. Geese faeces were collected at sites A (blue) and B (green) on a single day in October 2024. Specific locations of faeces collections are shown by black dots, with red dots indicating a location where a faecal pellet tested positive for *Candida*.

## 2.3 | Antifungal Drug Resistance Assays

Minimum inhibitory concentration (MIC) analysis, following the European Committee on Antimicrobial Susceptibility Testing (EUCAST) antifungal MIC method for yeasts [30] (with slight modifications) [18], was conducted on all confirmed isolates of *Candida*. Each isolate was grown overnight at 37°C in 5 mL of YPD broth, and cells were recovered by centrifugation at 4000 × *g* for 4 minutes, washed, resuspended in 5 mL PBS, and concentrations adjusted to $10^5$ cells/mL. Four antifungal drugs were prepared in 10 two-fold dilutions in Roswell Park Memorial Institute (RPMI) 1640 medium (Fisher Scientific, UK): amphotericin B (0.008–4 mg/L), caspofungin (0.008–4 mg/L), fluconazole (0.125–64 mg/L), voriconazole (0.008–4 mg/L) (Fisher Scientific, UK), and 100 μL of each drug concentration and 100 μL of each *Candida* isolate were added to each well of a 96-well plate in triplicate. Control wells containing sterile drug-free media, with 100 μL of each *Candida* isolate, were prepared and wells with no culture or drugs were also prepared. Plates were incubated at 37°C in a static incubator for 24 h. Growth was determined by measuring absorbance at 530 nm using a spectrophotometer (Infinite M200 plate reader; Tecan, Switzerland). The MIC of caspofungin, fluconazole and voriconazole was determined as the lowest concentration giving inhibition of 50% growth compared to a drug-free control, whilst the MIC of amphotericin B was determined as inhibition of 90% growth.

## 2.4 | Mesocosm Analysis of *C. albicans* Persistence in Soil

Three *C. albicans* isolates (CA05, CA10 and CA13) from goose faeces were selected to determine persistence in two common agricultural soil types with contrasting pH profiles (a loam and a podzol). Goose faecal pellets which tested negative for *Candida* on CHROMagar *Candida* Plus agar were used to create a faecal slurry: 6 g of goose faeces was mixed with 60 mL of PBS and thoroughly homogenised using a vortex for 60 s. The three selected *C. albicans* isolates originating from goose faeces were mixed with 60 mL of the faecal slurry to make a final volume of 120 mL, with final concentrations of $1.85 \times 10^8$ (CA05), $1.8 \times 10^8$ (CA10) and $1.85 \times 10^8$ (CA13).

Replicate mesocosms were prepared by adding either 100 g of podzol or loam soil (pre-screened to confirm the absence of any *Candida* species, dried at room temperature for 24 h and sieved to a uniform 4 mm) to sterile plastic pots (total volume 150 mL). To each mesocosm, 10 mL of one of the *C. albicans* faecal slurry inocula were added and thoroughly homogenised using a sterile spatula. A total of 52 mesocosms were set up, with five replicates



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for each of the three *C. albicans* isolates and one culture-negative control for both soil types. All mesocosm pots were kept in a glasshouse with lids loosely attached, and the temperature was monitored using iButton temperature logger chips (iButtonLink, WI, 176 USA) (temperature range 9–16°C).

At each timepoint (1, 2, 3, 4, 7, 10, 14, 21, 28, 40 and 60 days) a sterile spatula was used to remove 5 g of soil from each replicate mesocosm, which was placed in a sterile 30 mL glass universal tube. Soil was mixed with 10 mL sterile PBS and vortexed for 30 s, serially diluted in PBS and plated out on SGA agar with gentamycin (10 mg/L), incubated overnight at 37°C and colony-forming units (CFUs) enumerated. All colonies recovered from each mesocosm at each timepoint were phenotypically identical, and representative colonies were positively identified by PCR. At each time point 0.5 g of soil was also removed from each mesocosm to determine moisture content (105°C for 24 h) to calculate the concentration of *Candida* per soil dry weight.

### 2.5 | Challenging *G. mellonella* With *Candida* Isolates

The pathogenicity of confirmed *Candida* isolates was tested in a *G. mellonella* (greater wax moth) larval infection model. Colonies from *C. tropicalis* (CT01) and three *C. albicans* isolates (obtained by sweeping the surface of plates) were resuspended in 150 μL of PBS, and six 10-fold dilutions were made in PBS. *G. mellonella* larvae (Livefood, Axbridge, UK) were set up in groups of 10, and each individual larva was injected in the haemocoel via the last right pro-limb with 10 μL of the *Candida* isolate using a sterile Hamilton syringe and a 0.45 mm gauge needle and kept at 37°C for 10 days. In addition, three groups ($n = 10$) of larvae were injected with sterile PBS as negative injection controls. Larvae were considered dead when they did not respond to touch.

### 2.6 | MLST of *C. albicans* Isolated From Geese and Sheep Faeces

MLST analysis, based on the amplification and sequence alignment of seven housekeeping genes, AAT1a, ACC1, ADP1, MPIb, SYA1, VPS13 and ZWF1 [31, 32], was used to determine the relatedness of *C. albicans* isolated from geese and sheep faeces. Seven independent PCRs were performed for each gene for each isolate using previously published primers [31] using the following reaction set up; a 2x master mix (Qiagen, Germany), 0.4 μM forward and reverse primer and 5 μL of the heat-shocked colony solution, made up to 25 μL with nuclease-free water (Ambion, UK). PCR cyclical conditions were 94°C for 30 s, 50°C for 30 s and 72°C for 1 min, and run for 34 cycles, with an initial 3 min at 94°C and final extension of 72°C for 10 min. The resulting products were visualised using 1% agarose gel electrophoresis and purified using a Wizard SV Gel and PCR Clean Up Kit (Promega, UK). Quantified fragments were Sanger sequenced, and the resulting FASTA files were trimmed, aligned and concatenated in MEGA X [33]. The concatenated sequences were aligned using MUSCLE with 300 *C. albicans* reference sequences, taken from the *C. albicans* MLST database. The 300 *C. albicans* reference sequences were selected at random from the list of 4486 sequences and were used to determine the relatedness of the *C. albicans* isolated from geese and sheep faeces in this study, rather than how these isolates fit into the wider context of global *C. albicans* sequences. Using MEGA X, a maximum-likelihood phylogenetic tree was constructed using 500-bootstrap iterations, and the final image was generated using iTOL [34].

### 2.7 | Statistical Analyses

*C. albicans* die-off rates in soil were calculated by first transforming concentrations to $\log_{10}$ CFU/g. Linear regression analysis was then used to determine the dynamics of *C. albicans* die-off (Minitab v18; Minitab Inc.; State College, PA, USA). Briefly, a log-linear regression model was fitted to the $\log_{10}$-transformed data, which is described by the equation:

$$\mathrm{Log}_{10}(C) = \mathrm{Log}_{10}(C0) - kt,$$

where $C0$ is the cell concentration at $t = 0$ and $k$ is the die-off rate constant (day minus one).

The percentage decrease in *C. albicans* concentration per unit time was determined as constant using the log-linear model. Following a log-linear die-off profile, decimal reduction times ($D$-values; the number of days to reduce viable yeast by 90%) were calculated based on the decline rates for each population.

Statistical analyses of the Kaplan–Meier survival curves were calculated in Graphpad Prism (v10). A Mantal-Cox log-rank statistical analysis for the Kaplan–Meier survival curves for each 10-fold dilution was performed with values determined by comparing the differences in survival between each of the three *C. albicans* isolates examined.

## 3 | Results

### 3.1 | Recovery of *C. albicans* From Goose Faeces at Two Field Sites

During the first round of field sampling, *C. albicans* was detected in seven goose faecal pellets at site A (7/100) and three faecal pellets at site B (3/100), which were confirmed by Sanger sequencing of the ITS region (Table 1). Additionally, *C. tropicalis* was detected in one soil sample from site A, *Candida guilliermondii* was detected in a single goose faecal pellet at site B and some additional faecal pellets gave false positives on CHROMagar *Candida* Plus agar for other *Candida* species (Table 1). On the second visit to site A (visit AA), 9/25 goose faecal pellets were positive for *Candida*, with four isolates positively confirmed as *C. albicans* and three confirmed as *P. kudriavzevii* (formerly *C. krusei*). Four of the eight sheep faecal pellets tested positive for *C. albicans* (Table 1, Figure S1).

### 3.2 | Screening *Candida* Isolates for Antifungal Resistance

All *Candida* isolates exhibited some resistance to at least one of the four classes of antifungal drugs they were screened against (Figure 2). *C. tropicalis* isolated from soil showed some tolerance to voriconazole (0.0625 mg/L) and resistance to amphotericin B (4 mg/L) and fluconazole (8 mg/L). Most of the *C. albicans* isolates from the goose and sheep faeces (with the exception of one isolate) showed resistance to amphotericin B (>1 mg/L), and some level of tolerance to fluconazole (2 mg/L), although they



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**TABLE 1** | Fungal species isolated from goose and sheep faeces, soil and stover.

| Site | Isolate | Sample | Putative morphology | Top BLAST match | Accession number |
|---|---|---|---|---|---|
| A | CT01 | Soil | *C. tropicalis* | *C. tropicalis* | PQ860519 |
| A | CA01 | Goose faeces | *C. albicans* | *C. albicans* | PQ860520 |
| A | CA02 | Goose faeces | *C. albicans* | *C. albicans* | PQ860521 |
| A | CA03 | Goose faeces | *C. albicans* | *C. albicans* | PQ860522 |
| A | CA04 | Goose faeces | *C. albicans* | *C. albicans* | PQ860523 |
| A | CA05 | Goose faeces | *C. albicans* | *C. albicans* | PQ860524 |
| A | CA06 | Goose faeces | *C. albicans* | *C. albicans* | PQ860525 |
| A | CA07 | Goose faeces | *C. albicans* | *C. albicans* | PQ860526 |
| | — | — | — | — | — |
| B | AK01 | Goose faeces | *C. albicans* | *Arthrographis kalrae* | PQ860527 |
| B | BR01 | Goose faeces | *C. albicans* | *Blastobotrys raffinosifermentans* | PQ860528 |
| B | MG01 | Goose faeces | *C. tropicalis* | *Meyerozyma guilliermondii* | PQ860529 |
| B | CA08 | Goose faeces | *C. albicans* | *C. albicans* | PQ860530 |
| B | CA09 | Goose faeces | *C. albicans* | *C. albicans* | PQ860531 |
| B | CA10 | Goose faeces | *C. albicans* | *C. albicans* | PQ860532 |
| B | CM01 | Goose faeces | — | *Cutaneotrichosporon mucoides* | PQ860533 |
| B | AK02 | Stover | *C. albicans* | *Arthrographis kalrae* | PQ860534 |
| B | AK03 | Stover | *C. albicans* | *Arthrographis kalrae* | PQ860535 |
| B | AP01 | Soil | — | *Arxiozyma pintolopesii* | PQ860536 |
| B | AK04 | Soil | *C. albicans* | *Arthrographis kalrae* | PQ860537 |
| B | AK05 | Soil | *C. albicans* | *Arthrographis kalrae* | PQ860538 |
| B | AP02 | Soil | — | *Arxiozyma pintolopesii* | PQ860539 |
| | — | — | — | — | — |
| AA | PK01 | Goose faeces | *C. tropicalis* | *Pichia kudriavzevii* (*C. krusei*) | PQ860540 |
| AA | PK02 | Goose faeces | *C. tropicalis* | *Pichia kudriavzevii* (*C. krusei*) | PQ860541 |
| AA | KM01 | Goose faeces | *C. tropicalis* | *Kluyveromyces marxianus* | PQ860542 |
| AA | AP03 | Goose faeces | — | *Arxiozyma pintolopesii* | PQ860543 |
| AA | CA11 | Goose faeces | *C. albicans* | *C. albicans* | PQ860544 |
| AA | CA12 | Goose faeces | *C. albicans* | *C. albicans* | PQ860545 |
| AA | CA13 | Goose faeces | *C. albicans* | *C. albicans* | PQ860546 |
| AA | CA14 | Goose faeces | *C. albicans* | *C. albicans* | PQ860547 |
| AA | PK03 | Goose faeces | *C. tropicalis* | *Pichia kudriavzevii* (*C. krusei*) | PQ860548 |
| AA | CA15 | Sheep faeces | *C. albicans* | *C. albicans* | PQ860549 |
| AA | CA16 | Sheep faeces | *C. albicans* | *C. albicans* | PQ860550 |
| AA | CA17 | Sheep faeces | *C. albicans* | *C. albicans* | PQ860551 |
| AA | CA18 | Sheep faeces | *C. albicans* | *C. albicans* | PQ860552 |

*Note:* Putative species identification from morphology on CHROMagar *Candida* Plus agar together with the top accession match by NCBI BLAST. The final column indicates the NCBI accession number for each isolate that has been deposited in Genbank.

were all susceptible to voriconazole (<0.06 mg/L). No EUCAST breakpoints are available for caspofungin, but *C. albicans* isolated from sheep faeces were more susceptible to caspofungin than isolates from geese faeces.

### 3.3 | Persistence of *C. albicans* in Agricultural Soil

The three *C. albicans* isolates (CA05, CA10 and CA13) were able to persist in both loam and podzol soils for a minimum of 60 days



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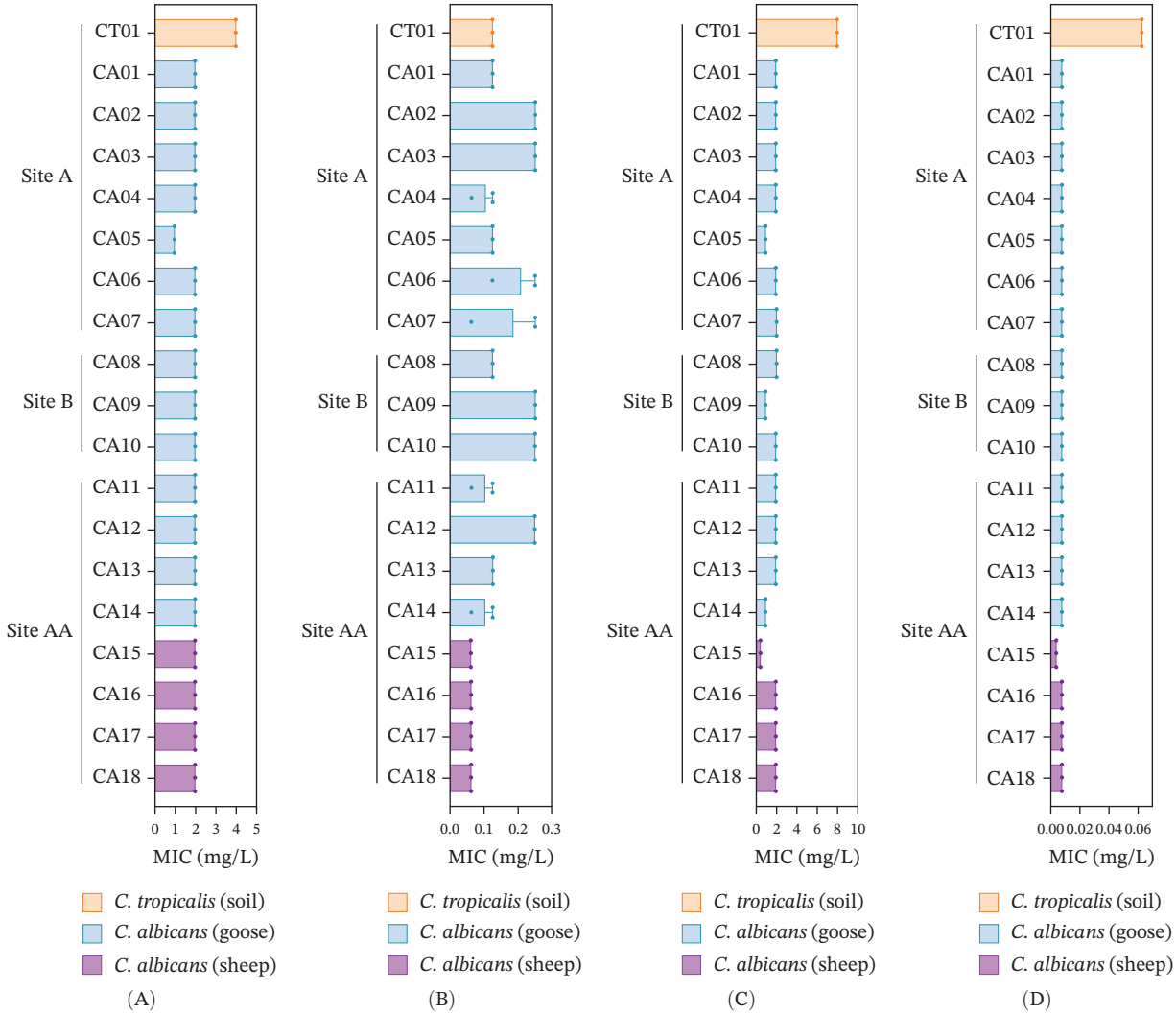


**FIGURE 2** | Minimum inhibitory concentration (MIC) of all confirmed *Candida* isolates from goose and sheep faeces, and soil. (A) Amphotericin B (0.008–4 mg/L), (B) caspofungin (0.008–4 mg/L), (C) fluconazole (0.125–32 mg/L) and (D) voriconazole (0.008–4 mg/L). There were three replicates per isolate, error bars indicate the SEM.

(Figure 3). By day 60, in both soil types, concentrations of *C. albicans* had only decreased by ~1 log CFU/g, with all isolates remaining viable as determined by their recovery on selective media. Log-linear regression models were used to determine the linear decline rate constants (*K*) and decimal reduction times (*D*-values) of the three *C. albicans* isolates in both soil types (Table S1). Although all three isolates remained detectable at high concentrations for the duration of the study, the *D*-values varied, with *C. albicans* isolate CA10 having the lowest *D*-value in podzol (52.8). All isolates recovered from the podzol had higher *D*-values than the isolates recovered from the loam.

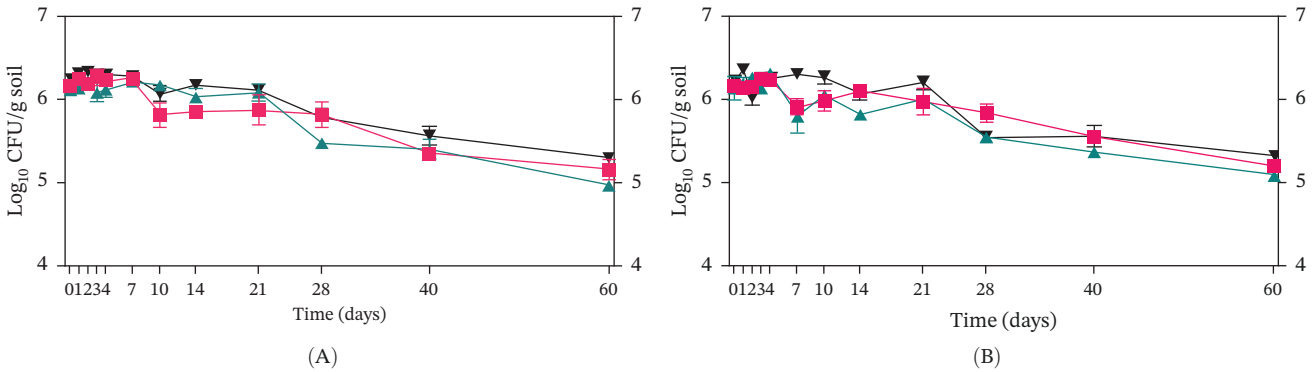


**FIGURE 3** | Persistence of *C. albicans* CA05 (red squares), CA10 (green triangles) and CA13 (black inverse triangles) isolates from goose faeces in (A) loam soil and (B) podzol. Data points represent the mean (n7= 5) ± SEM.



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### 3.4 | Pathogenicity of *Candida* Isolates

All three *C. albicans* isolates were pathogenic in the *G. mellonella* infection model, with the undiluted inoculum causing >95% probability of death within 24 h (Figure 4). Larvae injected with the $10^{-1}$ dilutions had a 5%–20% probability of survival by day 10, with no statistically significant difference between the three isolates; however, survival of larvae injected with the $10^{-2}$ dilution did significantly differ ($p < 0.05$) with *G. mellonella* injected with isolates CA10 and CA13 having a higher probability of survival. At lower concentrations ($10^{-4}$ and $10^{-5}$) there were no significant differences in pathogenicity between the three *C. albicans* isolates, with a probability of larval survival >60% (Figure 4, Table S2). However, injection of larvae with *C. albicans* at the lowest concentrations still had a lower survival probability than being injected with just PBS, which had a 100% survival rate after 10 days.

### 3.5 | Phylogenetic Analysis of *C. albicans* Isolates From Goose and Sheep Faeces Using MLST

Maximum likelihood phylogenetic analysis of the MLST sequences revealed that *C. albicans* isolates from both field sites and from goose and sheep faeces were relatively conserved; however, isolates from the sheep and geese clustered independently from one another on separate clades (Figure 5). The three *C. albicans* isolates from sheep all differed from one another but still clustered closely on the same clade, whilst the isolates from the goose faeces formed two closely related clades (CA01, CA07 and CA09 in one, and CA08, CA11 and CA12 in the other). The closest reference sequences on the same clade are isolates from the USA, Germany and South Korea (DST1085, 414 and 1597, respectively). The two closest sequences, DST1597 from South Korea and DST1085 from the USA, share the same allelic matches for VPS13 and MP1b and AAT1 as some of the isolates in this study (CA07, CA12 and CA18).

The allelic profile of each isolate was compared for each of the seven genes using the *C. albicans* MLST database (Table S3). Comparing the allelic matches for the individual genes indicated some similarities between isolates from geese (CA12) and sheep (CA18) and between two isolates from sheep (CA16 and CA17); however, none of the sequences had exactly the same allelic matches for all seven genes (Table S3).

## 4 | Discussion

Viable isolates of *C. albicans* were isolated from the faeces of migratory pink-footed geese and domestic sheep; however, our data were unable to resolve whether *C. albicans* was being introduced into agricultural environments by the migrating birds or whether sheep are a long-term host and geese are being exposed to *C. albicans* by sharing fields with grazing sheep and their faeces. Alternatively, both geese and sheep may ingest *C. albicans* after being exposed to agricultural soil that has been contaminated via surface water irrigation or flooding, or from the faeces of other species frequenting the sites [20]. However, despite the origin of infection remaining unknown, it is clear that the faeces from migratory geese can act as a potential source of *C. albicans*, and due to the transient habit of these birds, this opportunistic pathogen could be dispersed over a wide geographical range of agricultural and food production environments.

It has been estimated that ~300,000 pink-footed geese migrate from Iceland to Scotland in the autumn [35], although there are also significant populations migrating from Greenland and Svalbard, which together with small numbers of several other migratory geese species, for example light-bellied brent goose and Svalbard barnacle goose, produce a large volume of faecal material deposited into the environment every day. At the second sampling time point, some of the goose faeces remained in the field and continued to test positive for *C. albicans*. These goose faecal pellets were visibly older, partially desiccated and beginning to break down into the soil, indicating that *C. albicans* can persist outside the host for an extended period of time. Despite *C. albicans* being present in multiple faecal pellets at each site visit, it was not recovered from the soil or stover that was in close proximity to the faecal pellets. This suggests that transitory loading of faeces from these migratory birds was the de novo input of *C. albicans* into this environment, and cells had not yet dispersed into the soil from this primary source (e.g., by rain splash).

*C. albicans* has previously been isolated from the oesophagus of geese and ducks [27], and multidrug-resistant *C. albicans* has been associated with disease in several species of tropical birds. Although *Candida* is not generally considered to be zoonotic, geese may be acting as a reservoir for multiple species of *Candida*. The majority of *Candida* isolates recovered from the faeces of pink-footed geese were *C. albicans*, but several other species of opportunistic yeast were also isolated, including *P. kudriavzevii* (formerly *C. krusei*) and *Meyerozyma guilliermondii* (*C. guilliermondii*).

In the environment, *P. kudriavzevii* is often isolated from soils (although not in this study), with some indications that it may even be beneficial for soil health [36]. However, *P. kudriavzevii* is also becoming of increasing concern as an emerging nosocomial pathogen and was added to the WHO Fungal Pathogen Priority List [8] due to its natural resistance to fluconazole and potential to cause opportunistic invasive infections [37]. In this study, a single positive isolate of multidrug-resistant *C. tropicalis* was also recovered from the soil. This species is also on the WHO Fungal Pathogen Priority List and is also commonly isolated from the environment, including in soil [10, 17]. Other isolates from the soil and stover putatively identified as *Candida* were later confirmed as *Arthrographis kalrae* by Sanger sequencing. *A. kalrae* is commonly associated with soils but can cause fungal keratitis, and very rarely more severe infections [38, 39].

Three *C. albicans* isolates recovered from goose faecal pellets were used to simulate the delivery of *C. albicans* in goose faeces into agricultural soils. All three isolates persisted at fairly high concentrations for at least 60 days, indicating that once shed from a host, *C. albicans* can persist and remain culturable in the environment. Importantly, *C. albicans* was equally able to tolerate the edaphic conditions of both the loam and the more acidic podzol, with no difference in the decay rate over 60 days. *C. albicans* can dimorphically switch between yeast and hyphal forms, which is usually triggered by a change in environmental and nutritional cues and is characterised by an increased adaptability and pathogenicity [40]. Therefore, when *C. albicans* leaves a host in its faeces and subsequently enters the soil environment, with stressors such as changes in temperature and pH, it may switch from



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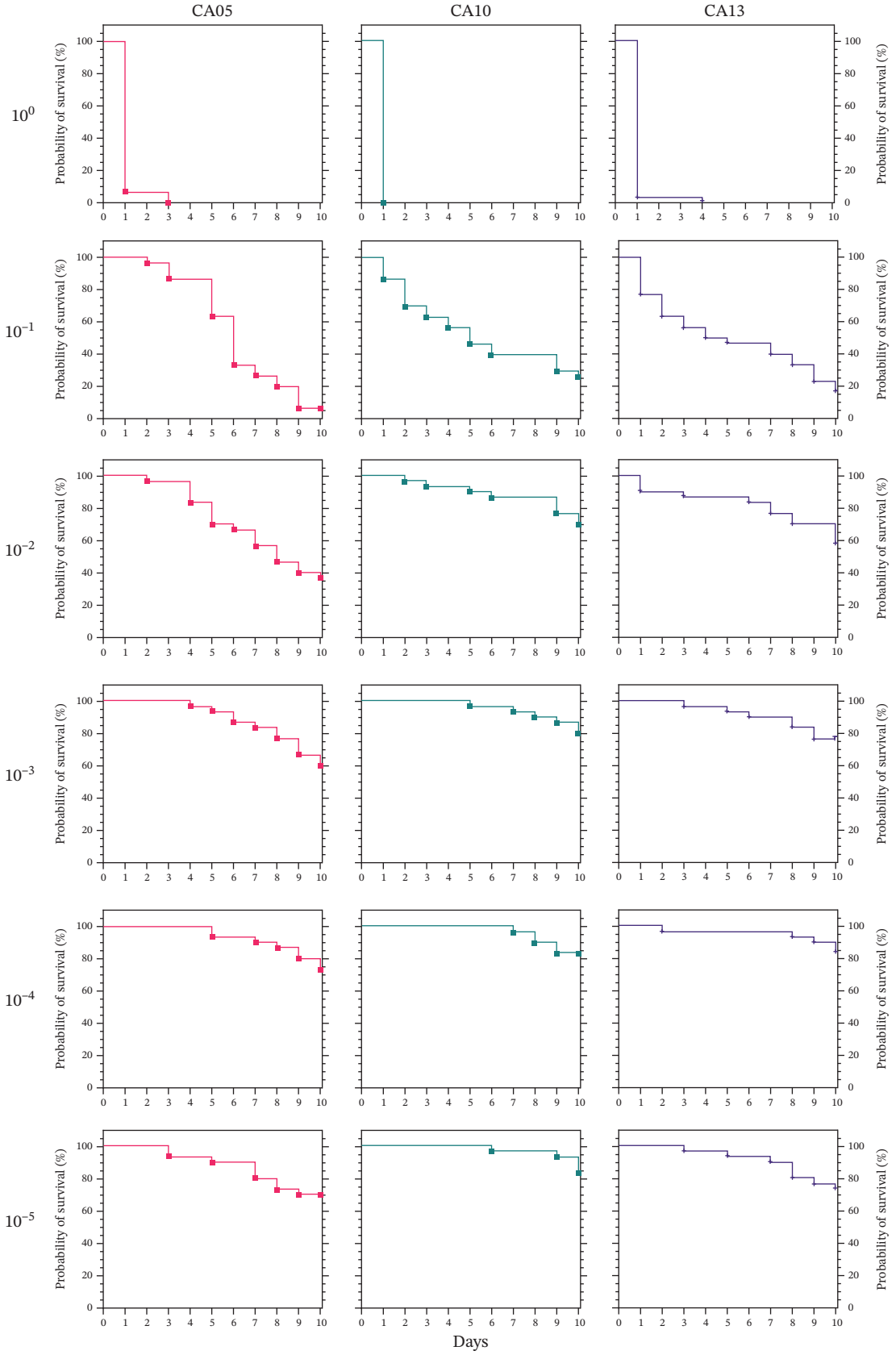


**FIGURE 4** | Kaplan–Meier survival curves for a *Galleria mellonella* infection model challenged with three *C. albicans* isolates. Initial undiluted ($10^0$) concentrations were $6.17 \times 10^6$/injection for CA05, $1.07 \times 10^7$/injection for CA10 and $8.50 \times 10^6$/injection for CA13, and a series of 10-fold dilutions down to $10^{-5}$ were used as inoculum. Survival was recorded over 10 days. Each line represents the survival proportion of 30 *G. mellonella* injected with a 10-fold dilution for each concentration.



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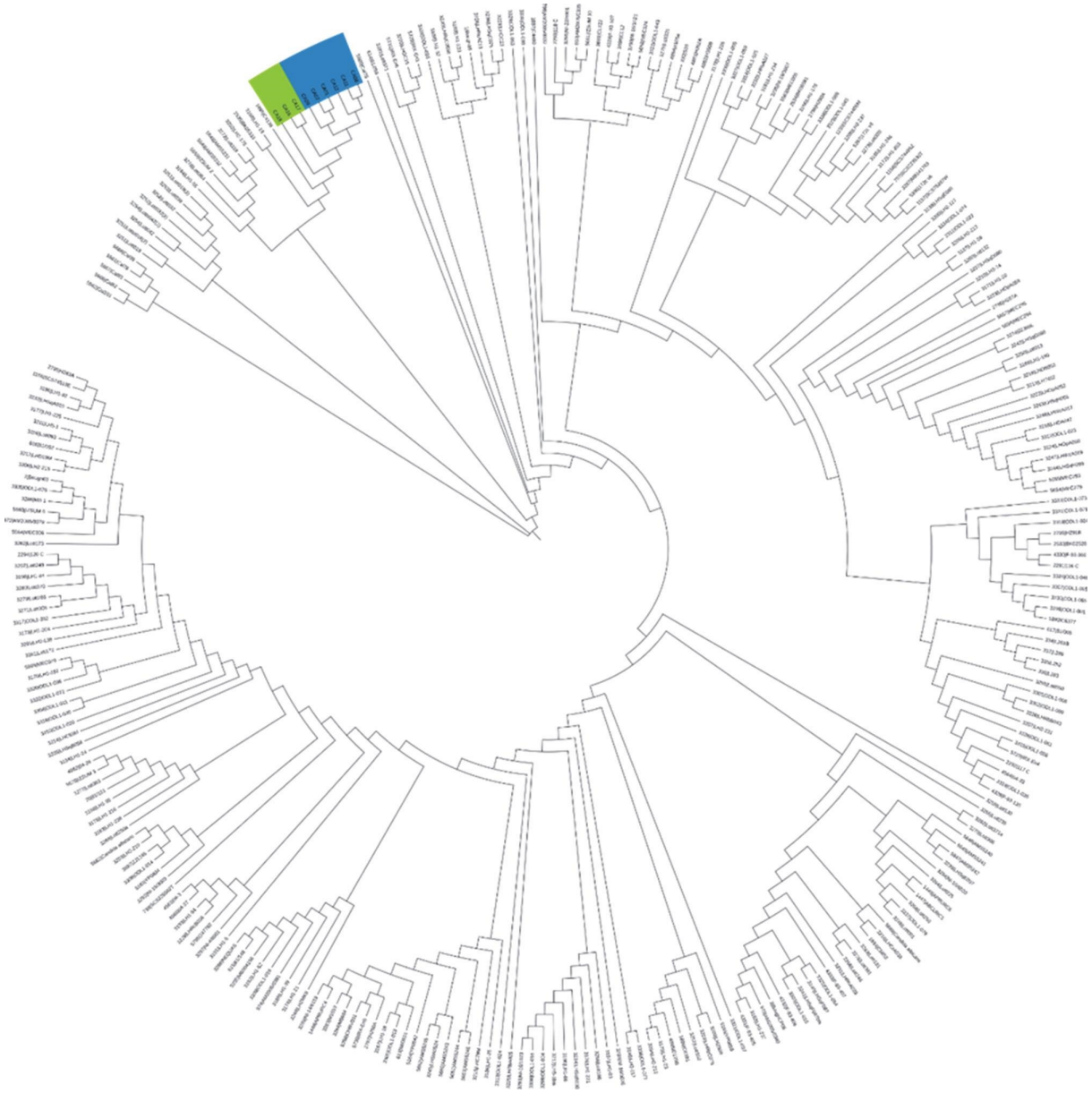

**FIGURE 5** | Maximum likelihood phylogenetic analysis of seven *C. albicans* isolates from goose and sheep faeces and 300 known *C. albicans* isolates. *C. albicans* isolates from geese and sheep faeces are highlighted in blue and green respectively. Sequences were aligned using MUSCLE and the phylogenetic tree was generated using 500-bootstrap iterations in MEGA X. Isolates CA05, CA10 and CA13 were excluded from analysis as good quality VPS13 sequences were not obtained.

one morphological form to the other in a way that is beneficial for its long-term environmental survival.

All sequenced isolates of *C. albicans* from goose faeces clustered together using an MLST analysis approach, and although all three of the sequenced isolates from sheep faeces clustered independently from the goose isolates, they were positioned on a neighbouring clade of the maximum likelihood phylogenetic tree. When compared to ~300 reference *C. albicans* sequences, all the isolates from this study clustered closely together, indicating a higher degree of relatedness between the isolates recovered from both the geese and sheep faeces. Furthermore, analysis of individual genes indicated several allelic matches between the different isolates, with one goose and one sheep isolate sharing four out of seven allelic matches. Although the sequences clustered by either goose or sheep host, they were closely aligned to each other. It has previously been shown that *C. albicans* sequences do not cluster into species-specific lineages [41], despite some degrees of separation, as observed here. The close relatedness between the different isolates from this study and the isolates from the USA, Germany and South Korea potentially provides evidence that animals could be reservoirs of *C. albicans* isolates that can also cause human infection [42], in a similar way to the transmission patterns of *C. glabrata* between gulls and humans [43].

Although no *C. albicans* were detected in the limited soil samples collected at either site in this study, potentially pathogenic *C. albicans* isolates can persist in soil, which allows them to come into contact with a range of mammalian and avian hosts in a shared environmental space [21]. Agricultural soils are also likely exposed to fungicides, for example, through the spraying of crops,



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seed coating applications, or through irrigation with potentially contaminated surface waters (e.g., rivers) containing fungicide residues [44]. Constant exposure to trace amounts of fungicides in the soil could induce adaptive changes in *C. albicans* introduced into the soil via faeces, potentially resulting in enhanced resistance or increased virulence of the fungal pathogen [6]. This could be further exacerbated by environmental stresses such as pH changes and extremes of temperature, as *C. albicans* responds differently to antifungal exposure when under stress in acidic environments [45, 46], such as the podzol soil.

## 5 | Conclusion

The unrestricted movement of migratory birds provides significant opportunity for the widespread dissemination of pathogens [47]. The cross-boundary nature of animal migration increases the geographical transmission of emerging pathogens, or novel variants of common pathogens (e.g., with enhanced drug resistance or virulence), by facilitating exposure to new hosts or environments. Here we have demonstrated the presence of viable isolates of *C. albicans* in the faeces of migratory geese deposited in agricultural fields, which were subsequently able to survive in agricultural soils for an extended period. Environmental persistence of *C. albicans* has the potential to facilitate transmission between animal species or humans despite them never actually coming into direct contact with each other. Such zoonotic potential of an opportunistic pathogen such as *C. albicans* in agricultural systems could be further intensified by repeated exposure to low levels of fungicides and the potential to develop resistance to antifungals.

### Author Contributions

**Luke Woodford**: conceptualisation, investigation, methodology, data curation, formal analysis, writing – original draft preparation. **Craig J. Engelbrecht**: investigation, writing – reviewing and editing. **Maiken Skov**: investigation, writing – reviewing and editing. **Richard S. Quilliam**: conceptualisation, writing – reviewing and editing, supervision.


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### Disclosure

The funder had no role in study design, data collection and analysis, the decision to publish, or the preparation of the manuscript.

### Ethics Statement

Ethical approval for this project was authorised by the General University Ethics Panel (Ref. GUEP 6748) from the University of Stirling.

### Conflicts of Interest

The authors declare no conflicts of interest.

### Data Availability Statement

All data are available from authors upon request.

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## Supporting Information

Additional supporting information can be found online in the Supporting Information section. (*Supporting Information*)

Table S1: Linear decline analysis of persistence of *Candida albicans* isolates in loam and podzol soils. Table S2: Log-rank statistical analysis for the Kaplan-Meier survival curves for each 10-fold dilution. Table S3: Allelic matches for 12 *C. albicans* isolates using seven housekeeping genes. Figure S1: All fungi identified by ITS Sanger sequencing from CHROMagar *Candida* Plus agar colony isolation.



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