Individual repeatability in dietary specialisation across years and competitive regimes in wild birds

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Abstract

Dietary variation reflects fitness trade-offs shaped by environmental conditions and individual traits. According to optimal foraging theory, individuals should specialise when profitable prey is abundant, yet empirical evidence remains limited. We hypothesised that specialisation is driven by individual personality and competition intensity. Following the pace-of-life syndrome (POLS) framework, we predicted that ”faster” explorers, often securing higher-quality habitats, would show greater specialisation than ”slower” explorers, and that selectivity would in- or decrease with competition intensity. We tested this in sympatric breeding blue (*Cyanistes caeruleus*) and great tits (*Parus major*) by combining breeding density manipulations with DNA metabarcoding of faecal samples. By quantifying environmental arthropod abundance, we identified preferred prey as those used proportionally more than available. Contrary to our predictions, specialisation was unrelated to exploration behaviour or competitive intensity. Crucially, however, we found strong individual repeatability in specialisation across years within these relatively short-lived species. While specialisation appears independent of risk-taking personality and experimental densities, this high longitudinal consistency reveals that individuals maintain distinct dietary compositions regardless of environmental or behavioural drivers. These findings call for studies addressing the ecological and evolutionary forces maintaining individualised dietary specialisation in the wild.

Keywords: dietary specialisation, competition, optimal foraging, behaviour, exploration

Introduction

Understanding why individuals vary in dietary specialisation remains a central challenge in evolutionary ecology. Explanations for this variation typically involve fitness-related trade-offs derived from optimal foraging theory (Charnov, 1976; Pyke et al., 1977). This framework predicts that individuals should base prey selection on profitability and encounter rates. Thus, a focal prey item should only be included in the diet when its profitability exceeds a threshold determined by the availability of more profitable alternatives (Charnov, 1976; Krebs et al., 1977; MacArthur, 1984). Consequently, dietary specialisation is predicted to emerge from a dynamic interplay between external ecological constraints and internal, individual-specific traits.

Competition is a primary environmental driver predicted to shift these foraging trade-offs (Araújo et al., 2011). Under the compression hypothesis, high intra- and interspecific competition reduce encounter rates with profitable prey, forcing animals to expand their diet breadth (MacArthur & Pianka, 1966). Conversely, the niche variation hypothesis predicts that competition can actually increase individual specialisation, as individuals diverge to avoid overlap (Van Valen, 1965). This theoretical ambiguity highlights the need for large-scale experimental manipulations of competitive regimes to clarify how density-dependent pressures truly reshape foraging strategies in the wild.

Beyond environmental drivers, dietary decisions can be influenced by internal traits that change the benefit to cost ratio of specialisation (Toscano et al., 2016). Life-history theory predicts that selection favours the integration of behaviour and life-history into an overarching pace-of-life syndrome (POLS), where ”faster” (compared to ”slower”) individuals facilitate high resource acquisition through increased risk-taking (Réale et al., 2010; Stearns, 1998). Because fast-paced individuals prioritize current over future reproduction, they require high energy intake (Charnov, 1976; Stearns, 1998). In wild passerines, faster types are more dispersive and successful at securing high-quality habitats (Both et al., 2005; Duckworth & Badyaev, 2007; Korsten et al., 2013). We therefore expected faster individuals to specialise on more profitable prey.

We tested this hypothesis in blue (*Cyanistes caeruleus*) and great tits (*Parus major*); study systems with extensive knowledge of personality and diet (Krebs et al., 1977; Mouchet & Dingemanse, 2021; Pagani-Núñez et al., 2016), where key factors can be experimentally decoupled. These species compete for nesting sites and food, but differ distinctly in their life-history and ecological strategies (Branston et al., 2021; Corsini et al., 2022; Dhondt, 2012). Blue tits generally have a faster strategy,

as they are bolder and more aggressive, exploit a wider range of arthropods, and forage more extensively in canopy foliage (Bookwalter et al., 2023; Perrins, 1979; Török & Tóth, 1999). We quantified exploration behaviour (a proxy for risk-taking; (Hollander et al., 2008; Stuber et al., 2013)) and tested whether key behavioural and ecological drivers of species differences also explain dietary variation among individuals within and among these species.

Crucially, the hypothesized drivers of diet are hierarchically structured (Dingemanse et al., 2010; Réale et al., 2026; Van de Pol & Wright, 2009). That is, behavioural traits vary within individuals (e.g. across life stages) but also among individuals (e.g., over time). For example, tit parents are repeatable in provisioning behaviour (Mutzel et al., 2013; Santema et al., 2024) but also plastically adjust their provisioning to nestling age, for example, in terms of arthropod composition (García-Navas et al., 2012; Naef-Daenzer et al., 2000). Similarly, environmental conditions like competitive regimes fluctuate among and within hierarchical levels, such as populations and years (Bolnick et al., 2003; Nicolaus et al., 2016). As we hypothesize trait- and environment-specific cost-benefit ratios, we thus also expect dietary variation among species, populations, life-stages and individuals.

To test this framework, we combined multi-year breeding density manipulations with faecal collections from wild birds and environmental samples from frass collectors. We subjected both sample types to DNA metabarcoding (Höhn et al., 2024; Rytkönen et al., 2019) to quantify prey availability and actual consumption. Comparing them confirmed that caterpillars dominate the diet of both tit species, validating our comparison between environmental frass collections and bird diet. By identifying prey taxa eaten significantly more than expected by random, we were able to quantify variation in consumption of ”preferred” prey across years and competitive regimes. We collected data of the same individuals across years to assess whether foraging strategies were repeatable and/or plastic to test three main predictions: first, that an individual’s speed of exploration behaviour positively predicts degree of specialisation on preferred prey; second, that specialisation changes with breeding densities; and third that the relative amount of consumed preferred prey positively impacts reproductive fitness. By combining individual behavioural phenotypes with population-level density dependence and prey measurements, this study clarifies the ecological mechanisms that maintain dietary variation in wild populations.

Material and methods

Field methods

Study site and species. We conducted the study in a deciduous forest area in the south-west of Munich, Germany (48°2'49"N, 11°27'40"E). The site consists of 420 nest boxes distributed across six plots, each containing two subplots with 70 nest boxes each, and has been monitored since 2019 (Gaona-Gordillo et al., 2026). We studied blue and great tits, two small passerines that breed in sympatry and compete for nesting sites and foraging habitats (Dhondt, 2012). Both are secondary cavity breeders that readily breed in nest boxes (Lambrechts et al., 2010). During the breeding season, caterpillars from families such as Geometridae and Tortricidae constitute a major key dietary component affecting nestling growth (García-Navas & Sanz, 2011; Höhn et al., 2024; Naef-Daenzer et al., 2000).

Population monitoring and personality assessment. In 2023 and 2024, we monitored our population twice a week beginning in late March, determining clutch size (number of eggs when the clutch is complete) and hatching date (day the first nestling hatches; Verhulst et al., 1995). Adult breeders were captured at the nest box using a spring trap ten days after hatching, identified, and fitted with a ring if they had not been ringed previously. Individual nestling morphology and weight were taken on day 14 for great tits and day 15 for blue tits (hereafter referred to as day 15; Perrins, 1979). From day 19 onward, nest boxes were visited daily to check if the nestlings had fledged (Perrins, 1979; Van Balen, 1973). Nests were considered successfully fledged when no signs of predation (e.g. destroyed nests, feathers, dead nestlings) were present (Van Balen, 1973). In 2023 and 2024, we recorded 140 measures of fledging success for blue tits and 138 for great tits.

Personality assessment Ten days post-hatching, we measured exploration behaviour in adult breeders using a standardized cage test (Stuber et al., 2013). Following a 1-minute acclimation period, we recorded the number of position changes within the cage over a two-minute interval using BORIS software (GoPro Hero8, model SPJB1; Araya-Ajoy et al., 2016; Friard and Gamba, 2016). Between 2023 and 2024, we collected 534 observations for blue tits (137 individuals; 73 females, 64 males) and 235 for great tits (188 individuals; 91 females, 97 males). Because we captured many individuals across multiple breeding attempts and years, these repeated measurements allowed us to partition behavioural variation into repeatable among-individual differences (personality) and within-individual plasticity (Dingemanse et al., 2010).

Experimental density treatment. To manipulate breeding density, we varied intra- and interspecific

densities of nest boxes across six plots, each containing two subplots (Figure 1, Gaona-Gordillo et al., 2026). To control occupancy, we used species-specific nest boxes with entrance diameters of 28 mm for blue tits (B) and 32 mm for great tits (G) (Dhondt, 2010). Nest box densities were manipulated at the subplot level with low (L; 10 boxes) or high (H; 25 boxes) densities for each species, resulting in a full-factorial design: B_LG_L, B_LG_H, B_HG_L, and B_HG_H (Figure 1). Treatments were randomly reassigned each breeding season. As tits are territorial and show high site-fidelity, this design ensured that individuals experienced different competitive environments over time (Abbey-Lee & Dingemanse, 2019). This allowed us to test for within-individual plasticity while preventing density treatments from being confounded with fixed plot characteristics or local habitat quality (Gaona-Gordillo et al., 2026).

Dietary and environmental sampling

Adult and nestling diet. Adult faecal samples were collected as part of the exploration test. The floor of the exploration cage and side compartment was lined with paper sheets for faecal collection and replaced for each bird. Samples were collected using wooden toothpicks and stored in 95% ethanol. If no sample was present in the cage, we checked the bird bag or attempted collection while measuring morphology (no sample obtained for 157 individuals). Nestling samples were collected on days 10 and 15 post-hatching during the collection of nestling morphometric data. Faecal sacs were pooled per nest and ruptured with a wooden toothpick to ensure preservation (Rytkönen et al., 2019; Verkuil et al., 2022). No faecal samples could be obtained from 53 nests. Across 2023 and 2024, we collected 853 samples: 386 from blue tits (148 adults (78 females, 70 males), 233 nestling pools (123 day 10, 110 day 15)) and 467 from great tits (218 adults (109 females, 109 males), 229 nestling pools (129 day 10, 100 day 15)).

Prey abundance. Prey abundance was estimated by sampling frass, the droppings of canopy-defoliating arthropods, following established methods (Fischbacher et al., 1998; Tinbergen & Dietz, 1994; Visser et al., 2006). In early April, we installed one collector per subplot (Figure 1), placing each under an oak tree (*Quercus robur*) to account for canopy variation (Mägi et al., 2009). Each collector consisted of a 1 m^2 wooden frame spanning a cheesecloth funnel that directed frass into a capped tube (Nadolski et al., 2021). The cap contained a small piece of cloth to allow moisture evaporation and drainage during rainfall. Samples were collected twice weekly (or on the first dry day following rain), dried at room temperature for 24 h (additional 12 h if necessary) and sequentially sieved (2 mm and 0.5 mm meshes). Following Blondel et al. (1991), samples were rolled down an angled glass plate to separate frass from debris, and remaining contaminants (seeds, larvae, stones)

were removed under a stereomicroscope. Eight samples were lost due to vandalism in 2023, resulting in 236 samples over both years.

Environmental controls and sample storage. To control for airborne environmental DNA contamination during processing, we collected a weekly control sample following the same procedures used for biological material but without adding sample matter. All samples (diet, frass, control) were stored in 95% ethanol at -20 °C.

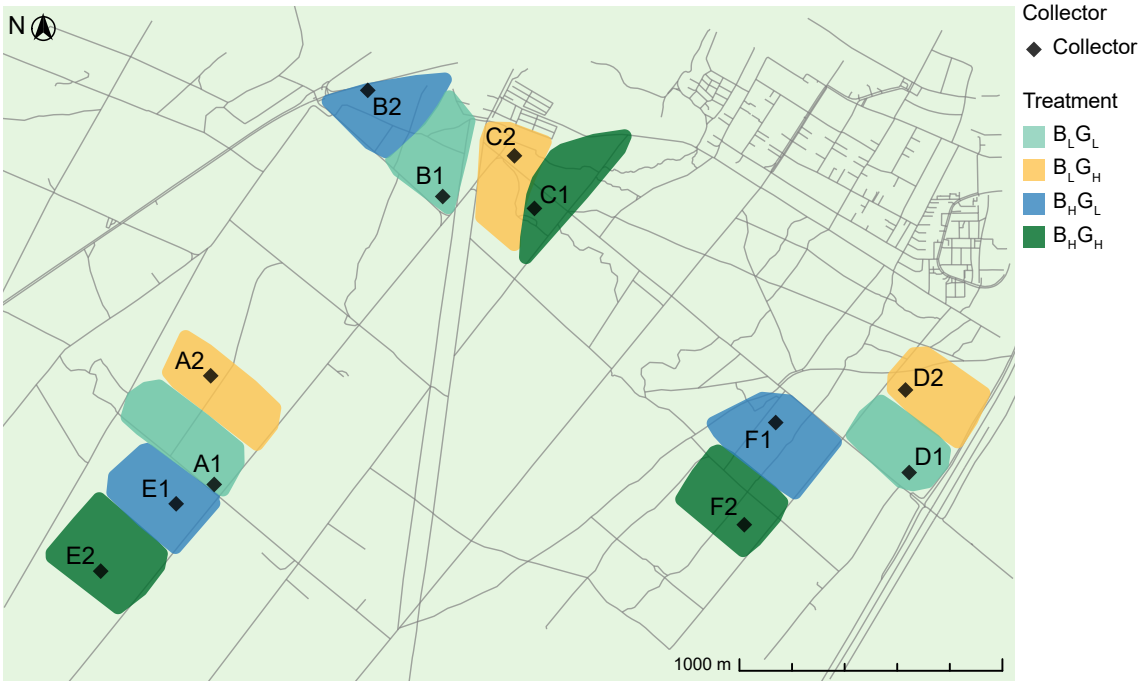

Figure 1: Study setup with location of frass collectors. Letters indicate plot (A, B, C, D, E, F) and numbers subplot identity (1 or 2). We show the density treatments applied in 2023 with colours indicating: low nest box density for blue and great tits (light green; B_LG_L), low density for blue tits and high density for great tits (yellow; B_LG_H), high density for blue tits and low density for great tits (blue; B_HG_L) and high density for both species (dark green; B_HG_H).

DNA extraction, metabarcoding and sample processing

DNA was extracted using the Qiagen Blood and Tissue Kit in 96-well format following the manufacturer's protocol. The 5P region of the mitochondrial COI gene was amplified with the primers mlCOIntf and dgHco (Folmer et al., 1994; Leray et al., 2013). Oligonucleotide indices were attached in a second amplification step using Supreme NZYTaq 2× Green Master Mix (NZYTech). Negative and positive controls were included in each library. Libraries were pooled in equimolar amounts based on Qubit dsDNA HS Assay quantification (Thermo Fisher Scientific) and sequenced on a NovaSeq PE250 flow cell (Illumina) targeting approximately 15 gigabases. Library preparation and sequencing were carried out by AllGenetics & Biology SL. Bioinformatic processing followed the

metabarcoding pipeline of Leonhardt et al. (2022). Reads were merged, quality filtered (ee > 1), length filtered (200–500 bp), dereplicated and denoised into amplicon sequence variants (ASVs) using VSEARCH v2.18.0 (Rognes et al., 2016). Taxonomy was assigned through iterative alignments against reference databases of German and Central European invertebrates (Keller et al., 2020) and the BOLD database (Ratnasingham & Hebert, 2007). Only sequences classified as invertebrates (Arthropoda and Mollusca) were retained, and classifications not resolved to at least family level were excluded. Low-abundance filtering removed ASVs representing $< 0.2\%$ of reads per sample. Filtered read counts were converted to relative abundances. For analyses of diet composition, reads were aggregated at the taxonomic level of order, while analyses of preferred prey were conducted at the family level. Samples with insufficient DNA or sequencing errors were excluded from further analysis. Detailed sequencing protocol information including database construction details, pipeline steps, failure diagnostics, and R processing can be found in the electronic supplementary material (ESM; Section 1).

Statistical analysis

All analyses were performed in R (v4.4.3) using Bayesian mixed models implemented in STAN Stan Development Team, 2025. Models were fitted with four chains using weakly informative priors, with 2,000 warm-up and 3,000 sampling iterations (increased to 3,000 warm-up and up to 6,000 for complex models). Statistical significance was determined based on whether 95% credible intervals overlapped zero Bürkner, 2017. Residual variances for the Beta and Bernoulli distributions were calculated following Nakagawa and Schielzeth (2010). Analyses were restricted to first broods (defined as clutches initiated within 30 days after the first clutch of the year; Noordwijk et al., 1995). In three cases where frass samples were split across multiple tubes for storage and barcoding, one tube per sample was randomly selected. Detailed model structures are provided in the ESM (Section 2). The subsequent analysis was performed in two parts, first verifying key assumptions followed by prediction testing:

Variation in general diet. We analysed variation in the relative read abundance (response variable) using zero-inflated Beta hurdle models. Fixed effects included species, competitive treatment (low/high density), bird type (female, male, nestling day 10, nestling day 15), date, and year. Random effects accounted for repeated sampling within broods and spatio-temporal variation among subplots. Models were fitted separately for each of the five most abundant prey orders, both across the full dataset and for each tit species.

Identification of preferred prey in the diet. To classify prey families as preferred, we compared

the relative abundance of potential prey in the environment (frass) versus bird diet (faecal samples). From 194 families detected in frass and 307 families detected in bird faecal samples, we retained 28 candidate prey families known to include canopy defoliators (Table S34, S35; GBIF, 2025; iNaturalist, 2025). Data for these families were extracted from the bird diet data set, with zeros imputed for Curculionidae (absent from faecal data); relative abundances were then recalculated based only on these 28 families for each sample. We used a zero-inflated Beta hurdle model with the relative abundances of each family from all samples as the response variable. We fitted the fixed effect of source (frass vs. faeces) to determine whether tits consumed a family significantly more than its relative abundance in frass. We included year and date as fixed effects, while controlling for spatio-temporal effects using random effects of location (nest box or frass collector), year, and subplot–year. From this, a "proportion of preferred prey" index was calculated for each sample by summing the relative abundances of preferred families and dividing by the total abundance of the 28 defoliator families.

Variation in preferred prey. To identify the sources of variation in preferred prey, we applied the same analysis as detailed above (section variation in general diet).

Personality, specialisation and competition. To examine how personality and competitive environments influenced diet, we fitted errors-in-variable models, an approach to resolve multiple connected equations simultaneously (while avoiding attenuation bias; see Dingemanse et al., 2021; Martin et al., 2025; Ponzi et al., 2018). In the first equation, exploration behaviour was modelled with a Gaussian error distribution, including test sequence, time since sunrise, sex, and species as fixed effects, and individual identity and subplot–year fitted as random effects. In the second equation, the proportion of preferred prey was modelled using a zero-inflated Beta hurdle distribution. To test whether behavioural differences influenced diet specialisation, the mean best linear unbiased predictor (BLUP) of the individual exploration score from the first equation was linked as a predictor in the second equation, along with competitive treatment, their interactions, date, year, and species. For the second equation we fitted the random effects of individual identity and subplot–year combinations. These analyses were repeated separately for each species and sex, incorporating nestling diet as the response for the second equation to assess parental influence.

Specialisation and reproductive success. To test if the relative amount of consumed preferred prey impacts reproductive fitness, we fitted a bivariate mixed model where the first equation modelled the proportion of preferred prey (zero-inflated Beta hurdle) and the second modelled individual nestling weight at day 15 (Gaussian distribution). Similar to the behavioural models, the mean individual

BLUP of the preferred prey index for each brood ID from the first equation was used as a predictor in the second equation to test its influence on brood survival. Models further included competitive treatment and its interactions with diet composition as fixed effects, with random effects accounting for repeated sampling within broods and subplot–year combinations. Directional selection gradients were calculated after Lande and Arnold (1983). We repeated the same bivariate mixed model for the total weight of a brood (sum of nestling weights; Gaussian) and fledging success (0/1; Bernoulli distribution). For the logistic regression of fledging success, we estimated the selection gradients following Janzen and Stern (1998). All analyses were repeated separately for each species.

Results

Variation in diet and preferred prey

Variation in general diet. The five most abundant orders out of 34 total orders of prey in tit diet were Lepidoptera, Diptera, Hymenoptera, Coleoptera and Araneae (Table S33). Species (blue vs. great tits) and life stages (nestlings vs. adults) differed in the relative abundance of these arthropod orders in their faeces (measured as the proportion of DNA reads assigned to each taxon; Table S4 - S6). Blue tits had relatively more Araneae in their faeces, while great tits had more Diptera, Hymenoptera and Coleoptera (Figure 2; S7). Blue tits adults had relatively more Araneae and Coleoptera, while nestlings had more Lepidoptera, Diptera, Hymenoptera, in their faeces (Figure 2; Table S8). Great tit adults had relatively more Lepidoptera, Coleoptera and Araneae in their faeces, while nestlings had more Diptera (Figure 2; Table S9). Blue tit nestlings at day 10 had relatively more Lepidoptera, and nestlings at day 15 Hymenoptera, in their faeces (Table S8). Great tit nestling diet did not differ between day 10 and 15 (Table S9). Brood identity in blue tits explained approximately 6% of the variation in Diptera, Araneae, Coleoptera and $\sim$ 15% in Lepidoptera and Hymenoptera. In great tits, brood and spatio-temporal effects explained 10% of the variance in Hymenoptera and 5–10% of the variance in Lepidoptera, Diptera, Araneae, and Coleoptera. For blue tits, spatio-temporal effects explained between 10 and 22 %. Within-brood effects explained 66 % of variation for Lepidoptera in great tits and less than 5% of the variation in all remaining arthropod orders in great tits and across all arthropod orders in blue tits. (Table S8, S9).

Identification of preferred prey in the diet. Of the 28 families, both species showed higher proportions of Geometridae in their diet than expected based on our environmental (frass) sampling (Figure 3, 5, Table S10 - S15). Blue tits had higher proportions of Noctuidae, and great tits higher proportions of Erebidae in their diet than expected.

Variation in preferred prey. Great tits consumed higher proportions of preferred prey (= families more abundant in their diet than expected) than blue tits (Table S19). Blue and great tit proportions of preferred prey did not vary between females and males or nestlings at day 10 and 15, but differed between nestlings and adults (Table S20, S21). Nestlings consumed larger proportions of preferred prey than the adults. The proportions of the preferred prey did not vary depending on the intensity of competitive treatment (Table S19 - S21). Variation in proportion of preferred prey was mainly explained by the variation within broods, explaining 88% of the total variation in blue and 92% in great tits, with spatio-temporal effects explaining $\sim$ 1% (Table S20, S21).

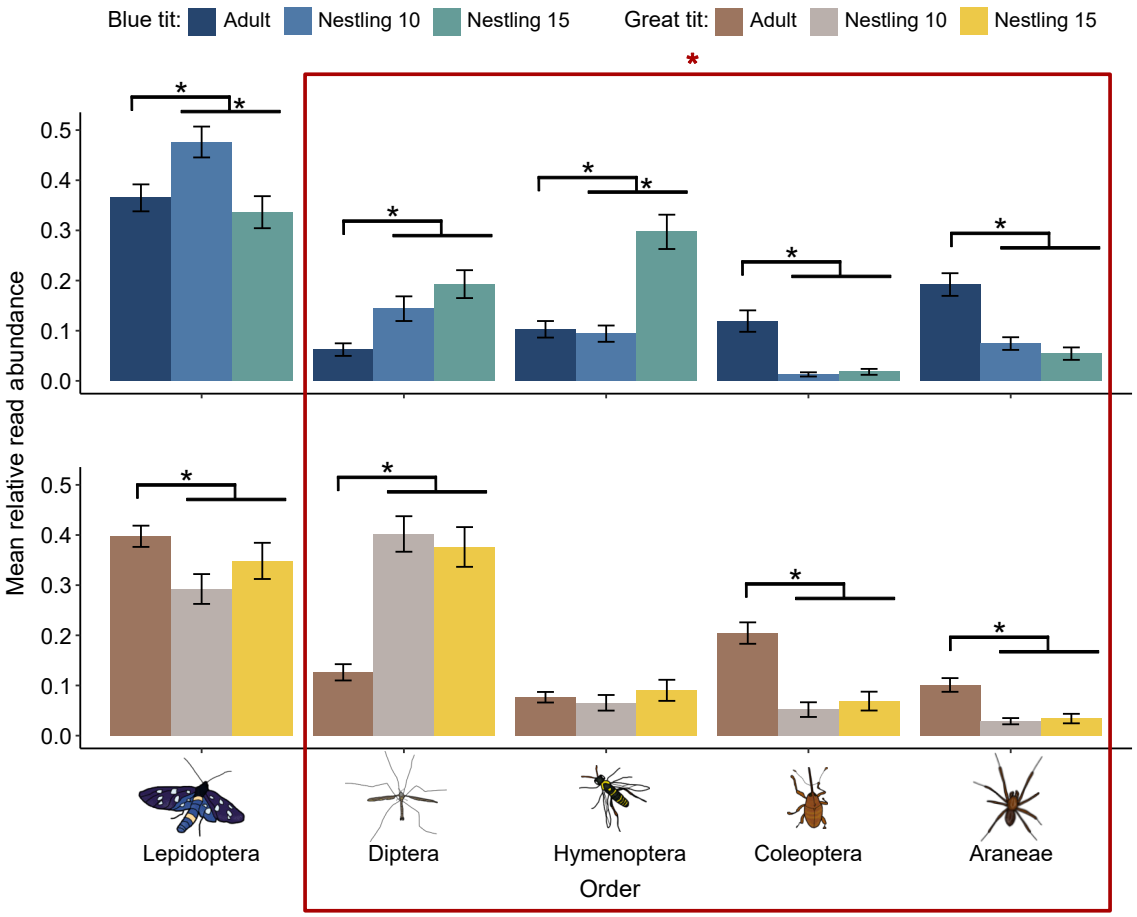

Figure 2: Mean diet compositions of blue and great tits for the five most abundant orders in their diet. On the X-axis are the diet orders and on the y-axis their mean read abundance per species and age class with blue tits adults (dark blue), nestlings measured at day 10 (nestling 10, blue), nestlings measured at day 15 (nestling 15, mint) and great tits with adults (brown), nestlings at day 10 (grey) and nestlings at day 15 (yellow). Significant differences between adults and nestlings and between nestlings at day 10 and day 15 are shown with a black $*$. Species differences are depicted with a red box spanning both compositions, significant difference is shown with a red $*$. These five most abundant orders are visualized using a drawing of an exemplary species in its adult stage: tiger moth (Lepidoptera), crane fly (Diptera), sawfly (Hymenoptera), weevil (Coleoptera) and sheet-weaver (Araneae). Number of faecal samples = 853 (blue tit = 386, great tit = 467).

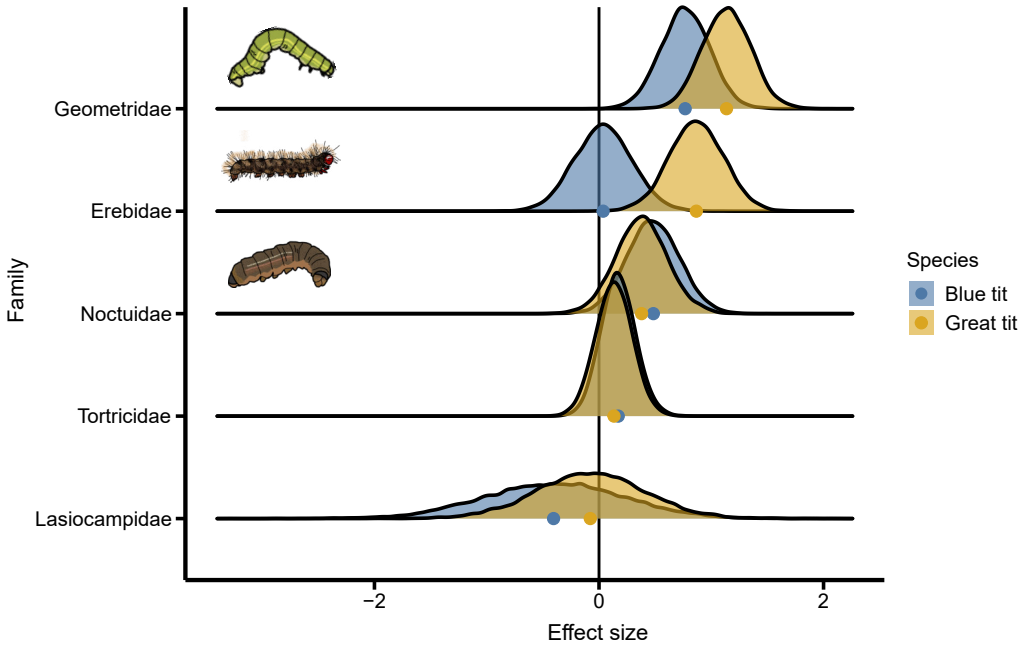

Figure 3: Ridge line plot showing effect sizes (X-axis) with posterior distributions across the main prey families (Y-axis) identified from the literature (Geometridae, Noctuidae, Tortricidae, Lasiocampidae; García-Navas and Sanz, 2011; Höhn et al., 2024; Pagani-Núñez et al., 2016) and our analysis (Erebidae), based on environmental frass samples. For a full listing of all 28 families see Figure 5. Points indicate posterior means, with ridge line densities showing the full posterior distributions. There is strong evidence for prey preference when intervals do not overlap zero (vertical line) and the estimate is positive. For those families, exemplary visualization is shown. Results are shown separately for blue tits (blue) and great tits (yellow). Number of samples = 1089 (frass = 236, blue tit = 386, great tit = 467).

Personality, specialisation and competition

The proportion of preferred prey did not vary with an individual's average exploration behaviour (personality). The main effect of density treatment also did not explain variation nor did its interaction with personality (Table S22 - S24). Individual exploration behaviour did not influence the proportion of preferred prey in their own diet or that consumed by their nestlings (Table S25, S26). Individuals in both species were highly repeatable in the proportion of preferred prey (adjusted R: blue tit = 0.865, great tit = 0.803). Spatio-temporal effects explained around $\sim$ 5% of the variation (Table S22 - S26).

Specialisation and reproductive success. Individual nestling weight, total brood weight and fledging success of a brood was not dependent on the proportion of preferred prey in nestling diet of both species (Table S27 - S32). Brood identity explained 37% of variation in individual nestling weight in blue and 29 % in great tits. Spatio-temporal effects explained $<$ 11 % in individual nestling weight and total weight of the brood in both species. For fledging success spatio-temporal effects explained 19% in blue tits and 16% in great tits. Standardised selection gradients for the proportion

of preferred prey did not differ significantly from zero in any treatment for nestling weight, total brood weight or fledging success.

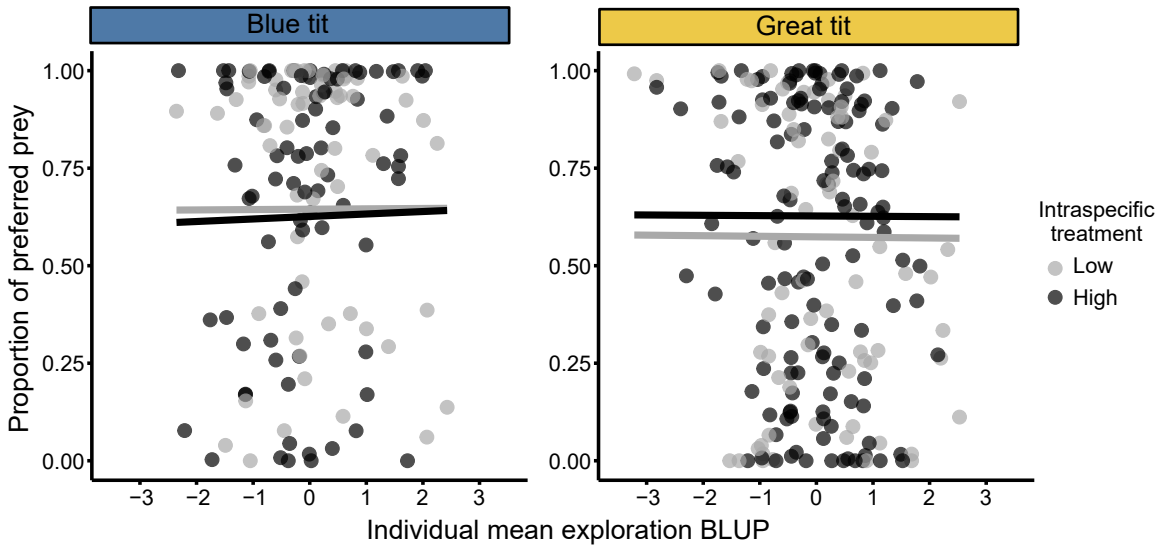

Figure 4: Proportion of preferred prey consumed by adult birds in relation to individual mean exploration behaviour and competitive environment. Exploration scores on the x-axis are expressed in units of among-individual standard deviations of the BLUP (best linear unbiased predictor), such that one unit corresponds to one standard deviation difference between individuals. The y-axis shows the proportion of preferred prey in the diet. Panels show results for blue tits and great tits. Colours indicate intraspecific competition treatment, with light grey representing low competition and dark grey representing high competition. Regression lines show the relationship between diet composition and exploration behaviour under each competitive treatment. Number of observations blue tit = 145 and great tit = 207.

Discussion

Our study reveals an unexpected ecological pattern: wild blue and great tits maintain highly repeatable individual differences in dietary preferences across years, yet these individualised strategies operate independently of classic ecological and behavioural drivers. Contrary to our original pace-of-life and density-dependent predictions, an individual's risk-taking personality and variation in breeding density failed to predict dietary specialisation. Instead, our variance partitioning demonstrates that dietary variation is primarily explained by pair- and brood-level factors rather than macro-environmental fluctuations. This repeatable among-individual variance across years suggests that individual dietary strategies persist as a relatively rigid phenotypic feature, influencing how these short-lived passerines navigate resource spaces.

Interspecific differences in dietary composition vs. intraspecific specialisation

Our dietary analyses confirmed that Lepidoptera dominate the breeding season diet of both sympatric tit species, validating our environmental frass sampling approach (Fischbacher et al., 1998; Nour

et al., 1998). However, beneath this shared reliance on caterpillars, our results reveal clear baseline niche partitioning between the two species. Blue tits incorporated significantly more Araneae and Hymenoptera from dense canopy foliage, whereas great tits consumed higher proportions of Diptera and Coleoptera from open and bark-dwelling micro-habitats (Cowie & Hinsley, 1988; Höhn et al., 2024). These differences align with previous literature (García-Navas & Sanz, 2011; Höhn et al., 2024), where species-specific foraging tendencies reduce interspecific resource overlap during high-demand breeding phases (Dhondt, 2012; Dhondt, 1977). Crucially, both species showed repeatable individual differences in dietary preferences for Geometridae and species-specific preferences for Noctuidae families in blue tits and Erebidae families in great tits. Yet, contrary to classic optimal foraging theory (Charnov, 1976; Krebs et al., 1977), a higher proportion of preferred prey did not translate into an increased nestling or brood-level weight, nor fledging success, suggesting that the proportion of preferred prey does not influence nestling weight or fledging success of a brood. Moreover, standardised selection gradients were close to zero, and the narrow credible intervals for fledging success indicate that directional selection on prey preference was weak or absent. However, the credible intervals for individual nestling weight and total weight of the brood were broad, such that we cannot confidently determine the effect of selection. The absence of selection on preferred prey might be influenced by external factors such as predation, temporal variation, or environmental conditions (Deeming & Pike, 2015; Naef-Daenzer et al., 2001; Visser & Verboven, 1999), which may explain the high residual variance observed in our models. Long-term population studies show that years with high caterpillar abundance are also years with high reproductive success (Mägi et al., 2009). Nevertheless, our findings suggest that such fitness mechanisms do not necessarily operate via individual dietary optimisation within a single season. Longer-term studies combining diet and environmental sampling across a broader range of seasonal qualities could help reveal potential mid- and long-term effects (Clutton-Brock & Sheldon, 2010).

Furthermore, optimal foraging in wild passerines is not only shaped by absolute biomass or caloric intake, but includes the nutritional quality of prey (Wright et al., 1998). Developing nestlings face strict physiological bottlenecks requiring micronutrients that are patchily distributed among insect taxa, such as specific essential amino acids, carotenoids for immune function, and arachidonic acid for skeletal and neural development (Arnold et al., 2010; Isaksson & Andersson, 2008). Consequently, specialised individual preferences may represent distinct decisions to balance nutritional demands (Han et al., 2016). Alternatively, individualised specialisations might optimise personal foraging efficiencies, such as minimising searching and handling costs (Araújo et al., 2011), that benefit other fitness components than nestling quality or quantity, such as the breeder's survival.

Stability of diet across environmental and behavioural contexts

Contrary to our pace-of-life syndrome (POLS) predictions, an individual's average exploration behaviour was not associated with its dietary specialisation. Exploration traits frequently inform spatial habitat decisions, such as choosing a territory or predation risk across larger areas (Abbey-Lee & Dingemanse, 2019; Toscano et al., 2016), but our results do not support the idea that they influence fine-scale prey selection. Personality may instead influence spatial foraging behaviour rather than direct diet composition (Toscano et al., 2016). For example, fast-exploring great tits can actively compensate for localised resource depletion by extending their foraging ranges (van Overveld & Matthysen, 2010). Such spatial and behavioural flexibility could effectively mask relationships between exploration behaviour and diet composition (Dingemanse et al., 2010; Wolf & Weissing, 2012). Our findings suggest that faster individuals might not secure higher quality habitats or specialise in higher quality prey compared to slow-exploring individuals, raising the possibility that the predictions of pace-of-life theory are incomplete (Royauté et al., 2018) and future frameworks might have to explore alternative pathways.

Furthermore, our breeding density manipulations did not alter individual dietary preferences. This outcome presents an apparent challenge to the compression and niche variation hypotheses, which predict systematic dietary shifts under changing population pressures (MacArthur & Pianka, 1966; Van Valen, 1965). However, our variance components show that spatio-temporal fluctuations explained less than 5% of dietary variation, while within-brood factors explained 88% to 92%. This suggests that our experimental manipulations did not actually alter the experienced intensity of resource competition. Increased breeding density may not directly affect the consumed proportion of preferred prey if tits compete for alternative resources, or if it shifts alternative foraging strategies such as overall foraging distance (Lamb et al., 2017). Multi-year experiments in this study system confirm that while nest box additions successfully alter breeding densities, they can leave demographic and reproductive traits unaffected (Gaona-Gordillo et al., 2026). During the peak breeding season, absolute prey abundance in our study might have been high enough that birds faced little increased competition or limitation in accessing food (Perrins, 1991; Visser et al., 2006). Assuming resource availability never dropped below the critical threshold required to trigger local depletion, encounter rates with preferred prey may have remained stable across treatments. Thus, our results do not falsify the structural logic of the compression or niche variation hypothesis. Rather, they suggest that individual foraging strategies are highly robust because abundant resources limited density-dependent competition (Dhondt, 2010; Milligan et al., 2017).

Deconstructing the statistics and mechanisms of cross-year repeatability

To our knowledge, only a handful of studies have demonstrated individual repeatability of diet (Class et al., 2021; Stewart et al., 2022; Zango et al., 2019), with even fewer on tits (Olivé-Muñiz et al., 2021), and ours is the first to do so using fine-scale metabarcoding data and dietary preferences in both adults and nestlings. DNA metabarcoding is a non-invasive method that provides high taxonomic resolution data and, unlike provisioning-based methods (e.g. through video observations), allows the simultaneous assessment of diet in breeding adults and nestlings (Ando et al., 2020; Bookwalter et al., 2023; Rytkönen et al., 2019; Verkuil et al., 2022). In this study, we furthermore tracked dietary preferences and exploration behaviour of the exact same individuals over consecutive years. Over short timescales, elevated repeatability is highly susceptible to pseudo-repeatability, where temporary environmental micro-patches confound true among-individual differences (Araya-Ajoy et al., 2015; Dingemanse et al., 2010; Réale et al., 2026). Thus, our study provides rare evidence of true long-term, individual repeatability in wild foraging choices.

Crucially, we implemented errors-in-variables models to simultaneously estimate this average behaviour while taking its statistical uncertainty forward into the second equation (Dingemanse et al., 2021; Ponzi et al., 2018). This approach preserves the full uncertainty of the behavioural trait. The resulting rigorous partitioning suggests that when environmental confounds and measurement errors are analytically controlled, dietary specialisation and the personality axis operate independently. Because diet appears to be independent of variation in breeding density, this cross-year repeatability could reflect localised or intrinsic mechanisms (Bolnick et al., 2003). Our variance components reveal that shared brood identity explains 88% to 92% of the variation in preferred prey. This suggests meaningful among-brood variation in preferred prey, providing a solid basis for subsequent individual analyses. Because a single pair provisions the entire nest, a brood identity effect represents an unavoidable conflation of specific territory characteristics and shared parental traits, meaning both factors may operate simultaneously (Poorboy et al., 2018). We propose two non-mutually exclusive hypotheses to explain this pattern, alongside clear avenues to test them:

Micro-Geographic Territory Quality: Because breeding adults highly favour the same nest box or swap boxes within close proximity to their territory across years (Lambrechts et al., 2010), they occupy a highly stable micro-environment. If a specific territory contains localised canopy structures that consistently harbours distinct arthropod families year-on-year, the cross-year repeatability may emerge partly as an environmental artifact of high site fidelity to a localised micro-niche (Baflbura et al., 1994; Blondel et al., 1991).

Heritable Parental Traits: Alternatively, given that parents are highly repeatable in their diet across years, a strong brood identity effect is inherently expected due to consistent parental provisioning, indicating stable foraging strategies. This consistency could reflect heritable individual strategies, such as learned search images or specialised motor skills (Svensson et al., 2001). Previous cross-population syntheses comparing behavioural repeatability and heritability suggest that approximately 52% of long-term repeatable among-individual variance is attributable to additive genetic effects (Dochtermann et al., 2019).

These hypotheses, together with the fine-scale taxonomic resolution of our DNA metabarcoding approach, may further explain our finding of high repeatability in dietary specialisation across years, in contrast to previous studies in breeding birds reporting low to moderate individual repeatability in diet (Nicolaus et al., 2019; Olivé-Muñiz et al., 2021; Zango et al., 2019). Disentangling the environmental and intrinsic pathways in future field studies will require quantitative genetic analyses (Charmantier et al., 2014). Explicitly modelling the heritability of parental diet and partitioning the additive genetic variance from permanent environmental territory effects will resolve whether these stable foraging strategies are driven by micro-niche fidelity, inherited genetic traits, or an interaction of both.

Methodological considerations

Our approach successfully captured dietary variation across multiple hierarchical levels, linking consumed prey directly to environmental prey availability. However, technical limitations warrant consideration. Low DNA detection rates in approximately one-quarter of our avian samples and more than half of our environmental frass samples may have introduced systematic biases when estimating preferred prey proportions. For example, nests characterised by lower faecal volume, potentially reflecting reduced parental provisioning rates or poor nestling condition, may have failed to amplify successfully prior to sequencing. Consequently, our estimates could be subtly skewed toward nests with higher focal provisioning and good nestling conditions. Future field studies utilising environmental frass metabarcoding could improve DNA recovery rates by minimising drying times, potentially using lightweight fleece substrates (Smith & Smith, 2019). Furthermore, increasing the density of collectors per forest subplot and pooling collections might effectively maximise arthropod DNA concentration (Rytkönen et al., 2019). Nonetheless, local climatic features, such as the high seasonal precipitation observed in our study area, will possibly continue to present ongoing challenges for field-based DNA preservation.

Evolutionary and ecological implications

In a broader ecological context, distinct individual dietary strategies are classically expected to reduce intra-specific competition by allowing individuals to partition resources (Bolnick et al., 2003). Although our experimental density manipulations suggest that competition was not a limiting factor during our study period, due to the classic, temporary peak abundance of caterpillars in the breeding season, individualised specialisation may act as a vital evolutionary buffer when resources decline (Bolnick et al., 2003). If a population encounters harsher environmental conditions or moves outside the window of peak caterpillar abundance, long-term specialist populations would show less overlap in resource use than flexible population of generalist competing for the same optimal prey (Futuyma & Moreno, 1988; Visser et al., 2006). In conclusion, our study underscores that dietary preference is a remarkably stable individual trait that persists across breeding seasons beyond shifts in environmental and social contexts, and characterizes both tit species. However, this lack of short-term dietary plasticity exposes individuals to significant evolutionary risks when anthropogenic environmental changes are rapid or permanent (Dingemanse & Wolf, 2010). If individual birds maintain rigidity in their dietary choices across years, they may lack the behavioural flexibility needed to shift when faced with climate-driven phenological mismatches, such as earlier caterpillar emergences (Branston, 2019; García-Navas & Sanz, 2011). Understanding the genetic architecture and environmental limits of this long-term dietary repeatability will remain crucial for predicting the persistence of wild populations in rapidly altering ecosystems.

Data availability statement

The data and code used to generate the results of this study are available on:
https://github.com/MeritFPokriefke/Dietary_specialisation

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References

Abbey-Lee RN, & Dingemanse NJ. (2019). Adaptive individual variation in phenological responses to perceived predation levels. *Nature Communications*, *10*(1), 1601. https://doi.org/10.1038/s41467-019-09138-5

Agetsuma-Yanagihara Y, Inoue E, & Agetsuma N. (2017). Effects of time and environmental conditions on the quality of dna extracted from fecal samples for genotyping of wild deer in a warm temperate broad-leaved forest. *Mammalian Research*, *62*(2), 201–207. https://doi.org/10.1007/s13364-016-0305-x

Ando H, Mukai H, Komura T, Dewi T, Ando M, & Isagi Y. (2020). Methodological trends and perspectives of animal dietary studies by noninvasive fecal dna metabarcoding. *Environmental DNA*, *2*, 391–406. https://doi.org/10.1002/edn3.117

Araújo MS, Bolnick DI, & Layman CA. (2011). The ecological causes of individual specialisation. *Ecology Letters*, *14*(9), 948–958. https://doi.org/10.1111/j.1461-0248.2011.01662.x

Araya-Ajoy YG, Kuhn S, Mathot KJ, Mouchet A, Mutzel A, Nicolaus M, Wijmenga JJ, Kempenaers B, & Dingemanse NJ. (2016). Sources of (co) variation in alternative siring routes available to male great tits (*Parus major)*. *Evolution*, *70*(10), 2308–2321. https://doi.org/10.1111/evo.13024

Araya-Ajoy YG, Mathot KJ, & Dingemanse NJ. (2015). An approach to estimate short-term, long-term and reaction norm repeatability. *Methods in Ecology and Evolution*, *6*(12), 1462–1473. https://doi.org/10.1111/2041-210X.12430

Arnold KE, Ramsay SL, Henderson L, & Larcombe SD. (2010). Seasonal variation in diet quality: Antioxidants, invertebrates and blue tits Cyanistes caeruleus. *Biological Journal of the Linnean Society*, *99*(4), 708–717. https://doi.org/10.1111/j.1095-8312.2010.01377.x

Baflbura J, Blondel -Hilde de Wilde-Lambrechts Marie-Jose Galan -Marie Maistre J, Bafibura J, & de Wilde-Lambrechts M-J Galan M Maistre BH. (1994). Nestling diet variation in an insular mediterranean population of blue tits *Parus caeruleus*: Effects of years, territories and individuals. *Oecologia*, *100*(4), 413–420. https://doi.org/10.1007/BF00317863.

Bates D, Mächler M, Bolker B, & Walker S. (2015). Fitting linear mixed-effects models using lme4. *Journal of Statistical Software*, *67*(1), 1–48. https://doi.org/10.18637/jss.v067.i01

Blondel J, Dervieux A, Maistre M, & Perret P. (1991). Feeding ecology and life history variation of the blue tit in mediterranean deciduous and sclerophyllous habitats. *Oecologia*, *88*(1), 9–14. https://doi.org/10.1007/BF00328397

Bolnick DI, Svanbäck R, Fordyce JA, Yang LH, Davis JM, Hulsey CD, & Forister ML. (2003). The ecology of individuals: Incidence and implications of individual specialization. *The American Naturalist*, *161*(1), 1–28. https://doi.org/10.1086/343878

Bookwalter J, Niyas AM, Caballero-López B, Villari C, Marco-Tresserras J, Burgas A, Ferrandiz-Rovira M, & Claramunt-López B. (2023). Dna metabarcoding passerine bird feces at tree-line uncovers little intra- and inter-species dietary overlap. *Community Ecology*, *24*(2), 147–157. https://doi.org/10.1007/s42974-023-00148-4

Both C, Dingemanse NJ, Drent PJ, & Tinbergen JM. (2005). Pairs of extreme avian personalities have highest reproductive success. *Journal of Animal Ecology*, *74*(4), 667–674. https://doi.org/10.1111/j.1365-2656.2005.00962.x

Branston CJ, Capilla-Lasheras P, Pollock CJ, Griffiths K, White S, & Dominoni DM. (2021). Urbanisation weakens selection on the timing of breeding and clutch size in blue tits but not in great tits. *Behavioral Ecology and Sociobiology*, *75*(11), 155. https://doi.org/10.1007/s00265-021-03096-z

Branston CJ. (2019). *The effects of climate and habitat on breeding blue tits (Cyanistes caeruleus) and their prey* [Doctoral dissertation, Durham University].

Bürkner P.-C. (2017). Brms: An r package for bayesian multilevel models using stan. *Journal of Statistical Software*, *80*, 1–28. https://doi.org/10.18637/jss.v080.i01

Charmantier A, Garant D, & Kruuk LE. (2014). *Quantitative genetics in the wild*. OUP Oxford.

Charnov EL. (1976). Optimal foraging: Attack strategy of a mantid. *The American Naturalist*, *110*(971), 141–151. https://doi.org/doi.org/10.1086/283054

Class B, Masoero G, Terraube J, & Korpimäki E. (2021). Estimating the long-term repeatability of food-hoarding behaviours in an avian predator. *Biology Letters*, *17*(7), 20210286. https://doi.org/10.1098/rsbl.2021.0286

Clutton-Brock T, & Sheldon BC. (2010). Individuals and populations: The role of long-term, individual-based studies of animals in ecology and evolutionary biology. *Trends in Ecology & Evolution*, *25*(10), 562–573. https://doi.org/10.1016/j.tree.2010.08.002

Corsini M, Leanza P, Rodewald AD, Sudyka J, Dhondt AA, & Szulkin M. (2022). Coping with novelty across an urban mosaic: Provisioning latency increases closer to roads and is associated with species-specific reproductive success in two urban adapters. *Science of The Total Environment*, *847*, 157450. https://doi.org/10.1016/j.scitotenv.2022.157450

Cowie RJ, & Hinsley SA. (1988). Feeding ecology of great tits (*Parus major*) and blue tits (*Parus caeruleus*), breeding in suburban gardens. *Journal of Animal Ecology*, *57*, 611–626. https://doi.org/10.2307/4928

Deeming DC, & Pike TW. (2015). Nest surface temperature predicts fledging success of blue tits *Cyanistes caeruleus* but not great tits *Parus major*. *Acta Ornithologica*, *50*(2), 247–251. https://doi.org/10.3161/00016454AO2015.50.2.012

Dhondt AA. (2010). Effects of competition on great and blue tit reproduction: Intensity and importance in relation to habitat quality. *Journal of Animal Ecology*, *79*(1), 257–265. https://doi.org/10.1111/j.1365-2656.2009.01624.x

Dhondt AA. (2012). *Interspecific competition in birds* (Vol. 2). Oxford University Press.

Dhondt AA. (1977). Interspecific competition between great and blue tit. *Nature*, *268*(5620), 521–523. https://doi.org/10.1038/268521a0

Dingemanse NJ, Kazem AJ, Réale D, & Wright J. (2010). Behavioural reaction norms: Animal personality meets individual plasticity. *Trends in Ecology & Evolution*, *25*(2), 81–89. https://doi.org/10.1016/j.tree.2009.07.013

Dingemanse NJ, & Wolf M. (2010). Recent models for adaptive personality differences: A review. *Philosophical Transactions of the Royal Society B: Biological Sciences*, *365*(1560), 3947–3958. https://doi.org/10.1098/rstb.2010.0221

Dingemanse NJ, Araya-Ajoy YG, & Westneat DF. (2021). Most published selection gradients are underestimated: Why this is and how to fix it. *Evolution*, *75*(4), 806–818. https://doi.org/10.1111/evo.14198

Dochtermann NA, Schwab T, Anderson Berdal M, Dalos J, & Royauté R. (2019). The heritability of behavior: A meta-analysis. *Heredity*, *110*(4), 403–410. https://doi.org/10.1093/jhered/esz023

Duckworth RA, & Badyaev AV. (2007). Coupling of dispersal and aggression facilitates the rapid range expansion of a passerine bird. *Proceedings of the National Academy of Sciences*, *104*(38), 15017–15022. https://doi.org/10.1073/pnas.0706174104

Edgar RC. (2016). Sintax: A simple non-bayesian taxonomy classifier for 16s and its sequences. *bioRxiv*. https://doi.org/10.1101/074161

Fischbacher M, Naef-Daenzer B, & Naef-Daenzer L. (1998). Estimating caterpillar density on trees by collection of frass droppings. *Ardea*, *86*(1), 121–129.

Folmer O, Hoeh W, Black M, & Vrijenhoek R. (1994). Dna primers for amplification of mitochondrial cytochrome c oxidase subunit i from diverse metazoan invertebrates. *Molecular Marine Biology and Biotechnology*, *3*, 294–299.

Friard O, & Gamba M. (2016). *Boris: Behavioral observation research interactive software* [Version 7.13, https://boris.readthedocs.io].

Futuyma DJ, & Moreno G. (1988). The evolution of ecological specialization. *Annual Review of Ecology and Systematics*, *19*, 207–233.

Gaona-Gordillo I, Białas JT, Cones AG, Dingemanse NJ, & Holtmann B. (2026). Intra- and interspecific competition interact: Multi-factorial experiments in two tit species. *Behavioral Ecology*, *37*(3), arag026. https://doi.org/10.1093/beheco/arag026

García-Navas V, & Sanz JJ. (2011). The importance of a main dish: Nestling diet and foraging behaviour in mediterranean blue tits in relation to prey phenology. *Oecologia*, *165*, 639–649. https://doi.org/10.1007/s00442-010-1858-z

García-Navas V, Ferrer ES, & Sanz JJ. (2012). Prey selectivity and parental feeding rates of blue tits cyanistes caeruleus in relation to nestling age. *Bird Study*, *59*(2), 236–242. https://doi.org/10.1080/00063657.2012.662939

GBIF. (2025). *Global biodiversity information facility* [Accessed: 2025-09-08]. https://www.gbif.org/

Han CS, Jäger HY, & Dingemanse NJ. (2016). Individuality in nutritional preferences: A multi-level approach in field crickets. *Scientific Reports*, *6*(1), 29071. https://doi.org/10.1038/srep29071

Höhn D, Masello JF, Kümmel MN, Griep S, Goesmann A, & Quillfeldt P. (2024). Nestling diet of two sympatric insectivorous passerines in different habitats — a metabarcoding study. *Birds*, *5*(1), 67–89. https://doi.org/10.3390/birds5010005

Hollander FA, Van Overveld T, Tokka I, & Matthysen E. (2008). Personality and nest defence in the great tit (*Parus major*). *Ethology*, *114*(4), 405–412. https://doi.org/10.1111/j.1439-0310.2008.01488.x

iNaturalist. (2025). *Inaturalist* [Accessed: 2025-09-08]. https://www.inaturalist.org/

Isaksson C, & Andersson S. (2008). Oxidative stress does not influence carotenoid mobilization and plumage pigmentation. *Proceedings of the Royal Society B: Biological Sciences*, *275*(1632), 309–314. https://doi.org/10.1098/rspb.2007.1474

Janzen FJ, & Stern HS. (1998). Logistic regression for empirical studies of multivariate selection. *Evolution*, *52*(6), 1564–1571. https://doi.org/10.1111/j.1558-5646.1998.tb02237.x

Keller A, Hohlfeld S, Kolter A, Schultz J, Gemeinholzer B, & Ankenbrand MJ. (2020). Bcdatabaser: On-the-fly reference database creation for (meta-)barcoding. *Bioinformatics*, *36*(8), 2630–2631. https://doi.org/10.1093/bioinformatics/btz960

Korsten P, van Overveld T, Adriaensen F, & Matthysen E. (2013). Genetic integration of local dispersal and exploratory behaviour in a wild bird. *Nature Communications*, *4*, 2362. https://doi.org/10.1038/ncomms3362

Krebs J, Erichsen J, Webber M, Charnov E, Krebs JR, Erichsen J, Webber M, & Charnov EL. (1977). Optimal prey selection in the great tit (*Parus major*). *Animal Behavior*, *25*, 30–38. https://doi.org/10.1016/0003-3472(77)90064-1

Lamb JS, Satgé YG, & Jodice PGR. (2017). Influence of density-dependent competition on foraging and migratory behavior of a subtropical colonial seabird. *Ecology & Evolution*, *7*(16), 6469–6481. https://doi.org/10.1002/ece3.3216

Lambrechts MM, Adriaensen F, Ardia DR, Artemyev AV, Atiénzar F, Bańbura J, Barba E, Bouvier J.-C, Camprodon J, Cooper CB, et al. (2010). The design of artificial nestboxes for the study of secondary hole-nesting birds: A review of methodological inconsistencies and potential biases. *Acta Ornithologica*, *45*(1), 1–26. https://doi.org/10.3161/000164510X516047

Lande R, & Arnold SJ. (1983). The measurement of selection on correlated characters. *Evolution*, *37*(6), 1210–1226. https://doi.org/10.2307/2408842

Leonhardt SD, Peters B, & Keller A. (2022). Do amino and fatty acid profiles of pollen provisions correlate with bacterial microbiomes in the mason bee *Osmia bicornis*? *Philosophical Transactions of the Royal Society B: Biological Sciences*, *377*, 20210171. https://doi.org/10.1098/rstb.2021.0171

Leray M, Yang J, Meyer C, Mills S, Agudelo N, Ranwez V, Boehm J, & Machida R. (2013). A new versatile primer set targeting a short fragment of the mitochondrial coi region for metabarcoding metazoan diversity: Application for characterizing coral reef fish gut contents. *Frontiers in Zoology*, *10*, 1–14. https://doi.org/10.1186/1742-9994-10-34

MacArthur RH. (1984). *Geographical ecology: Patterns in the distribution of species*. Princeton University Press.

MacArthur RH, & Pianka ER. (1966). On optimal use of a patchy environment. *The American Naturalist*, *100*(916), 603–609.

Mägi M, Mänd R, Tamm H, Sisask E, Kilgas P, & Tilgar V. (2009). Low reproductive success of great tits in the preferred habitat: A role of food availability. *Ecoscience*, *16*(2), 145–157. https://doi.org/10.2980/16-2-3215

Martin JS, Araya-Ajoy YG, Dingemanse NJ, Wilson AJ, & Westneat DF. (2025). Estimating (non)linear selection on reaction norms: A general framework for labile traits [e72298 ECE-2024-11-02439.R1]. *Ecology and Evolution*, *15*(10), e72298. https://doi.org/https://doi.org/10.1002/ece3.72298

McLaren M. (2025). *Speedyseq: Faster implementations of phyloseq functions* [R package version 0.5.3.9021, commit 0057652ff7a4244ccef2b786dca58d901ec2fc62].

McMurdie PJ, & Holmes S. (2013). Phyloseq: An r package for reproducible interactive analysis and graphics of microbiome census data. *PLoS ONE*, *8*(4), e61217. https://doi.org/10.1371/journal.pone.0061217

Milligan ND, Radersma R, Cole EF, & Sheldon BC. (2017). To graze or gorge: Consistency and flexibility of individual foraging tactics in tits. *Journal of Animal Ecology*, *86*(4), 826–836. https://doi.org/10.1111/1365-2656.12651

Mouchet A, & Dingemanse NJ. (2021). A quantitative genetics approach to validate lab- versus field-based behavior in novel environments. *Behavioral Ecology*, *32*(5), 903–911. https://doi.org/10.1093/beheco/arab059

Mutzel A, Dingemanse NJ, Araya-Ajoy YG, & Kempenaers B. (2013). Parental provisioning behaviour plays a key role in linking personality with reproductive success. *Proceedings of the Royal Society B: Biological Sciences*, *280*(1764). https://doi.org/10.1098/rspb.2013.1019

Nadolski J, Marciniak B, Loga B, Michalski M, & Bańbura J. (2021). Long-term variation in the timing and height of annual peak abundance of caterpillars in tree canopies: Some effects on a breeding songbird. *Ecological Indicators*, *121*, 107120. https://doi.org/10.1016/j.ecolind.2020.107120

Naef-Daenzer B, Widmer F, & Nuber M. (2001). Differential post-fledging survival of great and coal tits in relation to their condition and fledging date. *Journal of Animal Ecology*, *70*(5), 730–738. https://doi.org/10.1046/j.0021-8790.2001.00533.x

Naef-Daenzer L, Naef-Daenzer B, & Nager RG. (2000). Prey selection and foraging performance of breeding great tits *Parus major* in relation to food availability. *Journal of Avian Biology*, *31*(2), 206–214. https://doi.org/10.1034/j.1600-048X.2000.310212.x

Nakagawa S, & Schielzeth H. (2010). Repeatability for gaussian and non-gaussian data: A practical guide for biologists. *Biological Reviews*, *85*(4), 935–956. https://doi.org/10.1111/j.1469-185X.2010.00141.x

Nicolaus M, Barrault SCY, & Both C. (2019). Diet and provisioning rate differ predictably between dispersing and philopatric pied flycatchers. *Behavioral Ecology*, *30*(1), 114–124. https://doi.org/10.1093/beheco/ary152

Nicolaus M, Tinbergen JM, Ubels R, Both C, & Dingemanse NJ. (2016). Density fluctuations represent a key process maintaining personality variation in a wild passerine bird. *Ecology Letters*, *19*(4), 478–486. https://doi.org/10.1111/ele.12584

Noordwijk AV, McCleery R, & Perrins C. (1995). Selection for the timing of great tit breeding in relation to caterpillar growth and temperature. *Journal of Animal Ecology*, *64*(4), 451–458. https://doi.org/10.2307/5648

Nour N, Currie D, Matthysen E, Van Damme R, & Dhondt AA. (1998). Effects of habitat fragmentation on provisioning rates, diet and breeding success in two species of tit (great tit and blue tit). *Oecologia*, *114*(4), 522–530. https://doi.org/10.1007/s004420050476

Olivé-Muñiz M, Pagani-Núñez E, & Senar JC. (2021). Breeding great tit parus major individuals have moderately consistent foraging niches across years. *BioOne*, *68*(2), 409–422. https://doi.org/10.13157/arla.68.2.2021.ra6

Pagani-Núñez E, Barnett CA, Gu H, & Goodale E. (2016). The need for new categorizations of dietary specialism incorporating spatio-temporal variability of individual diet specialization. *Journal of Zoology*, *300*(1), 1–7. https://doi.org/10.1111/jzo.12364

Perrins CM. (1979). *British tits*. Collins.

Perrins C. (1991). Tits and their caterpillar food supply. *Ibis*, *133*, 49–54. https://doi.org/10.1111/j.1474-919X.1991.tb07668.x

Ponzi E, Keller LF, Bonnet T, & Muff S. (2018). Heritability, selection, and the response to selection in the presence of phenotypic measurement error: Effects, cures, and the role of repeated measurements. *Evolution*, *72*(10), 1992–2004. https://doi.org/10.1111/evo.13573

Poorboy D, Bowers EK, Sakaluk SK, & Thompson CF. (2018). Experimental cross-fostering of eggs reveals effects of territory quality on reproductive allocation. *Behavioral Ecology*, *29*(5), 1190–1198. https://doi.org/10.1093/beheco/ary098

Pyke GH, Pulliam HR, Charnov E, & Charnov EL. (1977). Optimal foraging: A selective review of theory and tests. *Quarterly Review of Biology*, *52*, 137–154. https://doi.org/10.1086/409852

Quaresma A, Ankenbrand MJ, Garcia CAY, et al. (2024). Semi-automated sequence curation for reliable reference datasets in its2 vascular plant dna (meta-)barcoding. *Scientific Data*, *11*(1), 129. https://doi.org/10.1038/s41597-024-02962-5

669 Ratnasingham S, & Hebert PDN. (2007). BOLD: The barcode of life data system (\NoCaseChange{http:
670 //www.barcodinglife.org}). *Molecular Ecology Notes*, *7*(3), 355–364. https://doi.org/10.
671 1111/j.1471-8286.2007.01678.x
672 Réale D, Allegue H, Araya-Ajoy YG, Dochtermann NA, Nakagawa S, Pick JL, Schielzeth H, Westneat DF,
673 & Dingemanse NJ. (2026). Avoiding misleading estimates of among-individual variance
674 caused by non-random sampling of individuals in a changeable environment. *Methods in*
675 *Ecology and Evolution*, *17*(4), 1161–1174. https://doi.org/10.1111/2041-210x.70202
676 Réale D, Dingemanse NJ, Kazem AJ, & Wright J. (2010). Evolutionary and ecological approaches to
677 the study of personality. *Philosophical Transactions of the Royal Society B: Biological Sciences*,
678 *365*(1560), 3937–3946. https://doi.org/10.1098/rstb.2010.0222
679 Rognes T, Flouri T, Nichols B, Quince C, & Mahé F. (2016). Vsearch: A versatile open source tool for
680 metagenomics. *PeerJ*, *4*, e2584. https://doi.org/10.7717/peerj.2584
681 Royauté R, Berdal MA, Garrison CR, & Dochtermann NA. (2018). Paceless life? a meta-analysis
682 of the pace-of-life syndrome hypothesis. *Behavioral Ecology and Sociobiology*, *72*(3). https:
683 //doi.org/10.1007/s00265-018-2472-z
684 Rytkönen S, Vesterinen EJ, Westerduin C, Leviäkangas T, Vatka E, Mutanen M, Välimäki P, Hukkanen
685 M, Suokas M, & Orell M. (2019). From feces to data: A metabarcoding method for analyzing
686 consumed and available prey in a bird-insect food web. *Ecology & Evolution*, *9*(1), 631–639.
687 https://doi.org/10.1002/ece3.4787
688 Santema P, Forstmeier W, & Kempenaers B. (2024). Variance partitioning of nest provisioning rates
689 in blue tits: Individual repeatability, heritability, and partner interactions. *Evolution*, *78*(11),
690 1751–1760. https://doi.org/10.1093/evolut/qpae131
691 Smith KW, & Smith L. (2019). Does the abundance and timing of defoliating caterpillars influence
692 the nest survival and productivity of the great spotted woodpecker *Dendrocopos major? Bird*
693 *Study*, *66*(2), 187–197. https://doi.org/10.1080/00063657.2019.1637396
694 Stan Development Team. (2025). *RStan: The R interface to Stan* [R package version 2.32.7].
695 Stearns SC. (1998). *The evolution of life histories*. Oxford University Press.
696 Stewart C, Lang SL, Iverson S, & Bowen WD. (2022). Measuring repeatability of compositional diet
697 estimates: An example using quantitative fatty acid signature analysis. *Ecology & Evolution*,
698 *12*(10). https://doi.org/10.1002/ece3.9428
699 Stuber EF, Araya-Ajoy YG, Mathot KJ, Mutzel A, Nicolaus M, Wijmenga JJ, Mueller JC, & Dingemanse
700 NJ. (2013). Slow explorers take less risk: A problem of sampling bias in ecological studies.
701 *Behavioral Ecology*, *24*(5), 1092–1098. https://doi.org/10.1093/beheco/art035

Svensson E, Sinervo B, & Comendant T. (2001). Condition, genotype-by-environment interaction, and correlational selection in lizard life-history morphs. *Evolution*, *55*(10), 2053–2069. https://doi.org/10.1111/j.0014-3820.2001.tb01321.x.

Taberlet P, Waits LP, & Luikart G. (1999). Noninvasive genetic sampling: Look before you leap. *Trends in Ecology & Evolution*, *14*(8), 323–327. https://doi.org/10.1016/S0169-5347(99)01637-7

Tinbergen JM, & Dietz MW. (1994). Parental energy expenditure during brood rearing in the great tit (*Parus major*) in relation to body mass, temperature, food availability and clutch size. *Functional Ecology*, *8*(5), 563–572. https://doi.org/10.2307/2389916

Török J, & Tóth L. (1999). Asymmetric competition between two tit species: A reciprocal removal experiment. *Journal Animal Ecology*, *68*(2), 338–345. https://doi.org/10.1046/j.1365-2656.1999.00283.x

Toscano BJ, Gownaris NJ, Heerhartz SM, & Monaco CJ. (2016). Personality, foraging behavior and specialization: Integrating behavioral and food web ecology at the individual level. *Oecologia*, *182*(1), 55–69. https://doi.org/10.1007/s00442-016-3648-8

Van Balen JH. (1973). A comparative sudy of the breeding ecology of the great tit parus major in different habitats. *Ardea*, *55*(1–2), 1–93. https://doi.org/10.5253/arde.v61.p1

Van de Pol M, & Wright J. (2009). A simple method for distinguishing within-versus between-subject effects using mixed models. *Animal Behaviour*, *77*(3), 753. https://doi.org/10.1016/j.anbehav.2008.11.006

Van Valen L. (1965). Morphological variation and width of ecological niche. *The American Naturalist*, *99*(908), 377–390.

van Overveld T, & Matthysen E. (2010). Personality predicts spatial responses to food manipulations in free-ranging great tits (*Parus major*). *Biology Letters*, *6*(2), 187–190. https://doi.org/10.1098/rsbl.2009.0764

Verhulst S, Van Balen J, & Tinbergen J. (1995). Seasonal decline in reproductive success of the great tit: Variation in time or quality? *Ecology*, *76*(8), 2392–2403. https://doi.org/10.2307/2265815

Verkuil YI, Nicolaus M, Ubels R, Dietz MW, Samplonius JM, Galema A, Kiekebos K, de Knijff P, & Both C. (2022). Dna metabarcoding quantifies the relative biomass of arthropod taxa in songbird diets: Validation with camera-recorded diets. *Ecology & Evolution*, *12*(5). https://doi.org/10.1002/ece3.8881

Visser ME, & Verboven N. (1999). Long-term fitness effects of fledging date in great tits. *Oikos*, *85*(3), 445–450. https://doi.org/10.2307/3546694

Visser M, Holleman L, & Gienapp P. (2006). Shifts in caterpillar biomass phenology due to climate change and its impact on the breeding biology of an insectivorous bird. *Oecologia*, *147*, 164–172. https://doi.org/10.1007/s00442-005-0299-6

Wedrowicz F, Karsa M, Mosse J, & Hogan FE. (2013). Reliable genotyping of the koala (*P hascolarctos cinereus*) using dna isolated from a single faecal pellet. *Molecular Ecology Resources*, *13*(4), 634–641. https://doi.org/10.1111/1755-0998.12101

Wolf M, & Weissing FJ. (2012). Animal personalities: Consequences for ecology & evolution. *Trends in Ecology & Evolution*, *27*(8), 452–461. https://doi.org/10.1016/j.tree.2012.05.001

Wright, Both, Cotton & Bryant. (1998). Quality vs. quantity: Energetic and nutritional trade-offs in parental provisioning strategies. *Journal of Animal Ecology*, *67*(4), 620–634. https://doi.org/10.1046/j.1365-2656.1998.00221.x

Zango L, Reyes-González JM, Militão T, Zajková Z, Álvarez-Alonso E, Ramos R, & González-Solís J. (2019). Year-round individual specialization in the feeding ecology of a long-lived seabird. *Scientific Reports*, *9*(1), 11812. https://doi.org/10.1038/s41598-019-48214-0

Electronic supplementary material (ESM)

Notation Table

Explanation of distribution notations and abbreviations used in tables

Abbreviation	Meaning
B	Blue tit
G	Great tit
$_{\text{H}}$	High treatment density
$_{\text{L}}$	Low treatment density
p	Probability
σ^2	Variance
ZIH	Zero-inflated hurdle
μ	Mean

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1 Detailed sequencing protocol

DNA was extracted using the Qiagen Blood and Tissue Kit in 96-well format following the manufacturer's protocol. The 5P region of the mitochondrial COI gene was amplified with the primers mlCOIntf and dgHco (Folmer et al., 1994; Leray et al., 2013). PCR products were verified through gel electrophoresis. The oligonucleotide indices were attached in a second amplification step using the Supreme NZYTaq 2x Green Master Mix (NZYTech) and ultrapure water. Negative and positive controls were added as individual samples. Library sizes were confirmed by 3% agarose gels stained with GreenSafe (NZYTech) imaged under UV light. Finished libraries were pooled in equimolar amounts according to the results of a Qubit dsDNA HS Assay (Thermo Fisher Scientific) quantification. The pool was sequenced in a fraction of a NovaSeq PE250 flow cell (Illumina) aiming for a total output of 15 gigabases. DNA metabarcoding library preparation and sequencing were carried out by AllGenetics & Biology SL (www.allgenetics.eu). Bioinformatic processing followed the pipeline available at https://github.com/chiras/metabarcoding_pipeline (version 400d87c; Leonhardt et al., 2022). The pipeline used VSEARCH v2.18.0 (Rognes et al., 2016) for paired-read merging, quality (ee <1) and length (200-500bp) filtering and truncation, primer and adapter removal, dereplication, and denoising to amplicon sequence variants (ASVs). Taxonomy was assigned to ASVs with an iterative approach, direct global alignments and a threshold of 97% against local fauna databases. These databases were created using BCdatabaser (Keller et al., 2020) with invertebrate lists from Germany and Central Europe Quaresma et al. (2024). Sequences were classified first against the German reference database, then against Central European, and finally against entire BOLD (Ratnasingham & Hebert, 2007). Any remaining unclassified reads were classified using SINTAX (Edgar, 2016) against the BOLD database curated and unified according to (Quaresma et al., 2024) with a threshold of 0.8. Of all ASVs, only sequences classified as invertebrates (phyla Arthropoda and Mollusca) were retained. Furthermore, unspecific classifications that were not resolved at least at the level of taxonomic family were excluded. If multiple ASVs belonged to the same biological species, they were collated per sample. We used targeted filtering (see Table S2, S3, S30, S31) and converted the read numbers into relative data. We then applied low-abundance filtering by discarding ASVs 0.2% of relative reads per sample. To process barcoded data, we used phyloseq and speedyseq in R (McLaren, 2025; McMurdie & Holmes, 2013). For the general diet overview, we agglomerated the filtered data of the relative abundances per sample at the taxonomic level of order and extracted the relative read abundances of the five largest orders (calculated over all orders in the sample). For the analysis of preferred prey, we agglomerated the filtered data at the taxonomic level of family per sample and extracted the relative abundances for all families detected. DNA detection rates in 26.4% of all bird samples were too low for reliable metabarcoding. These samples arose mainly from adult and nestling samples, where the samples consisted primarily of urates and contained little to no faecal matter. Further, two samples had sequencing problems, and these samples were not used in the analyses. In frass samples, 55% of all samples had DNA concentrations too low for successful metabarcoding. A generalised linear mixed effects model (Bates et al., 2015) revealed that longer drying times and later sampling dates explained these low DNA counts (Table S1). Longer drying times are connected to higher initial humidity of the sample, which can lead to faster DNA deterioration (Agetsuma-Yanagihara et al., 2017; Taberlet et al., 1999; Wedrowicz et al., 2013). Furthermore, the later in the season a sample was collected, the smaller the amount of frass within the sample, ranging as low as 0.00005 g, thus leading to a low DNA detection rate.

2 Detailed model structures

2.1 Variation in general diet

We estimated variation between consumed dietary orders using zero-inflated hurdle models with Beta distributions. For each of the five most abundant prey orders, we used the relative read abundances (combined for both species) as the response variable.

To see if intra- and interspecific competition influenced species-specific dietary preferences, we added the fixed effects of species and competitive treatment low/high for each species and their interaction. Furthermore, we added the fixed effect of female, male, and nestling measured on day 10 and nestling measured on day 15 to estimate differences between different bird types. To account for spatial and temporal effects, we fitted the size of the Subplot, the date the sample was taken (in April days, with the first of April being 0), and the year. Moreover, as our high competitive density treatments lead to some boxes being in close proximity to one another, we added a fixed effect of nest box in close proximity (yes/no). To account for repeated brood data, within-nest repeated samples, e.g., multiple nestling samples stored in separate tubes (e.g., four nestling samples were taken at day 10 and stored in two tubes) and spatio-temporal effects, we fitted the random effects of brood identity, a combined identifier for brood ID and sex and age (Nestling repeat), the Subplot identity, and Subplot year combinations.

Because the effects of bird type differed among prey orders (sex and age), we tested for each order whether diet composition differed between females and males, between nestlings measured at day 10 and day 15, and between adults and nestlings. Depending on the outcome, we refitted the model for each order using a new fixed effect (e.g. if adults and nestlings were not different, we used a new two-level effect of adult and nestling; Table S4). We

repeated these steps for a model only including blue tit diet and again for a model only using great tit specific diet samples (Table S5, S6).

2.2 Identification of preferred prey in the diet

We analysed the families that were more abundant in the diet (bird faecal data) than in the environment (frass data) using a zero inflated hurdle model with Beta distribution with the relative abundances for each family from all samples (frass and bird diet) as the response variable. We fitted the fixed effect of frass, blue and great tit to determine whether tits ate more of a family compared to the relative abundance in the frass samples. To catch temporal effects, we added the year and date the sample was taken as fixed effects, while controlling small- and large scale spatio-temporal effects using the random effects of location (nest box or frass collector) and year as well as Subplot year.

2.3 Variation in preferred prey

To identify the sources of variation in preferred prey, we applied the same model described in section 2.1, using the same distribution and the same set of fixed and random effects, but with the index of preferred prey as the response variable. This analysis was conducted both across all birds combined and separately by species. We also used the same approach to determine whether a difference existed between the bird types existed or not and refitted the models accordingly (Table S16 - S18).

2.4 Personality, specialisation and competition

To see whether personality and dietary specialisation are connected and vary with the competitive environment, we fitted a bivariate mixed model with exploration behaviour and the consumed proportion of preferred prey as the two key variables. In the first equation, we used the exploration test score of each individual as response variable using a Gaussian distribution. The number of times a bird repeated the exploration test we added as the fixed effect of sequence (2, 3 and 4). We furthermore added the fixed effects of time the test was taken calculated in hours after sunrise, the sex of the individual, and the species. As random effects, we fitted individual ID and Subplot year combinations to catch spatio-temporal effects. From this equation, we extracted the mean best linear unbiased predictor (BLUP) of the exploration score for each individual (Ponzi et al., 2018).
In the second equation of the bivariate model, within the same model, we used the proportions of preferred prey as the second response variable, again using a zero inflated hurdle model with Beta distribution. We then used the mean exploration scores calculated from the first equation as a fixed effect to estimate the effect of behaviour on the proportion of preferred prey. We further fitted the competitive treatment of blue and great tits, their interaction with each other, and the interaction between individual exploration score and the blur tit treatment, exploration score and the great tit treatment and the interaction of both treatments with individual mean exploration scores to estimate whether exploration behaviour changes with diet, depending on the competitive treatment a bird is experiencing. As before, for temporal effects, we added the fixed effect of date and year, as well as the fixed effect of species. For the spatio-temporal effect, we added the random effect of Subplot year combinations and the random effect of individual ID, as a few individuals showed repeated measures of diet.
To analyse how the exploration behaviour of a parent influences the proportion of preferred prey consumed by their nestlings, we repeated the analyses separately for each species and sex by adding to the second response variable the diet of the nestlings. The fixed and random effects structure of the first equation remained the same as before, except removing the effect of sex and species. For the second equation, we fitted mean exploration behaviour from the first equation, the fixed effect of life stage (female and nestling / male and nestling), date and year effects, and the interaction between the mean exploration behaviour of the female/male and nestling diet. As random effect, we used Subplot year and added the random effect of within nest repeats, to control for multiple tubes taken within a nest. Additionally, the random effect of individual ID now included the nestling measures, making it a female/male with nestlings identifier.

2.5 Specialisation and reproductive success

To test whether the proportion of preferred prey from nestlings was related to reproductive success, we fitted a bivariate mixed model for each species with the same structure as used for the behavioural analysis. In this model, the first equation described the proportion of preferred prey of nestlings using a zero-inflated Beta hurdle distribution, including a random effect of nestling repeat to correct for multiple samples per nest and brood ID. The second equation modelled individual nestling weight at day 15 (Gaussian distribution) as the response variable. We used the best linear unbiased predictor (BLUP) of the proportion of preferred prey for each brood ID from the

first equation as a fixed effect to test its influence on individual nestling weight. We fitted the fixed effect of each species treatment, the effect of a box in close proximity (DoubleBox), year, the time when the nestlings had been weighted (in minutes after sunrise) and the number of nestlings within a brood to account for the negative effect of brood size on individual weight. Further, we included the interaction between brood proportion of preferred prey and each species treatment, as well as the interaction between treatments and the interaction of both treatments combined with brood proportion of preferred prey. We corrected for spatio-temporal effects and repeated brood measures by fitting the random effects of a subplot and year combination and brood ID. Directional selection gradients were calculated after Lande and Arnold (1983).

We repeated the analysis twice, first using the total weight of a brood (sum of the individual weights) in the second equation as a response variable (modelled with a Gaussian distribution), exempt the random effect of brood ID. Second, we modelled fledging success (0/1) with a Bernoulli distribution as the response variable in the second equation, exempt the fixed effect for time and brood size. Here, we estimated the selection gradients following Janzen and Stern (1998).

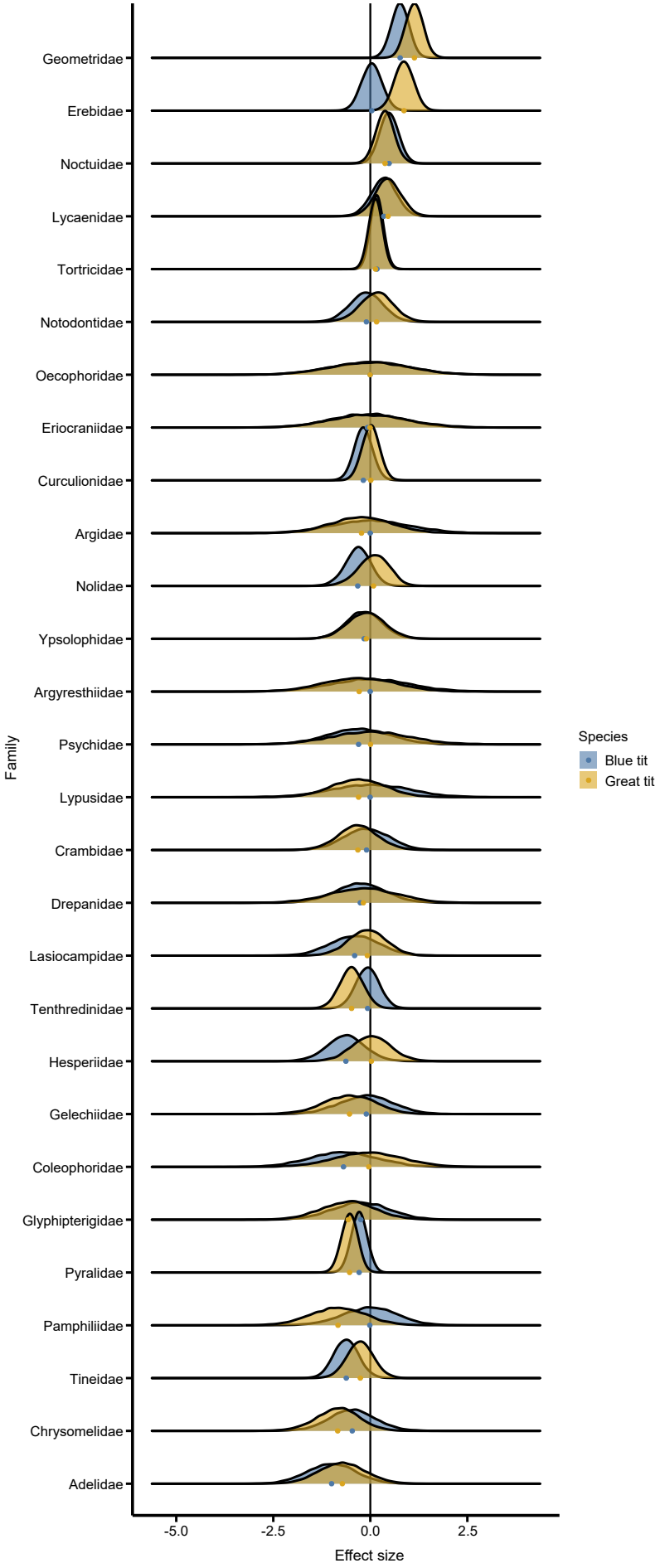

Figure 1: Ridge line plot showing prey preference (X-axis) across 28 quantified prey families (Y-axis) from environmental frass samples. Points indicate posterior means, with ridge line densities showing the full posterior distributions. There is strong evidence for prey preference when intervals do not overlap zero (vertical line) and the estimate is positive. For those families, exemplary visualization is shown. Results are shown separately for blue tits (blue) and great tits (yellow). Number of observations = 1089, with frass = 236, blue tit = 386 and great tit = 467.

Table S1: Summary for the generalized linear mixed model with DNA detection failure as response (DF, Binomial), the fixed effects of drying time (hours), day (in april days) and the random effect of collector ID. Shown are the estimates with standard error (SE), z-value (null-hypothesis testing, z), p-value (p) for significance and the model fit criteria of Akaike Information Criterion (AIC), Bayesian Information Criterion (BIC) as well as the log-likelihood (logLik). Number observations = 301.

$DetectionFailure \sim Bernoulli(p)$	Estimate	SE	z	p
Fixed effects				
Intercept	-2.16	0.37	-5.84	< 0.001
Drying time	0.020	0.005	3.86	< 0.001
April day	0.018	0.007	2.60	0.009
Random effects				
Collector (Intercept)	0.022	–	–	–
Model fit				
AIC	367.7			
BIC	382.5			
logLik	-179.9			

Table S2: Targeted filtering of taxa to exclude from the bird faecal data at different taxonomic levels.

Taxonomic Level	Filtered Taxa
Kingdom	Fungi, Plantae, Protista, Bacteria
Phylum	Rotifera, Nematoda, Platyhelminthes, Bryozoa, Cnidaria, Echinodermata, Gastrotricha, Porifera, Tardigrada, Nemertea, Chordata
Class	Actinopterygii, Amphibia, Bivalvia, Ascidiacea, Branchiopoda, Aves, Reptilia, Thecostraca, Polyplacophora, Polychaeta, Animalia spc, Arthropoda spc
Order	Arachnida spc, Insecta spc
Species	Homo sapiens, Meleagris gallopavo, Cyornis spc 1, Platorchestia platensis

Table S3: Targeted filtering of taxa to exclude from the arthropod faecal data (frass) at different taxonomic levels.

Taxonomic Level	Filtered Taxa
Kingdom	Fungi, Plantae, (empty), Protista, Bacteria
Phylum	Rotifera, Nematoda, Platyhelminthes, Bryozoa, Cnidaria, Echinodermata, Gastrotricha, Porifera, Tardigrada, Nemertea, Chordata, Animalia spc
Class	Actinopterygii, Amphibia, Bivalvia, Ascidiacea, Branchiopoda, Aves, Reptilia, Thecostraca, Polyplacophora, Polychaeta, Malacostraca, Arthropoda spc
Order	Arachnida spc, Insecta spc
Species	Homo sapiens, Meleagris gallopavo, Cyornis spc 1, Platorchestia platensis, Porcellanidae spc 1, Goniobranchus spc 1, Styliola spc 1, Zetela spc 1

Table S4: Model summaries for the dietary variation across the five most abundant orders for both species combined and all bird categories (female, male, nestling 10, nestling 15). Relative read abundance as response (zero-inflated Beta-hurdle, $RelativeReadAbundance \sim$ *ZIH-Beta*(μ, ϕ, π)) with posterior median and 2.5 to 97.5 credible intervals. Fitted are the fixed effects of competitive treatment of blue tits (Treatment B), great tits (Treatment G), the size of the Subplot, the effect of a close box proximity (Double box), bird category (female, male and nestling measured at day 10 and day 15), sample date, year, species (blue and great tit) and the interaction of both competitive treatments. As random effects fitted are brood ID, the Subplot, a combination of Subplot and year, a nestling stage and brood ID combination (nestling repeat) to account for multiple pooled tubes from one brood and the residual. Intercept and repeatabilities are shown as proportions on the original scale. Mean effects are calculated for the summarised effects for each species-specific treatment (blue and great tit treatment effect) and their four combinations ($B_L : G_L$, $B_L : G_H$, $B_H : G_L$, $B_H : G_H$). Mean effect for each bird category and their differences are estimated within the model. Distribution specific parameters phi (ϕ; precision parameter of beta distributions) and pi (π; hurdle pass probability (non-zero)) are shown. Fixed and random effects are shown on logit scale, intercept, mean effects and categories are shown on original scale. Number of observations = 853.

$RelativeReadAbundance \sim$ *ZIH-Beta*(μ, ϕ, π)	*Lepidoptera*	*Diptera*	*Araneae*	*Hymenoptera*	*Coleoptera*
Fixed effects					
Intercept	0.400 [0.383 ; 0.419]	0.312 [0.291 ; 0.333]	0.148 [0.135 ; 0.163]	0.198 [0.181 ; 0.217]	0.215 [0.195 ; 0.238]
Treatment B	-0.235 [-0.541 ; 0.104]	0.146 [-0.181 ; 0.461]	-0.118 [-0.394 ; 0.158]	0.099 [-0.177 ; 0.399]	0.211 [-0.183 ; 0.604]
Treatment G	-0.326 [-0.657 ; 0.032]	0.105 [-0.240 ; 0.446]	-0.267 [-0.555 ; 0.025]	0.053 [-0.286 ; 0.373]	0.076 [-0.387 ; 0.516]
Size subplot	-0.155 [-0.303 ; 0.001]	0.096 [-0.047 ; 0.244]	-0.049 [-0.174 ; 0.068]	0.042 [-0.099 ; 0.177]	0.136 [-0.065 ; 0.331]
Double box	0.098 [-0.257 ; 0.470]	-0.052 [-0.403 ; 0.294]	-0.113 [-0.433 ; 0.206]	0.307 [-0.018 ; 0.636]	-0.392 [-0.785 ; -0.001]
Male	-0.137 [-0.401 ; 0.133]	0.013 [-0.252 ; 0.290]	0.121 [-0.126 ; 0.360]	-0.115 [-0.384 ; 0.150]	0.124 [-0.157 ; 0.411]
Nestling 10	-0.065 [-0.317 ; 0.185]	0.652 [0.404 ; 0.912]	-0.338 [-0.563 ; -0.096]	-0.127 [-0.391 ; 0.137]	-0.432 [-0.716 ; -0.133]
Nestling 15	-0.208 [-0.477 ; 0.052]	0.737 [0.454 ; 1.011]	-0.416 [-0.682 ; -0.150]	0.274 [0.004 ; 0.550]	-0.384 [-0.692 ; -0.073]
Date	-0.014 [-0.032 ; 0.004]	0.008 [-0.010 ; 0.025]	0.008 [-0.009 ; 0.025]	0.017 [-0.002 ; 0.034]	0.008 [-0.011 ; 0.028]
Year 2024	-0.265 [-0.609 ; 0.073]	0.067 [-0.256 ; 0.391]	0.121 [-0.199 ; 0.440]	0.203 [-0.129 ; 0.538]	0.251 [-0.132 ; 0.645]
Species	-0.097 [-0.293 ; 0.093]	0.566 [0.366 ; 0.765]	-0.277 [-0.459 ; -0.100]	-0.256 [-0.446 ; -0.072]	0.322 [0.102 ; 0.557]
Treatment B x Treatment G	0.261 [-0.244 ; 0.720]	-0.243 [-0.722 ; 0.254]	0.217 [-0.186 ; 0.621]	-0.103 [-0.540 ; 0.341]	-0.015 [-0.616 ; 0.580]
Random effects					
Brood ID	0.014 [0.000 ; 0.105]	0.004 [0.000 ; 0.040]	0.002 [0.000 ; 0.025]	0.003 [0.000 ; 0.039]	0.003 [0.000 ; 0.041]
Subplot	0.008 [0.000 ; 0.096]	0.004 [0.000 ; 0.067]	0.003 [0.000 ; 0.037]	0.004 [0.000 ; 0.066]	0.016 [0.000 ; 0.168]
Subplot year	0.006 [0.000 ; 0.063]	0.004 [0.000 ; 0.053]	0.003 [0.000 ; 0.033]	0.002 [0.000 ; 0.036]	0.021 [0.000 ; 0.140]
Nestlings repeat	0.294 [0.094 ; 0.540]	0.003 [0.000 ; 0.038]	0.002 [0.000 ; 0.023]	0.003 [0.000 ; 0.034]	0.003 [0.000 ; 0.035]
Residual	0.092 [0.080 ; 0.104]	0.098 [0.090 ; 0.106]	0.029 [0.025 ; 0.034]	0.050 [0.044 ; 0.057]	0.052 [0.045 ; 0.061]
Repeatability					
Brood ID	0.032 [0.000 ; 0.236]	0.030 [0.000 ; 0.253]	0.046 [0.000 ; 0.369]	0.044 [0.000 ; 0.368]	0.028 [0.000 ; 0.297]
Subplot	0.019 [0.000 ; 0.203]	0.035 [0.000 ; 0.357]	0.055 [0.000 ; 0.464]	0.052 [0.000 ; 0.497]	0.146 [0.001 ; 0.657]
Subplot year	0.013 [0.000 ; 0.141]	0.034 [0.000 ; 0.296]	0.055 [0.000 ; 0.439]	0.032 [0.000 ; 0.328]	0.184 [0.001 ; 0.628]
Nestlings repeat	0.674 [0.349 ; 0.830]	0.027 [0.000 ; 0.239]	0.044 [0.000 ; 0.345]	0.041 [0.000 ; 0.341]	0.027 [0.000 ; 0.261]
Residual	0.208 [0.115 ; 0.426]	0.763 [0.460 ; 0.959]	0.624 [0.281 ; 0.931]	0.681 [0.329 ; 0.939]	0.441 [0.165 ; 0.845]
Mean effects					
Treatment B	-0.026 [-0.087 ; 0.036]	0.004 [-0.030 ; 0.041]	-0.002 [-0.034 ; 0.031]	0.008 [-0.026 ; 0.043]	0.033 [-0.020 ; 0.085]
Treatment G	-0.048 [-0.106 ; 0.013]	-0.003 [-0.037 ; 0.032]	-0.025 [-0.057 ; 0.007]	0.000 [-0.037 ; 0.037]	0.011 [-0.041 ; 0.063]
$B_L : G_L$	0.510 [0.425 ; 0.589]	0.166 [0.121 ; 0.220]	0.211 [0.163 ; 0.264]	0.187 [0.141 ; 0.247]	0.179 [0.125 ; 0.252]
$B_L : G_H$	0.429 [0.345 ; 0.516]	0.181 [0.133 ; 0.239]	0.169 [0.131 ; 0.216]	0.196 [0.146 ; 0.255]	0.191 [0.132 ; 0.269]
$B_H : G_L$	0.451 [0.369 ; 0.538]	0.187 [0.138 ; 0.244]	0.192 [0.148 ; 0.242]	0.204 [0.156 ; 0.264]	0.212 [0.151 ; 0.290]
$B_H : G_H$	0.435 [0.349 ; 0.527]	0.167 [0.119 ; 0.226]	0.183 [0.138 ; 0.240]	0.196 [0.146 ; 0.260]	0.223 [0.153 ; 0.312]

Table S4: (continued)

$RelativeReadAbundance \sim$ ZIH-Beta(μ, ϕ, π)	*Lepidoptera*	*Diptera*	*Araneae*	*Hymenoptera*	*Coleoptera*
Categorys					
Female	0.510 [0.425 ; 0.589]	0.166 [0.121 ; 0.220]	0.211 [0.163 ; 0.264]	0.187 [0.141 ; 0.247]	0.179 [0.125 ; 0.252]
Male	0.476 [0.387 ; 0.563]	0.168 [0.124 ; 0.222]	0.230 [0.180 ; 0.287]	0.170 [0.127 ; 0.226]	0.198 [0.140 ; 0.280]
Nestling 10	0.494 [0.413 ; 0.572]	0.276 [0.216 ; 0.345]	0.160 [0.124 ; 0.203]	0.169 [0.128 ; 0.220]	0.125 [0.086 ; 0.178]
Nestling 15	0.458 [0.374 ; 0.543]	0.293 [0.226 ; 0.372]	0.149 [0.112 ; 0.194]	0.233 [0.177 ; 0.302]	0.130 [0.088 ; 0.190]
Adult	0.493 [0.413 ; 0.571]	0.167 [0.126 ; 0.217]	0.220 [0.176 ; 0.272]	0.179 [0.138 ; 0.231]	0.189 [0.135 ; 0.262]
Nestling	0.476 [0.399 ; 0.552]	0.285 [0.226 ; 0.353]	0.154 [0.121 ; 0.195]	0.201 [0.157 ; 0.257]	0.128 [0.089 ; 0.180]
Diff adults	0.034 [-0.033 ; 0.099]	-0.002 [-0.040 ; 0.035]	-0.021 [-0.062 ; 0.022]	0.017 [-0.023 ; 0.058]	-0.019 [-0.065 ; 0.024]
Diff nestlings	0.036 [-0.025 ; 0.098]	-0.016 [-0.070 ; 0.034]	0.010 [-0.023 ; 0.042]	-0.063 [-0.110 ; -0.023]	-0.005 [-0.042 ; 0.029]
Diff categories	0.017 [-0.028 ; 0.064]	-0.117 [-0.157 ; -0.082]	0.065 [0.038 ; 0.096]	-0.022 [-0.052 ; 0.008]	0.062 [0.031 ; 0.099]
Distribution parameters					
phi	1.476 [1.260 ; 1.750]	1.030 [0.936 ; 1.129]	2.606 [2.294 ; 2.943]	1.652 [1.470 ; 1.849]	1.360 [1.200 ; 1.533]
pi	0.968 [0.954 ; 0.979]	0.805 [0.779 ; 0.830]	0.702 [0.671 ; 0.731]	0.696 [0.664 ; 0.726]	0.575 [0.543 ; 0.607]

Table S5: Model summaries for the dietary variation across the five most abundant orders for blue tits using the same model structure and estimation as specified in Table S4, exempt the fixed effect for species. Number of observations = 386.

$RelativeReadAbundance \sim$ ZIH-Beta(μ, ϕ, π)	*Lepidoptera*	*Diptera*	*Araneae*	*Hymenoptera*	*Coleoptera*
Fixed effects					
Intercept	0.412 [0.385 ; 0.442]	0.211 [0.184 ; 0.240]	0.174 [0.153 ; 0.198]	0.238 [0.212 ; 0.266]	0.162 [0.136 ; 0.195]
Treatment B	-0.247 [-0.656 ; 0.204]	0.076 [-0.376 ; 0.516]	-0.015 [-0.411 ; 0.372]	0.259 [-0.182 ; 0.676]	0.089 [-0.382 ; 0.571]
Treatment G	-0.157 [-0.625 ; 0.390]	0.066 [-0.475 ; 0.559]	-0.192 [-0.652 ; 0.249]	-0.055 [-0.575 ; 0.419]	0.119 [-0.397 ; 0.647]
Size subplot	-0.049 [-0.291 ; 0.202]	0.004 [-0.222 ; 0.215]	0.006 [-0.208 ; 0.208]	0.035 [-0.201 ; 0.243]	0.001 [-0.239 ; 0.243]
Double box	0.287 [-0.215 ; 0.811]	-0.024 [-0.566 ; 0.503]	-0.342 [-0.819 ; 0.115]	0.456 [-0.052 ; 0.984]	-0.400 [-1.039 ; 0.201]
Male	-0.072 [-0.472 ; 0.324]	-0.010 [-0.429 ; 0.402]	0.303 [-0.057 ; 0.682]	-0.046 [-0.473 ; 0.392]	-0.177 [-0.680 ; 0.290]
Nestling 10	0.359 [0.013 ; 0.700]	0.193 [-0.169 ; 0.566]	-0.331 [-0.665 ; 0.000]	-0.133 [-0.514 ; 0.224]	-0.606 [-1.018 ; -0.190]
Nestling 15	-0.092 [-0.459 ; 0.297]	0.507 [0.089 ; 0.924]	-0.396 [-0.764 ; -0.048]	0.528 [0.154 ; 0.928]	-0.671 [-1.131 ; -0.195]
Date	-0.006 [-0.040 ; 0.026]	0.000 [-0.032 ; 0.031]	-0.012 [-0.040 ; 0.017]	0.011 [-0.020 ; 0.042]	0.013 [-0.023 ; 0.049]
Year 2024	-0.276 [-0.857 ; 0.295]	-0.039 [-0.642 ; 0.518]	-0.329 [-0.848 ; 0.192]	0.183 [-0.371 ; 0.733]	0.351 [-0.300 ; 0.976]
Treatment B x Treatment G	0.063 [-0.625 ; 0.715]	-0.236 [-0.903 ; 0.481]	0.253 [-0.358 ; 0.848]	0.000 [-0.648 ; 0.652]	0.022 [-0.701 ; 0.778]
Random effects					
Brood ID	0.037 [0.000 ; 0.216]	0.007 [0.000 ; 0.093]	0.005 [0.000 ; 0.064]	0.010 [0.000 ; 0.111]	0.007 [0.000 ; 0.073]
Subplot	0.023 [0.000 ; 0.253]	0.007 [0.000 ; 0.123]	0.011 [0.000 ; 0.152]	0.012 [0.000 ; 0.182]	0.013 [0.000 ; 0.168]
Subplot year	0.013 [0.000 ; 0.154]	0.014 [0.000 ; 0.148]	0.006 [0.000 ; 0.078]	0.007 [0.000 ; 0.097]	0.010 [0.000 ; 0.129]
Nestlings repeat	0.026 [0.000 ; 0.243]	0.005 [0.000 ; 0.061]	0.006 [0.000 ; 0.074]	0.009 [0.000 ; 0.117]	0.007 [0.000 ; 0.068]
Residual	0.097 [0.084 ; 0.107]	0.057 [0.047 ; 0.068]	0.037 [0.030 ; 0.046]	0.065 [0.055 ; 0.076]	0.034 [0.025 ; 0.044]
Repeatability					
Brood ID	0.146 [0.000 ; 0.567]	0.062 [0.000 ; 0.495]	0.061 [0.000 ; 0.482]	0.072 [0.000 ; 0.497]	0.072 [0.000 ; 0.495]
Subplot	0.094 [0.000 ; 0.566]	0.061 [0.000 ; 0.529]	0.124 [0.000 ; 0.699]	0.092 [0.000 ; 0.620]	0.142 [0.000 ; 0.702]
Subplot year	0.053 [0.000 ; 0.427]	0.120 [0.000 ; 0.622]	0.069 [0.000 ; 0.542]	0.054 [0.000 ; 0.454]	0.113 [0.000 ; 0.634]
Nestlings repeat	0.105 [0.000 ; 0.569]	0.044 [0.000 ; 0.393]	0.066 [0.000 ; 0.513]	0.067 [0.000 ; 0.526]	0.068 [0.000 ; 0.492]
Residual	0.376 [0.145 ; 0.790]	0.486 [0.174 ; 0.873]	0.415 [0.137 ; 0.848]	0.473 [0.171 ; 0.876]	0.350 [0.107 ; 0.802]
Mean effects					
Treatment B	-0.051 [-0.135 ; 0.037]	-0.006 [-0.060 ; 0.048]	0.018 [-0.035 ; 0.076]	0.038 [-0.016 ; 0.092]	0.016 [-0.047 ; 0.086]
Treatment G	-0.029 [-0.113 ; 0.069]	-0.007 [-0.062 ; 0.048]	-0.011 [-0.069 ; 0.047]	-0.008 [-0.066 ; 0.045]	0.022 [-0.040 ; 0.093]
$B_L : G_L$	0.465 [0.339 ; 0.584]	0.175 [0.115 ; 0.265]	0.232 [0.162 ; 0.320]	0.171 [0.110 ; 0.261]	0.178 [0.114 ; 0.269]
$B_L : G_H$	0.428 [0.315 ; 0.554]	0.184 [0.118 ; 0.280]	0.200 [0.135 ; 0.285]	0.162 [0.101 ; 0.253]	0.196 [0.123 ; 0.304]
$B_H : G_L$	0.406 [0.296 ; 0.517]	0.186 [0.125 ; 0.274]	0.229 [0.159 ; 0.316]	0.209 [0.142 ; 0.305]	0.192 [0.124 ; 0.283]
$B_H : G_H$	0.384 [0.264 ; 0.518]	0.162 [0.097 ; 0.260]	0.240 [0.157 ; 0.348]	0.200 [0.127 ; 0.305]	0.216 [0.122 ; 0.347]
Category					
Female	0.465 [0.339 ; 0.584]	0.175 [0.115 ; 0.265]	0.232 [0.162 ; 0.320]	0.171 [0.110 ; 0.261]	0.178 [0.114 ; 0.269]
Male	0.447 [0.319 ; 0.571]	0.174 [0.112 ; 0.264]	0.290 [0.204 ; 0.392]	0.164 [0.102 ; 0.253]	0.153 [0.092 ; 0.249]
Nestling 10	0.555 [0.438 ; 0.660]	0.206 [0.141 ; 0.296]	0.180 [0.125 ; 0.250]	0.152 [0.099 ; 0.228]	0.106 [0.066 ; 0.165]
Nestling 15	0.442 [0.310 ; 0.579]	0.261 [0.170 ; 0.383]	0.169 [0.110 ; 0.250]	0.258 [0.167 ; 0.386]	0.100 [0.056 ; 0.175]
Adult	0.455 [0.337 ; 0.567]	0.175 [0.118 ; 0.258]	0.262 [0.190 ; 0.348]	0.168 [0.111 ; 0.249]	0.166 [0.108 ; 0.249]
Nestling	0.499 [0.380 ; 0.612]	0.233 [0.160 ; 0.331]	0.175 [0.122 ; 0.245]	0.205 [0.137 ; 0.302]	0.103 [0.064 ; 0.165]
Diff adults	0.018 [-0.079 ; 0.114]	0.001 [-0.061 ; 0.063]	-0.058 [-0.134 ; 0.011]	0.006 [-0.055 ; 0.069]	0.024 [-0.044 ; 0.093]
Diff nestlings	0.110 [0.022 ; 0.196]	-0.055 [-0.133 ; 0.012]	0.010 [-0.044 ; 0.060]	-0.105 [-0.189 ; -0.044]	0.005 [-0.044 ; 0.047]
Diff categories	-0.043 [-0.105 ; 0.024]	-0.058 [-0.111 ; -0.011]	0.087 [0.045 ; 0.136]	-0.038 [-0.087 ; 0.006]	0.062 [0.026 ; 0.110]
Distribution parameters					
phi	1.412 [1.219 ; 1.693]	1.509 [1.271 ; 1.798]	2.455 [2.045 ; 2.924]	1.483 [1.258 ; 1.753]	1.689 [1.343 ; 2.088]
pi	0.980 [0.964 ; 0.991]	0.736 [0.692 ; 0.777]	0.775 [0.732 ; 0.814]	0.775 [0.733 ; 0.814]	0.534 [0.486 ; 0.579]

Table S6: Model summaries for the dietary variation across the five most abundant orders for great tits using the same model structure and estimation as specified in Table S4, exempt the fixed effect for species. Number of observations = 468.

$RelativeReadAbundance \sim$ ZIH-Beta(μ, ϕ, π)	*Lepidoptera*	*Diptera*	*Araneae*	*Hymenoptera*	*Coleoptera*
Fixed effects					
Intercept	0.387 [0.365 ; 0.412]	0.373 [0.345 ; 0.402]	0.127 [0.109 ; 0.148]	0.157 [0.136 ; 0.181]	0.254 [0.225 ; 0.285]
Treatment B	-0.191 [-0.698 ; 0.340]	0.150 [-0.327 ; 0.625]	-0.303 [-0.740 ; 0.112]	-0.207 [-0.644 ; 0.231]	0.386 [-0.183 ; 0.914]
Treatment G	-0.372 [-0.882 ; 0.157]	0.089 [-0.377 ; 0.548]	-0.274 [-0.700 ; 0.149]	0.120 [-0.314 ; 0.540]	0.053 [-0.539 ; 0.597]
Size subplot	-0.253 [-0.494 ; -0.023]	0.119 [-0.072 ; 0.319]	-0.079 [-0.272 ; 0.105]	0.087 [-0.109 ; 0.273]	0.239 [-0.022 ; 0.505]
Double box	-0.218 [-0.721 ; 0.309]	0.062 [-0.415 ; 0.513]	0.073 [-0.359 ; 0.508]	0.076 [-0.373 ; 0.512]	-0.338 [-0.824 ; 0.168]
Male	-0.124 [-0.502 ; 0.256]	-0.016 [-0.344 ; 0.330]	-0.010 [-0.320 ; 0.313]	-0.235 [-0.572 ; 0.107]	0.226 [-0.112 ; 0.582]
Nestling 10	-0.421 [-0.795 ; -0.055]	0.928 [0.582 ; 1.276]	-0.391 [-0.717 ; -0.063]	-0.161 [-0.528 ; 0.192]	-0.341 [-0.737 ; 0.063]
Nestling 15	-0.305 [-0.680 ; 0.093]	0.846 [0.447 ; 1.221]	-0.350 [-0.736 ; 0.042]	-0.096 [-0.462 ; 0.278]	-0.261 [-0.674 ; 0.134]
Date	-0.019 [-0.041 ; 0.004]	0.011 [-0.011 ; 0.032]	0.015 [-0.006 ; 0.036]	0.013 [-0.010 ; 0.035]	0.006 [-0.018 ; 0.029]
Year 2024	-0.233 [-0.716 ; 0.216]	0.043 [-0.377 ; 0.477]	0.410 [-0.019 ; 0.831]	0.189 [-0.234 ; 0.621]	0.168 [-0.312 ; 0.649]
Treatment B x Treatment G	0.368 [-0.394 ; 1.027]	-0.233 [-0.834 ; 0.437]	0.247 [-0.370 ; 0.852]	0.002 [-0.598 ; 0.633]	-0.204 [-0.973 ; 0.593]
Random effects					
Brood ID	0.014 [0.000 ; 0.126]	0.009 [0.000 ; 0.086]	0.005 [0.000 ; 0.055]	0.005 [0.000 ; 0.055]	0.009 [0.000 ; 0.106]
Subplot	0.019 [0.000 ; 0.217]	0.009 [0.000 ; 0.136]	0.006 [0.000 ; 0.098]	0.006 [0.000 ; 0.075]	0.029 [0.000 ; 0.293]
Subplot year	0.019 [0.000 ; 0.184]	0.014 [0.000 ; 0.133]	0.007 [0.000 ; 0.095]	0.006 [0.000 ; 0.077]	0.029 [0.000 ; 0.218]
Nestlings repeat	0.507 [0.200 ; 0.984]	0.008 [0.000 ; 0.088]	0.004 [0.000 ; 0.048]	0.004 [0.000 ; 0.046]	0.007 [0.000 ; 0.073]
Residual	0.082 [0.065 ; 0.098]	0.116 [0.107 ; 0.126]	0.022 [0.017 ; 0.028]	0.032 [0.025 ; 0.041]	0.066 [0.056 ; 0.078]
Repeatability					
Brood ID	0.020 [0.000 ; 0.191]	0.046 [0.000 ; 0.342]	0.078 [0.000 ; 0.531]	0.067 [0.000 ; 0.492]	0.053 [0.000 ; 0.439]
Subplot	0.029 [0.000 ; 0.257]	0.050 [0.000 ; 0.445]	0.112 [0.000 ; 0.680]	0.082 [0.000 ; 0.574]	0.176 [0.001 ; 0.707]
Subplot year	0.028 [0.000 ; 0.229]	0.079 [0.000 ; 0.448]	0.121 [0.000 ; 0.672]	0.085 [0.000 ; 0.586]	0.164 [0.001 ; 0.657]
Nestlings repeat	0.743 [0.440 ; 0.893]	0.044 [0.000 ; 0.352]	0.066 [0.000 ; 0.504]	0.056 [0.000 ; 0.455]	0.036 [0.000 ; 0.344]
Residual	0.119 [0.056 ; 0.264]	0.623 [0.307 ; 0.905]	0.345 [0.101 ; 0.799]	0.466 [0.171 ; 0.866]	0.359 [0.132 ; 0.767]
Mean effects					
Treatment B	-0.003 [-0.097 ; 0.088]	0.007 [-0.059 ; 0.080]	-0.021 [-0.060 ; 0.013]	-0.027 [-0.071 ; 0.017]	0.054 [-0.028 ; 0.142]
Treatment G	-0.045 [-0.138 ; 0.046]	-0.005 [-0.074 ; 0.060]	-0.018 [-0.055 ; 0.017]	0.017 [-0.027 ; 0.059]	-0.009 [-0.093 ; 0.069]
$B_L : G_L$	0.498 [0.385 ; 0.605]	0.252 [0.180 ; 0.341]	0.161 [0.114 ; 0.223]	0.165 [0.119 ; 0.229]	0.231 [0.158 ; 0.332]
$B_L : G_H$	0.405 [0.301 ; 0.522]	0.269 [0.196 ; 0.351]	0.127 [0.092 ; 0.179]	0.182 [0.130 ; 0.252]	0.242 [0.161 ; 0.337]
$B_H : G_L$	0.449 [0.337 ; 0.572]	0.282 [0.200 ; 0.381]	0.124 [0.085 ; 0.174]	0.140 [0.092 ; 0.201]	0.307 [0.212 ; 0.425]
$B_H : G_H$	0.448 [0.326 ; 0.565]	0.255 [0.180 ; 0.351]	0.120 [0.082 ; 0.173]	0.154 [0.106 ; 0.221]	0.275 [0.182 ; 0.395]
Category					
Female	0.498 [0.385 ; 0.605]	0.252 [0.180 ; 0.341]	0.161 [0.114 ; 0.223]	0.165 [0.119 ; 0.229]	0.231 [0.158 ; 0.332]
Male	0.465 [0.354 ; 0.582]	0.249 [0.180 ; 0.337]	0.159 [0.115 ; 0.216]	0.135 [0.095 ; 0.190]	0.274 [0.194 ; 0.379]
Nestling 10	0.393 [0.291 ; 0.501]	0.459 [0.361 ; 0.567]	0.115 [0.079 ; 0.162]	0.145 [0.099 ; 0.207]	0.177 [0.114 ; 0.269]
Nestling 15	0.424 [0.314 ; 0.538]	0.439 [0.333 ; 0.551]	0.119 [0.079 ; 0.175]	0.153 [0.105 ; 0.215]	0.188 [0.120 ; 0.288]
Adult	0.482 [0.377 ; 0.581]	0.250 [0.186 ; 0.333]	0.160 [0.117 ; 0.216]	0.150 [0.111 ; 0.204]	0.253 [0.181 ; 0.350]
Nestling	0.409 [0.310 ; 0.507]	0.450 [0.356 ; 0.550]	0.118 [0.083 ; 0.162]	0.150 [0.108 ; 0.204]	0.183 [0.122 ; 0.269]
Diff adults	0.030 [-0.063 ; 0.124]	0.003 [-0.062 ; 0.065]	0.001 [-0.041 ; 0.045]	0.029 [-0.014 ; 0.076]	-0.042 [-0.110 ; 0.022]
Diff nestlings	-0.031 [-0.118 ; 0.059]	0.021 [-0.069 ; 0.106]	-0.004 [-0.045 ; 0.033]	-0.008 [-0.057 ; 0.041]	-0.012 [-0.084 ; 0.057]
Diff categories	0.073 [0.003 ; 0.142]	-0.197 [-0.261 ; -0.135]	0.043 [0.012 ; 0.077]	0.002 [-0.033 ; 0.035]	0.069 [0.020 ; 0.124]
Distribution parameters					
phi	1.654 [1.310 ; 2.223]	0.926 [0.819 ; 1.045]	2.972 [2.461 ; 3.552]	2.157 [1.782 ; 2.593]	1.269 [1.078 ; 1.509]
pi	0.954 [0.932 ; 0.971]	0.860 [0.827 ; 0.890]	0.639 [0.595 ; 0.681]	0.629 [0.584 ; 0.672]	0.609 [0.564 ; 0.653]

Table S7: Model summaries for the dietary variation across the five most abundant for both species combined, orders using the same model structure and estimation as specified in Table S4, exempt adjusted fixed effect for significant differences in bird categories for each order.

$RelativeReadAbundance \sim$ *ZIH-Beta*(μ, ϕ, π)	*Lepidoptera*	*Diptera*	*Araneae*	*Hymenoptera*	*Coleoptera*
Fixed effects					
Intercept	0.400 [0.382 ; 0.420]	0.312 [0.291 ; 0.332]	0.148 [0.135 ; 0.163]	0.198 [0.181 ; 0.217]	0.215 [0.195 ; 0.237]
Treatment B	-0.236 [-0.553 ; 0.088]	0.137 [-0.183 ; 0.458]	-0.113 [-0.390 ; 0.164]	0.099 [-0.177 ; 0.399]	0.198 [-0.192 ; 0.590]
Treatment G	-0.323 [-0.676 ; 0.039]	0.095 [-0.251 ; 0.436]	-0.267 [-0.559 ; 0.019]	0.053 [-0.286 ; 0.373]	0.077 [-0.404 ; 0.489]
Size subplot	-0.144 [-0.300 ; 0.010]	0.092 [-0.054 ; 0.237]	-0.047 [-0.177 ; 0.076]	0.042 [-0.099 ; 0.177]	0.132 [-0.067 ; 0.331]
Double box	0.110 [-0.232 ; 0.455]	-0.058 [-0.391 ; 0.287]	-0.100 [-0.424 ; 0.206]	0.307 [-0.018 ; 0.636]	-0.396 [-0.787 ; -0.022]
Nestling	-	0.683 [0.486 ; 0.876]	-0.429 [-0.608 ; -0.247]	-	-0.475 [-0.692 ; -0.246]
Nestling 10	-	-	-	-0.115 [-0.384 ; 0.150]	-
Nestling 15	-	-	-	-0.127 [-0.391 ; 0.137]	-
Date	-0.018 [-0.034 ; -0.001]	0.009 [-0.008 ; 0.026]	0.007 [-0.009 ; 0.022]	0.274 [0.004 ; 0.550]	0.009 [-0.009 ; 0.028]
Year 2024	-0.312 [-0.636 ; 0.021]	0.089 [-0.242 ; 0.417]	0.103 [-0.200 ; 0.402]	0.017 [-0.002 ; 0.034]	0.282 [-0.097 ; 0.660]
Species	-0.091 [-0.287 ; 0.103]	0.565 [0.359 ; 0.770]	-0.269 [-0.458 ; -0.083]	0.203 [-0.129 ; 0.538]	0.327 [0.096 ; 0.557]
Treatment B x Treatment G	-	-0.223 [-0.698 ; 0.231]	0.213 [-0.221 ; 0.628]	-0.103 [-0.540 ; 0.341]	0.003 [-0.579 ; 0.617]
Random effects					
Brood ID	0.016 [0.000 ; 0.107]	0.004 [0.000 ; 0.043]	0.002 [0.000 ; 0.023]	0.003 [0.000 ; 0.039]	0.004 [0.000 ; 0.039]
Subplot	0.009 [0.000 ; 0.095]	0.005 [0.000 ; 0.069]	0.002 [0.000 ; 0.044]	0.004 [0.000 ; 0.066]	0.016 [0.000 ; 0.170]
Subplot year	0.006 [0.000 ; 0.068]	0.005 [0.000 ; 0.050]	0.003 [0.000 ; 0.034]	0.002 [0.000 ; 0.036]	0.019 [0.000 ; 0.133]
Nestlings repeat	0.287 [0.084 ; 0.552]	0.004 [0.000 ; 0.040]	0.002 [0.000 ; 0.023]	0.003 [0.000 ; 0.034]	0.003 [0.000 ; 0.035]
Residual	0.092 [0.080 ; 0.104]	0.098 [0.090 ; 0.105]	0.029 [0.025 ; 0.034]	0.050 [0.044 ; 0.057]	0.052 [0.045 ; 0.060]
Repeatability					
Brood ID	0.038 [0.000 ; 0.255]	0.031 [0.000 ; 0.262]	0.045 [0.000 ; 0.364]	0.044 [0.000 ; 0.368]	0.030 [0.000 ; 0.292]
Subplot	0.020 [0.000 ; 0.197]	0.037 [0.000 ; 0.356]	0.054 [0.000 ; 0.510]	0.052 [0.000 ; 0.497]	0.153 [0.000 ; 0.667]
Subplot year	0.013 [0.000 ; 0.148]	0.036 [0.000 ; 0.286]	0.058 [0.000 ; 0.437]	0.032 [0.000 ; 0.328]	0.168 [0.000 ; 0.620]
Nestlings repeat	0.664 [0.311 ; 0.830]	0.030 [0.000 ; 0.248]	0.042 [0.000 ; 0.372]	0.041 [0.000 ; 0.341]	0.027 [0.000 ; 0.262]
Residual	0.213 [0.115 ; 0.425]	0.760 [0.459 ; 0.957]	0.622 [0.280 ; 0.921]	0.681 [0.329 ; 0.939]	0.452 [0.171 ; 0.840]
Mean effects					
Treatment B	-0.027 [-0.087 ; 0.035]	0.003 [-0.031 ; 0.041]	-0.001 [-0.036 ; 0.033]	0.008 [-0.026 ; 0.043]	0.034 [-0.019 ; 0.087]
Treatment G	-0.048 [-0.107 ; 0.015]	-0.003 [-0.038 ; 0.031]	-0.026 [-0.060 ; 0.008]	0.000 [-0.037 ; 0.037]	0.012 [-0.041 ; 0.065]
$B_L : G_L$	0.488 [0.413 ; 0.561]	0.166 [0.126 ; 0.218]	0.220 [0.174 ; 0.273]	0.187 [0.141 ; 0.247]	0.188 [0.137 ; 0.259]
$B_L : G_H$	0.409 [0.338 ; 0.488]	0.180 [0.136 ; 0.233]	0.178 [0.140 ; 0.223]	0.196 [0.146 ; 0.255]	0.199 [0.141 ; 0.272]
$B_H : G_L$	0.430 [0.360 ; 0.502]	0.187 [0.142 ; 0.242]	0.202 [0.161 ; 0.249]	0.204 [0.156 ; 0.264]	0.221 [0.164 ; 0.291]
$B_H : G_H$	0.413 [0.334 ; 0.495]	0.167 [0.123 ; 0.223]	0.194 [0.148 ; 0.246]	0.196 [0.146 ; 0.260]	0.233 [0.164 ; 0.320]
Distribution parameters					
phi	1.465 [1.256 ; 1.757]	1.473 [1.261 ; 1.767]	1.029 [0.940 ; 1.128]	1.652 [1.470 ; 1.849]	1.357 [1.198 ; 1.547]
pi	0.968 [0.955 ; 0.978]	0.968 [0.955 ; 0.978]	0.805 [0.779 ; 0.830]	0.696 [0.664 ; 0.726]	0.575 [0.541 ; 0.608]

Table S8: Model summaries for the dietary variation across the five most abundant orders for blue tits using the same model structure and estimation as specified in Table S5, exempt adjusted fixed effect for significant differences in bird categories for each order.

$RelativeReadAbundance \sim$ ZIH-Beta(μ, ϕ, π)	*Lepidoptera*	*Diptera*	*Araneae*	*Hymenoptera*	*Coleoptera*
Fixed effects					
Intercept	0.412 [0.384 ; 0.440]	0.210 [0.183 ; 0.240]	0.174 [0.153 ; 0.197]	0.238 [0.212 ; 0.266]	0.163 [0.136 ; 0.196]
Treatment B	-0.245 [-0.675 ; 0.176]	0.060 [-0.390 ; 0.480]	0.002 [-0.388 ; 0.374]	0.010 [0.000 ; 0.106]	0.101 [-0.366 ; 0.565]
Treatment G	-0.148 [-0.641 ; 0.376]	0.050 [-0.464 ; 0.528]	-0.208 [-0.636 ; 0.256]	0.013 [0.000 ; 0.178]	0.108 [-0.429 ; 0.630]
Size subplot	-0.052 [-0.292 ; 0.192]	-0.024 [-0.246 ; 0.182]	0.004 [-0.202 ; 0.204]	0.007 [0.000 ; 0.091]	0.006 [-0.234 ; 0.247]
Double box	0.283 [-0.210 ; 0.758]	-0.004 [-0.512 ; 0.513]	-0.303 [-0.787 ; 0.175]	0.009 [0.000 ; 0.107]	-0.409 [-1.044 ; 0.225]
Nestling	-	0.318 [0.026 ; 0.609]	-0.498 [-0.754 ; -0.244]	-	-0.564 [-0.884 ; -0.240]
Nestling 10	0.395 [0.098 ; 0.711]	-	-	0.065 [0.056 ; 0.077]	-
Nestling 15	-0.057 [-0.377 ; 0.267]	-	-	0.074 [0.000 ; 0.497]	-
Date	-0.007 [-0.039 ; 0.025]	0.011 [-0.019 ; 0.041]	-0.014 [-0.040 ; 0.013]	0.096 [0.000 ; 0.605]	0.011 [-0.021 ; 0.043]
Year 2024	-0.274 [-0.825 ; 0.297]	0.133 [-0.401 ; 0.687]	-0.348 [-0.836 ; 0.141]	0.052 [0.000 ; 0.442]	0.300 [-0.286 ; 0.899]
Treatment B x Treatment G	0.074 [-0.599 ; 0.719]	-0.252 [-0.911 ; 0.435]	0.255 [-0.356 ; 0.855]	0.069 [0.000 ; 0.503]	0.055 [-0.697 ; 0.800]
Random effects					
Brood ID	0.037 [0.000 ; 0.222]	0.007 [0.000 ; 0.079]	0.005 [0.000 ; 0.057]	0.483 [0.179 ; 0.872]	0.006 [0.000 ; 0.074]
Subplot	0.021 [0.000 ; 0.248]	0.007 [0.000 ; 0.121]	0.010 [0.000 ; 0.137]	1.480 [1.261 ; 1.742]	0.012 [0.000 ; 0.171]
Subplot year	0.013 [0.000 ; 0.136]	0.011 [0.000 ; 0.130]	0.006 [0.000 ; 0.076]	0.775 [0.733 ; 0.813]	0.010 [0.000 ; 0.124]
Nestlings repeat	0.022 [0.000 ; 0.228]	0.005 [0.000 ; 0.061]	0.006 [0.000 ; 0.065]	0.038 [-0.013 ; 0.094]	0.006 [0.000 ; 0.066]
Residual	0.097 [0.085 ; 0.107]	0.057 [0.047 ; 0.069]	0.037 [0.030 ; 0.046]	-0.008 [-0.063 ; 0.045]	0.034 [0.026 ; 0.045]
Repeatability					
Brood ID	0.149 [0.000 ; 0.596]	0.059 [0.000 ; 0.469]	0.056 [0.000 ; 0.440]	0.168 [0.112 ; 0.245]	0.063 [0.000 ; 0.527]
Subplot	0.089 [0.000 ; 0.576]	0.063 [0.000 ; 0.551]	0.124 [0.000 ; 0.687]	0.160 [0.102 ; 0.237]	0.139 [0.000 ; 0.719]
Subplot year	0.051 [0.000 ; 0.400]	0.098 [0.000 ; 0.571]	0.074 [0.000 ; 0.543]	0.206 [0.144 ; 0.292]	0.109 [0.000 ; 0.649]
Nestlings repeat	0.091 [0.000 ; 0.564]	0.045 [0.000 ; 0.383]	0.069 [0.000 ; 0.496]	0.199 [0.124 ; 0.298]	0.060 [0.000 ; 0.487]
Residual	0.391 [0.155 ; 0.787]	0.519 [0.188 ; 0.887]	0.438 [0.151 ; 0.847]	0.238 [0.212 ; 0.266]	0.353 [0.108 ; 0.801]
Mean effects					
Treatment B	-0.052 [-0.134 ; 0.036]	-0.009 [-0.056 ; 0.044]	0.023 [-0.038 ; 0.084]	0.007 [0.000 ; 0.091]	0.019 [-0.045 ; 0.085]
Treatment G	-0.025 [-0.113 ; 0.067]	-0.010 [-0.059 ; 0.040]	-0.015 [-0.075 ; 0.051]	0.009 [0.000 ; 0.107]	0.021 [-0.041 ; 0.092]
$B_L : G_L$	0.457 [0.345 ; 0.566]	0.167 [0.112 ; 0.241]	0.260 [0.191 ; 0.343]	0.065 [0.056 ; 0.077]	0.171 [0.109 ; 0.254]
$B_L : G_H$	0.420 [0.308 ; 0.541]	0.175 [0.114 ; 0.251]	0.222 [0.156 ; 0.307]	0.074 [0.000 ; 0.497]	0.187 [0.119 ; 0.281]
$B_H : G_L$	0.395 [0.296 ; 0.505]	0.176 [0.120 ; 0.251]	0.259 [0.192 ; 0.342]	0.096 [0.000 ; 0.605]	0.185 [0.124 ; 0.267]
$B_H : G_H$	0.378 [0.267 ; 0.507]	0.148 [0.091 ; 0.230]	0.269 [0.183 ; 0.374]	0.052 [0.000 ; 0.442]	0.211 [0.123 ; 0.336]
Distribution parameters					
phi	1.410 [1.228 ; 1.676]	1.497 [1.260 ; 1.771]	2.430 [2.032 ; 2.903]	0.010 [0.000 ; 0.106]	1.684 [1.345 ; 2.070]
pi	0.980 [0.964 ; 0.991]	0.736 [0.692 ; 0.777]	0.774 [0.731 ; 0.815]	0.013 [0.000 ; 0.178]	0.533 [0.483 ; 0.583]

Table S9: Model summaries for the dietary variation across the five most abundant orders for great tits using the same model structure and estimation as specified in Table S6, exempt adjusted fixed effect for significant differences in bird categories for each order.

$RelativeReadAbundance \sim$ *ZIH-Beta*(μ, ϕ, π)	*Lepidoptera*	*Diptera*	*Araneae*	*Hymenoptera*	*Coleoptera*
Fixed effects					
Intercept	0.387 [0.364 ; 0.412]	0.373 [0.345 ; 0.402]	0.127 [0.110 ; 0.147]	0.156 [0.135 ; 0.181]	0.254 [0.225 ; 0.285]
Treatment B	-0.191 [-0.686 ; 0.305]	0.138 [-0.348 ; 0.616]	-0.304 [-0.750 ; 0.123]	-0.217 [-0.637 ; 0.208]	0.365 [-0.177 ; 0.879]
Treatment G	-0.385 [-0.902 ; 0.143]	0.088 [-0.413 ; 0.524]	-0.282 [-0.692 ; 0.136]	0.097 [-0.322 ; 0.516]	0.040 [-0.591 ; 0.558]
Size subplot	-0.260 [-0.491 ; -0.023]	0.128 [-0.063 ; 0.324]	-0.080 [-0.255 ; 0.109]	0.075 [-0.101 ; 0.253]	0.241 [-0.026 ; 0.493]
Double box	-0.230 [-0.731 ; 0.265]	0.079 [-0.389 ; 0.517]	0.067 [-0.387 ; 0.505]	0.096 [-0.335 ; 0.504]	-0.340 [-0.818 ; 0.115]
Nestling	-0.326 [-0.599 ; -0.058]	0.906 [0.642 ; 1.176]	-0.373 [-0.635 ; -0.123]	-	-0.416 [-0.717 ; -0.109]
Date	-0.017 [-0.039 ; 0.007]	0.009 [-0.012 ; 0.030]	0.016 [-0.005 ; 0.036]	0.012 [-0.009 ; 0.034]	0.006 [-0.018 ; 0.030]
Year 2024	-0.213 [-0.708 ; 0.242]	0.038 [-0.387 ; 0.461]	0.410 [0.003 ; 0.825]	0.187 [-0.211 ; 0.594]	0.161 [-0.320 ; 0.631]
Treatment B x Treatment G	0.379 [-0.314 ; 1.067]	-0.228 [-0.867 ; 0.462]	0.252 [-0.343 ; 0.864]	0.020 [-0.573 ; 0.600]	-0.173 [-0.934 ; 0.649]
Random effects					
Brood ID	0.014 [0.000 ; 0.135]	0.009 [0.000 ; 0.091]	0.004 [0.000 ; 0.051]	0.004 [0.000 ; 0.046]	0.009 [0.000 ; 0.097]
Subplot	0.021 [0.000 ; 0.217]	0.009 [0.000 ; 0.133]	0.006 [0.000 ; 0.093]	0.005 [0.000 ; 0.075]	0.027 [0.000 ; 0.276]
Subplot year	0.020 [0.000 ; 0.180]	0.014 [0.000 ; 0.132]	0.007 [0.000 ; 0.091]	0.005 [0.000 ; 0.068]	0.025 [0.000 ; 0.206]
Nestlings repeat	0.502 [0.184 ; 0.957]	0.007 [0.000 ; 0.082]	0.004 [0.000 ; 0.047]	0.004 [0.000 ; 0.045]	0.006 [0.000 ; 0.075]
Residual	0.082 [0.065 ; 0.099]	0.116 [0.106 ; 0.126]	0.022 [0.017 ; 0.028]	0.032 [0.025 ; 0.040]	0.066 [0.056 ; 0.078]
Repeatability					
Brood ID	0.020 [0.000 ; 0.204]	0.048 [0.000 ; 0.359]	0.072 [0.000 ; 0.541]	0.064 [0.000 ; 0.460]	0.050 [0.000 ; 0.424]
Subplot	0.031 [0.000 ; 0.278]	0.052 [0.000 ; 0.442]	0.112 [0.000 ; 0.665]	0.085 [0.000 ; 0.573]	0.166 [0.001 ; 0.706]
Subplot year	0.030 [0.000 ; 0.228]	0.075 [0.000 ; 0.438]	0.127 [0.000 ; 0.657]	0.079 [0.000 ; 0.564]	0.151 [0.001 ; 0.627]
Nestlings repeat	0.737 [0.405 ; 0.896]	0.037 [0.000 ; 0.337]	0.068 [0.000 ; 0.506]	0.057 [0.000 ; 0.456]	0.037 [0.000 ; 0.341]
Residual	0.119 [0.056 ; 0.265]	0.627 [0.301 ; 0.922]	0.350 [0.107 ; 0.808]	0.477 [0.175 ; 0.878]	0.384 [0.133 ; 0.782]
Mean effects					
Treatment B	-0.002 [-0.092 ; 0.093]	0.004 [-0.061 ; 0.072]	-0.021 [-0.058 ; 0.014]	-0.025 [-0.064 ; 0.015]	0.056 [-0.025 ; 0.143]
Treatment G	-0.046 [-0.139 ; 0.041]	-0.006 [-0.073 ; 0.058]	-0.019 [-0.056 ; 0.018]	0.013 [-0.027 ; 0.050]	-0.010 [-0.104 ; 0.068]
$B_L : G_L$	0.484 [0.383 ; 0.587]	0.252 [0.187 ; 0.335]	0.161 [0.118 ; 0.214]	0.150 [0.112 ; 0.198]	0.255 [0.182 ; 0.352]
$B_L : G_H$	0.390 [0.294 ; 0.487]	0.267 [0.201 ; 0.346]	0.127 [0.093 ; 0.168]	0.163 [0.123 ; 0.215]	0.263 [0.180 ; 0.350]
$B_H : G_L$	0.436 [0.332 ; 0.550]	0.278 [0.199 ; 0.370]	0.124 [0.087 ; 0.173]	0.125 [0.087 ; 0.176]	0.330 [0.237 ; 0.444]
$B_H : G_H$	0.434 [0.329 ; 0.547]	0.250 [0.183 ; 0.335]	0.121 [0.086 ; 0.167]	0.138 [0.101 ; 0.187]	0.301 [0.209 ; 0.406]
Distribution parameters					
phi	1.648 [1.298 ; 2.216]	0.927 [0.820 ; 1.049]	2.980 [2.471 ; 3.582]	2.140 [1.784 ; 2.564]	1.262 [1.070 ; 1.475]
pi	0.954 [0.933 ; 0.971]	0.860 [0.828 ; 0.890]	0.639 [0.595 ; 0.681]	0.628 [0.585 ; 0.670]	0.610 [0.566 ; 0.653]

Table S10: Model summaries for the enviornemnetal availability for the families of Noctuidae, Erebidae, Geometridae, Tineidae, Lasiocampidae and preference of blue and great tits. Subscript links to the order of the family, L = Lepidoptera, C = Coleoptera and H = Hymenoptera. Response variable is the relative read abundance of the family taxa (zero-inflated Beta-hurdle, $RelativeReadAbundance \sim ZIH\text{-}Beta(\mu, \phi, \pi)$) with with posterior median and 2.5 to 97.5 credible intervals. Fitted are the fixed effects of sample type (frass, blue tit, great tit), sample date and sample year. As random effect are fitted the combination of Subplot and year, the combination of location of the frass collector or nest box with the year and residual variance. Distribution specific parameters phi (ϕ; precision parameter of beta distributions) and pi (π; hurdle pass probability (non-zero)) are shown. Fixed and random effects are shown on logit scale, intercept is shown on original scale. Number of observations = 1089.

$RelativeReadAbundance \sim ZIH\text{-}Beta(\mu, \phi, \pi)$	$Noctuidae_L$	$Erebidae_L$	$Geometridae_L$	$Tineidae_L$	$Lasiocampidae_L$
Fixed effects					
Intercept	0.358 [0.340 ; 0.377]	0.265 [0.235 ; 0.298]	0.596 [0.578 ; 0.613]	0.148 [0.111 ; 0.198]	0.145 [0.103 ; 0.205]
Blue tit	0.481 [0.026 ; 0.948]	0.036 [-0.461 ; 0.540]	0.766 [0.339 ; 1.190]	-0.622 [-1.227 ; 0.004]	-0.399 [-1.634 ; 0.819]
Great tit	0.379 [-0.070 ; 0.849]	0.866 [0.388 ; 1.338]	1.137 [0.720 ; 1.564]	-0.258 [-0.916 ; 0.412]	-0.074 [-1.031 ; 0.877]
Date	0.639 [0.270 ; 0.984]	-0.167 [-0.620 ; 0.292]	-0.658 [-1.105 ; -0.177]	0.009 [-0.624 ; 0.574]	-0.697 [-1.700 ; 0.259]
Year 2024	0.032 [0.022 ; 0.042]	0.002 [-0.012 ; 0.016]	-0.031 [-0.042 ; -0.020]	-0.023 [-0.038 ; -0.007]	0.009 [-0.016 ; 0.036]
Random effects					
Subplot year	0.022 [0.000 ; 0.142]	0.013 [0.000 ; 0.138]	0.159 [0.047 ; 0.422]	0.106 [0.001 ; 0.501]	0.094 [0.000 ; 0.813]
LocationYear	0.939 [0.725 ; 1.217]	0.491 [0.256 ; 0.826]	0.643 [0.455 ; 0.880]	0.220 [0.006 ; 0.561]	2.340 [1.316 ; 3.967]
Residual	0.047 [0.042 ; 0.053]	0.061 [0.050 ; 0.074]	0.061 [0.053 ; 0.069]	0.035 [0.022 ; 0.057]	0.011 [0.006 ; 0.019]
Repeatability					
Subplot year	0.022 [0.000 ; 0.130]	0.023 [0.000 ; 0.216]	0.185 [0.059 ; 0.388]	0.296 [0.002 ; 0.840]	0.039 [0.000 ; 0.278]
LocationYear	0.930 [0.824 ; 0.960]	0.860 [0.660 ; 0.930]	0.743 [0.553 ; 0.869]	0.594 [0.023 ; 0.928]	0.957 [0.718 ; 0.996]
Residual	0.046 [0.035 ; 0.062]	0.105 [0.059 ; 0.199]	0.069 [0.048 ; 0.097]	0.088 [0.033 ; 0.325]	0.004 [0.002 ; 0.011]
Distribution parameters					
phi	1.704 [1.515 ; 1.913]	1.945 [1.535 ; 2.459]	1.058 [0.958 ; 1.167]	2.222 [1.483 ; 3.215]	11.509 [5.939 ; 19.490]
pi	0.762 [0.735 ; 0.786]	0.267 [0.241 ; 0.294]	0.861 [0.840 ; 0.881]	0.113 [0.095 ; 0.133]	0.074 [0.058 ; 0.091]

Table S11: Model summaries for the environmental availability for the families of Chrysomelidae, Ypsolophidae, Tortricidae, Lycaenidae, Pyralidae and preference of blue and great tits using the model structure as specified before in Table S10.

$RelativeReadAbundance \sim$ ZIH-Beta(μ, ϕ, π)	*Chrysomelidae*$_C$	*Ypsolophidae*$_L$	*Tortricidae*$_L$	*Lycaenidae*$_L$	*Pyralidae*$_L$
Fixed effects					
Intercept	0.232 [0.149 ; 0.350]	0.144 [0.096 ; 0.220]	0.136 [0.120 ; 0.155]	0.211 [0.174 ; 0.256]	0.120 [0.103 ; 0.141]
Blue tit	-0.094 [-1.446 ; 1.210]	-0.161 [-1.043 ; 0.736]	0.168 [-0.121 ; 0.482]	0.352 [-0.293 ; 0.966]	0.005 [-2.018 ; 1.944]
Great tit	-0.529 [-1.883 ; 0.718]	-0.103 [-1.022 ; 0.825]	0.134 [-0.178 ; 0.447]	0.453 [-0.195 ; 1.112]	-0.301 [-1.685 ; 1.086]
Date	-0.325 [-1.927 ; 1.260]	-0.278 [-1.281 ; 0.671]	-0.300 [-0.604 ; 0.006]	0.291 [-0.405 ; 0.968]	-0.447 [-1.839 ; 0.858]
Year 2024	0.009 [-0.065 ; 0.092]	-0.029 [-0.077 ; 0.017]	-0.011 [-0.023 ; 0.001]	0.010 [-0.015 ; 0.035]	-0.006 [-0.082 ; 0.070]
Random effects					
Subplot year	0.163 [0.000 ; 1.969]	0.022 [0.000 ; 0.349]	0.004 [0.000 ; 0.049]	0.103 [0.000 ; 0.533]	0.018 [0.000 ; 0.126]
LocationYear	0.325 [0.001 ; 3.662]	0.022 [0.000 ; 0.410]	0.004 [0.000 ; 0.044]	0.431 [0.123 ; 0.925]	0.314 [0.189 ; 0.486]
Residual	0.046 [0.011 ; 0.092]	0.023 [0.013 ; 0.038]	0.021 [0.017 ; 0.026]	0.049 [0.034 ; 0.069]	0.020 [0.015 ; 0.026]
Repeatability					
Subplot year	0.266 [0.001 ; 0.935]	0.274 [0.001 ; 0.883]	0.128 [0.000 ; 0.658]	0.179 [0.001 ; 0.622]	0.050 [0.000 ; 0.304]
LocationYear	0.549 [0.002 ; 0.985]	0.281 [0.001 ; 0.899]	0.118 [0.000 ; 0.632]	0.731 [0.272 ; 0.940]	0.890 [0.639 ; 0.957]
Residual	0.064 [0.003 ; 0.742]	0.257 [0.028 ; 0.914]	0.637 [0.225 ; 0.980]	0.078 [0.033 ; 0.213]	0.054 [0.032 ; 0.099]
Distribution parameters					
phi	2.225 [1.053 ; 12.371]	4.225 [2.793 ; 6.595]	3.762 [3.177 ; 4.420]	2.122 [1.465 ; 3.080]	3.342 [2.682 ; 4.111]
pi	0.028 [0.019 ; 0.039]	0.064 [0.050 ; 0.080]	0.320 [0.292 ; 0.350]	0.148 [0.127 ; 0.169]	0.327 [0.299 ; 0.356]

Table S12: Model summaries for the environmental availability for the families of Drepanidae, Gelechiidae, Argyresthiidae, Lypusidae, Notodontidae and preference of blue and great tits using the model structure as specified before in Table S10.

$RelativeReadAbundance \sim$ *ZIH-Beta*(μ, ϕ, π)	*Drepanidae*$_L$	*Gelechiidae*$_L$	*Argyresthiidae*	*Lypusidae*$_L$	*Notodontidae*$_L$
Fixed effects					
Intercept	0.204 [0.076 ; 0.424]	0.125 [0.057 ; 0.277]	0.316 [0.089 ; 0.620]	0.179 [0.062 ; 0.411]	0.252 [0.185 ; 0.339]
Blue tit	-0.102 [-0.918 ; 0.725]	-0.297 [-1.892 ; 1.277]	-0.315 [-0.988 ; 0.286]	-0.247 [-1.687 ; 1.176]	-0.256 [-1.561 ; 1.046]
Great tit	0.169 [-0.694 ; 0.987]	0.006 [-1.962 ; 2.005]	0.097 [-0.736 ; 0.805]	-0.554 [-1.970 ; 0.803]	-0.171 [-1.929 ; 1.496]
Date	0.138 [-0.710 ; 0.971]	-1.049 [-2.596 ; 0.544]	0.172 [-0.575 ; 0.877]	0.108 [-1.565 ; 1.738]	-0.987 [-2.689 ; 0.727]
Year 2024	0.006 [-0.024 ; 0.037]	0.016 [-0.078 ; 0.104]	0.010 [-0.008 ; 0.029]	-0.004 [-0.071 ; 0.067]	-0.052 [-0.127 ; 0.020]
Random effects					
Subplot year	0.168 [0.000 ; 2.409]	0.161 [0.000 ; 2.160]	0.522 [0.001 ; 5.079]	0.223 [0.000 ; 2.741]	0.068 [0.000 ; 0.583]
LocationYear	0.160 [0.000 ; 2.069]	0.163 [0.000 ; 1.845]	0.506 [0.002 ; 4.858]	0.205 [0.000 ; 2.599]	0.841 [0.302 ; 1.657]
Residual	0.020 [0.007 ; 0.062]	0.017 [0.005 ; 0.062]	0.027 [0.008 ; 0.086]	0.019 [0.005 ; 0.068]	0.061 [0.038 ; 0.096]
Repeatability					
Subplot year	0.438 [0.001 ; 0.977]	0.432 [0.002 ; 0.976]	0.466 [0.001 ; 0.984]	0.462 [0.001 ; 0.980]	0.069 [0.000 ; 0.465]
LocationYear	0.420 [0.001 ; 0.974]	0.439 [0.001 ; 0.976]	0.464 [0.002 ; 0.984]	0.430 [0.001 ; 0.979]	0.856 [0.452 ; 0.963]
Residual	0.039 [0.004 ; 0.602]	0.035 [0.003 ; 0.575]	0.018 [0.002 ; 0.357]	0.028 [0.003 ; 0.538]	0.059 [0.023 ; 0.182]
Distribution parameters					
phi	5.280 [1.686 ; 12.664]	4.542 [1.420 ; 11.746]	3.825 [0.819 ; 11.927]	5.215 [1.430 ; 13.675]	1.696 [1.025 ; 2.746]
pi	0.010 [0.005 ; 0.018]	0.013 [0.008 ; 0.021]	0.004 [0.002 ; 0.010]	0.008 [0.004 ; 0.015]	0.087 [0.071 ; 0.105]

Table S13: Model summaries for the environmental availability for the families of Nolidae, Glyphipterigidae, Adelidae, Hesperiidae, Coleophoridae and preference of blue and great tits using the model structure as specified before in Table S10.

$RelativeReadAbundance \sim$ ZIH-Beta(μ, ϕ, π)	$Nolidae_L$	$Glyphipterigidae_L$	$Adelidae_L$	$Hesperiidae_L$	$Coleophoridae_L$
Fixed effects					
Intercept	0.070 [0.045 ; 0.112]	0.133 [0.054 ; 0.318]	0.075 [0.039 ; 0.153]	0.158 [0.106 ; 0.235]	0.246 [0.080 ; 0.518]
Blue tit	-0.287 [-0.669 ; 0.086]	-0.070 [-1.900 ; 1.746]	-0.005 [-2.002 ; 1.996]	-0.997 [-2.220 ; 0.224]	-0.697 [-2.367 ; 0.962]
Great tit	-0.531 [-0.923 ; -0.156]	-0.028 [-1.943 ; 1.974]	-0.287 [-2.077 ; 1.479]	-0.724 [-1.888 ; 0.465]	-0.039 [-1.792 ; 1.669]
Date	-0.164 [-0.523 ; 0.184]	-0.025 [-1.999 ; 1.978]	0.009 [-1.951 ; 1.929]	-0.057 [-1.162 ; 0.996]	-0.478 [-2.294 ; 1.293]
Year 2024	-0.006 [-0.015 ; 0.003]	0.151 [0.006 ; 0.300]	-0.036 [-0.190 ; 0.127]	0.023 [-0.029 ; 0.082]	0.019 [-0.148 ; 0.201]
Random effects					
Subplot year	0.024 [0.000 ; 0.281]	0.163 [0.000 ; 2.216]	0.041 [0.000 ; 0.577]	0.039 [0.000 ; 0.451]	0.389 [0.001 ; 4.218]
LocationYear	0.018 [0.000 ; 0.246]	0.153 [0.000 ; 2.090]	0.051 [0.000 ; 0.723]	0.045 [0.000 ; 0.468]	0.388 [0.001 ; 4.274]
Residual	0.008 [0.004 ; 0.016]	0.016 [0.004 ; 0.060]	0.009 [0.003 ; 0.029]	0.035 [0.020 ; 0.060]	0.027 [0.007 ; 0.097]
Repeatability					
Subplot year	0.424 [0.001 ; 0.949]	0.454 [0.002 ; 0.979]	0.364 [0.001 ; 0.960]	0.282 [0.001 ; 0.893]	0.449 [0.002 ; 0.982]
LocationYear	0.318 [0.001 ; 0.933]	0.419 [0.001 ; 0.977]	0.457 [0.002 ; 0.971]	0.328 [0.001 ; 0.898]	0.455 [0.001 ; 0.981]
Residual	0.112 [0.015 ; 0.787]	0.032 [0.003 ; 0.562]	0.060 [0.006 ; 0.678]	0.222 [0.041 ; 0.874]	0.024 [0.002 ; 0.460]
Distribution parameters					
phi	7.199 [4.381 ; 11.032]	5.279 [1.567 ; 13.690]	6.615 [2.604 ; 13.754]	2.646 [1.629 ; 4.063]	3.506 [0.695 ; 11.348]
pi	0.054 [0.042 ; 0.069]	0.010 [0.005 ; 0.017]	0.021 [0.013 ; 0.031]	0.042 [0.031 ; 0.055]	0.005 [0.002 ; 0.011]

Table S14: Model summaries for the environmental availability for the families of Psychidae, Eriocraniidae, Crambidae, Argidae, Pamphiliidae and preference of blue and great tits using the model structure as specified before in Table S10.

$RelativeReadAbundance \sim$ *ZIH-Beta*(μ, ϕ, π)	*Psychidae*$_L$	*Eriocraniidae*$_L$	*Crambidae*$_L$	*Argidae*$_H$	*Pamphiliidae*$_H$
Fixed effects					
Intercept	0.243 [0.066 ; 0.530]	0.485 [0.233 ; 0.723]	0.155 [0.098 ; 0.243]	0.225 [0.072 ; 0.489]	0.165 [0.066 ; 0.367]
Blue tit	-0.626 [-1.614 ; 0.343]	-0.099 [-1.260 ; 1.036]	0.003 [-1.955 ; 1.953]	0.002 [-1.947 ; 1.927]	-0.002 [-1.441 ; 1.359]
Great tit	0.028 [-0.965 ; 1.019]	-0.322 [-1.339 ; 0.691]	0.001 [-1.973 ; 1.982]	-0.227 [-1.804 ; 1.328]	-0.833 [-2.242 ; 0.559]
Date	-0.027 [-0.849 ; 0.781]	-0.128 [-1.187 ; 0.893]	-0.004 [-1.971 ; 1.971]	0.349 [-1.398 ; 1.902]	-0.396 [-2.101 ; 1.292]
Year 2024	-0.007 [-0.035 ; 0.021]	0.009 [-0.028 ; 0.048]	-0.001 [-0.121 ; 0.127]	-0.031 [-0.078 ; 0.011]	-0.014 [-0.088 ; 0.053]
Random effects					
Subplot year	0.245 [0.001 ; 3.283]	0.309 [0.001 ; 3.805]	0.057 [0.000 ; 1.013]	0.203 [0.000 ; 2.598]	0.225 [0.001 ; 2.702]
LocationYear	0.216 [0.000 ; 3.041]	0.330 [0.001 ; 3.836]	0.045 [0.000 ; 1.672]	0.169 [0.000 ; 2.336]	0.246 [0.001 ; 2.703]
Residual	0.023 [0.006 ; 0.077]	0.022 [0.009 ; 0.062]	0.037 [0.010 ; 0.071]	0.020 [0.006 ; 0.067]	0.023 [0.007 ; 0.076]
Repeatability					
Subplot year	0.467 [0.002 ; 0.980]	0.438 [0.001 ; 0.981]	0.329 [0.001 ; 0.925]	0.474 [0.001 ; 0.979]	0.420 [0.001 ; 0.977]
LocationYear	0.413 [0.001 ; 0.978]	0.472 [0.002 ; 0.983]	0.284 [0.001 ; 0.944]	0.401 [0.001 ; 0.974]	0.462 [0.002 ; 0.977]
Residual	0.032 [0.003 ; 0.557]	0.022 [0.003 ; 0.430]	0.199 [0.005 ; 0.905]	0.035 [0.003 ; 0.554]	0.033 [0.003 ; 0.558]
Distribution parameters					
phi	4.710 [1.116 ; 13.329]	5.501 [1.500 ; 14.011]	2.326 [1.283 ; 9.834]	5.572 [1.584 ; 14.664]	3.766 [1.146 ; 10.412]
pi	0.006 [0.003 ; 0.012]	0.005 [0.002 ; 0.011]	0.035 [0.025 ; 0.048]	0.009 [0.005 ; 0.016]	0.010 [0.005 ; 0.017]

Table S15: Model summaries for the environmental availability for the families of Tenthredinidae, Oecophoridae, Curculionidae and preference of blue and great tits using the model structure as specified before in Table S10.

$RelativeReadAbundance \sim$ *ZIH-Beta*(μ, ϕ, π)	*Tenthredinidae*$_H$	*Oecophoridae*$_L$	*Curculionidae*$_C$
Fixed effects			
Intercept	0.262 [0.208 ; 0.324]	0.319 [0.076 ; 0.662]	0.303 [0.271 ; 0.336]
Blue tit	-0.068 [-0.651 ; 0.510]	-0.068 [-0.651 ; 0.510]	-0.068 [-0.651 ; 0.510]
Great tit	-0.483 [-1.072 ; 0.101]	-0.483 [-1.072 ; 0.101]	-0.483 [-1.072 ; 0.101]
Date	-0.196 [-0.867 ; 0.463]	-0.196 [-0.867 ; 0.463]	-0.196 [-0.867 ; 0.463]
Year 2024	0.014 [-0.005 ; 0.033]	0.014 [-0.005 ; 0.033]	0.014 [-0.005 ; 0.033]
Random effects			
Subplot year	0.114 [0.001 ; 0.588]	0.488 [0.001 ; 5.063]	0.054 [0.000 ; 0.275]
LocationYear	0.121 [0.000 ; 0.525]	0.510 [0.002 ; 5.362]	0.473 [0.229 ; 0.794]
Residual	0.085 [0.062 ; 0.110]	0.034 [0.009 ; 0.103]	0.081 [0.069 ; 0.094]
Repeatability			
Subplot year	0.346 [0.002 ; 0.825]	0.435 [0.001 ; 0.980]	0.090 [0.000 ; 0.359]
LocationYear	0.349 [0.002 ; 0.832]	0.471 [0.002 ; 0.983]	0.769 [0.506 ; 0.894]
Residual	0.226 [0.083 ; 0.752]	0.023 [0.002 ; 0.480]	0.129 [0.075 ; 0.242]
Distribution parameters			
phi	1.080 [0.803 ; 1.481]	2.876 [0.588 ; 10.018]	1.200 [0.996 ; 1.432]
pi	0.113 [0.095 ; 0.133]	0.004 [0.002 ; 0.010]	0.368 [0.339 ; 0.397]

Table S16: Model summary for the variation in preferred prey for blue and great tits combined. Response variable is the proportion of preferred prey combined for both species (zero-inflated Beta-hurdle, $ProportionPreferredPrey \sim$ *ZIH-Beta*(μ, ϕ, π)) with with posterior median and 2.5 to 97.5 credible intervals. Fitted are the fixed effects of competitive treatment of blue tits (Treatment B), great tits (Treatment G), the size of the Subplot, the effect of a close box proximity (Double box), bird category (female, male and nestling measured at day 10 and day 15), sample date, year, species (blue and great tit) and the interaction of both competitive treatments. As random effects fitted are brood ID, the Subplot, a combination of Subplot and year, a nestling stage and brood ID combination (nestling repeat) to account for multiple pooled tubes from one brood and the residual. Intercept and repeatabilities are shown as proportions on the original scale. Mean effects are calculated for the summarised effects for each species-specific treatment (blue and great tit treatment effect) and their four combinations ($B_L : G_L$, $B_L : G_H$, $B_H : G_L$, $B_H : G_H$). Mean effect for each bird category and their differences are estimated within the model. Distribution specific parameters phi (ϕ; precision parameter of beta distributions) and pi (π; hurdle pass probability (non-zero)) are shown. Fixed and random effects are shown on logit scale, intercept, mean effects and categories are shown on original scale. Number of observations = 853.

$ProportionPreferredPrey \sim$ *ZIH-Beta*(μ, ϕ, π)	
Fixed effects	
Intercept	0.831 [0.818 ; 0.844]
Treatment B	0.111 [-0.317 ; 0.577]
Treatment G	0.137 [-0.340 ; 0.671]
Size subplot	-0.305 [-0.531 ; -0.064]
Double box	0.133 [-0.325 ; 0.582]
Male	-0.035 [-0.370 ; 0.302]
Nestling 10	0.936 [0.611 ; 1.266]
Nestling 15	1.007 [0.660 ; 1.357]
Date	-0.025 [-0.049 ; -0.001]
Year 2024	-0.515 [-0.975 ; -0.042]
Great tit	0.521 [0.271 ; 0.771]
Treatment B x Treatment G	-0.013 [-0.697 ; 0.669]
Random effects	
Brood ID	0.025 [0.000 ; 0.198]
Subplot	0.022 [0.000 ; 0.220]
Subplot year	0.032 [0.000 ; 0.210]
Nestlings repeat	1.250 [0.848 ; 1.756]
Residual	0.056 [0.045 ; 0.066]
Repeatability	
Brood ID	0.017 [0.000 ; 0.135]
Subplot	0.015 [0.000 ; 0.135]
Subplot year	0.022 [0.000 ; 0.133]
Nestlings repeat	0.877 [0.720 ; 0.950]
Residual	0.039 [0.024 ; 0.061]
Mean effects	
Treatment B	0.016 [-0.040 ; 0.077]
Treatment G	0.021 [-0.035 ; 0.085]
$B_L : G_L$	0.783 [0.686 ; 0.851]
$B_L : G_H$	0.805 [0.718 ; 0.873]
$B_H : G_L$	0.801 [0.715 ; 0.864]
$B_H : G_H$	0.822 [0.732 ; 0.886]
Category	
Female	0.783 [0.686 ; 0.851]
Male	0.777 [0.675 ; 0.849]
Nestling 10	0.902 [0.846 ; 0.936]
Nestling 15	0.908 [0.852 ; 0.942]
Adult	0.780 [0.687 ; 0.846]
Nestling	0.905 [0.852 ; 0.938]
Diff adults	0.006 [-0.052 ; 0.066]
Diff nestlings	-0.006 [-0.037 ; 0.024]
Diff categories	-0.125 [-0.179 ; -0.083]
Distribution parameters	
phi	1.657 [1.319 ; 2.167]
pi	0.980 [0.969 ; 0.988]

Table S17: Model summary for the variation in preferred prey for blue tits using the same model structure and estimation as specified in Table S16, exempt the fixed effect for species. Number of observations = 386.

$ProportionPreferredPrey \sim$ *ZIH-Beta*(μ, ϕ, π)	
Fixed effects	
Intercept	0.779 [0.760 ; 0.796]
Treatment B	0.015 [-0.568 ; 0.662]
Treatment G	0.238 [-0.448 ; 0.987]
Size subplot	-0.496 [-0.868 ; -0.138]
Double box	0.137 [-0.586 ; 0.869]
Male	-0.165 [-0.712 ; 0.405]
Nestling 10	0.421 [-0.075 ; 0.940]
Nestling 15	0.914 [0.348 ; 1.469]
Date	-0.050 [-0.096 ; -0.004]
Year 2024	-0.772 [-1.579 ; 0.091]
Treatment B x Treatment G	-0.247 [-1.191 ; 0.682]
Random effects	
Brood ID	0.032 [0.000 ; 0.289]
Subplot	0.047 [0.000 ; 0.529]
Subplot year	0.049 [0.000 ; 0.408]
Nestlings repeat	2.016 [1.336 ; 2.909]
Residual	0.048 [0.035 ; 0.064]
Repeatability	
Brood ID	0.014 [0.000 ; 0.123]
Subplot	0.021 [0.000 ; 0.195]
Subplot year	0.022 [0.000 ; 0.157]
Nestlings repeat	0.888 [0.691 ; 0.969]
Residual	0.021 [0.011 ; 0.038]
Mean effects	
Treatment B	-0.012 [-0.088 ; 0.061]
Treatment G	0.013 [-0.061 ; 0.095]
$B_L : G_L$	0.839 [0.705 ; 0.914]
$B_L : G_H$	0.870 [0.750 ; 0.934]
$B_H : G_L$	0.843 [0.720 ; 0.914]
$B_H : G_H$	0.842 [0.699 ; 0.923]
Category	
Female	0.839 [0.705 ; 0.914]
Male	0.816 [0.662 ; 0.904]
Nestling 10	0.889 [0.786 ; 0.941]
Nestling 15	0.929 [0.841 ; 0.967]
Adult	0.827 [0.695 ; 0.903]
Nestling	0.908 [0.817 ; 0.952]
Diff adults	0.023 [-0.058 ; 0.115]
Diff nestlings	-0.038 [-0.097 ; 0.006]
Diff categories	-0.079 [-0.151 ; -0.034]
Distribution parameters	
phi	2.608 [1.821 ; 3.895]
pi	0.977 [0.959 ; 0.989]

Table S18: Model summary for the variation in preferred prey for great tits using the same model structure and estimation as specified in Table S16, exempt the fixed effect for species. Number of observations = 467.

$ProportionPreferredPrey \sim$ *ZIH-Beta*(μ, ϕ, π)	
Fixed effects	
Intercept	0.659 [0.641 ; 0.676]
Treatment B	0.085 [-0.571 ; 0.759]
Treatment G	0.388 [-0.294 ; 1.058]
Size subplot	-0.229 [-0.561 ; 0.111]
Double box	0.103 [-0.583 ; 0.811]
Male	-0.253 [-0.764 ; 0.242]
Nestling 10	1.137 [0.608 ; 1.657]
Nestling 15	0.912 [0.366 ; 1.474]
Date	-0.097 [-0.135 ; -0.062]
Year 2024	-1.778 [-2.484 ; -1.074]
Treatment B x Treatment G	-0.273 [-1.185 ; 0.643]
Random effects	
Brood ID	0.039 [0.000 ; 0.332]
Subplot	0.024 [0.000 ; 0.323]
Subplot year	0.050 [0.000 ; 0.410]
Nestlings repeat	2.669 [1.869 ; 3.636]
Residual	0.066 [0.053 ; 0.080]
Repeatability	
Brood ID	0.013 [0.000 ; 0.113]
Subplot	0.008 [0.000 ; 0.101]
Subplot year	0.017 [0.000 ; 0.129]
Nestlings repeat	0.916 [0.772 ; 0.971]
Residual	0.022 [0.014 ; 0.036]
Mean effects	
Treatment B	-0.008 [-0.109 ; 0.090]
Treatment G	0.045 [-0.054 ; 0.147]
$B_L : G_L$	0.714 [0.578 ; 0.823]
$B_L : G_H$	0.786 [0.662 ; 0.871]
$B_H : G_L$	0.732 [0.584 ; 0.843]
$B_H : G_H$	0.753 [0.607 ; 0.856]
Category	
Female	0.714 [0.578 ; 0.823]
Male	0.660 [0.504 ; 0.782]
Nestling 10	0.886 [0.803 ; 0.936]
Nestling 15	0.862 [0.760 ; 0.924]
Adult	0.686 [0.551 ; 0.794]
Nestling	0.873 [0.792 ; 0.926]
Diff adults	0.053 [-0.051 ; 0.166]
Diff nestlings	0.023 [-0.037 ; 0.099]
Diff life stages	-0.185 [-0.274 ; -0.111]
Distribution parameters	
phi	3.896 [2.650 ; 5.798]
pi	0.919 [0.892 ; 0.941]

Table S19: Model summary for the variation in preferred prey for both species combined using the same model structure and estimation as specified in as specified in Table S16, exempt adjusted fixed effect for significant differences in bird categories for each order.

$ProportionPreferredPrey \sim$ *ZIH-Beta*(μ, ϕ, π)	
Fixed effects	
Intercept	0.831 [0.818 ; 0.844]
Treatment B	0.110 [-0.324 ; 0.570]
Treatment G	0.136 [-0.352 ; 0.665]
Size subplot	-0.309 [-0.534 ; -0.075]
Double box	0.124 [-0.309 ; 0.571]
Nestling	0.997 [0.755 ; 1.246]
Date	-0.023 [-0.046 ; -0.001]
Year 2024	-0.497 [-0.945 ; -0.028]
Great tit	0.518 [0.264 ; 0.773]
Treatment B x Treatment G	-0.010 [-0.703 ; 0.670]
Random effects	
Brood ID	0.024 [0.000 ; 0.195]
Subplot	0.022 [0.000 ; 0.219]
Subplot year	0.031 [0.000 ; 0.210]
Nestlings repeat	1.248 [0.837 ; 1.758]
Residual	0.056 [0.045 ; 0.067]
Repeatability	
Brood ID	0.017 [0.000 ; 0.137]
Subplot	0.016 [0.000 ; 0.139]
Subplot year	0.022 [0.000 ; 0.132]
Nestlings repeat	0.878 [0.718 ; 0.950]
Residual	0.039 [0.024 ; 0.063]
Mean effects	
Treatment B	0.017 [-0.040 ; 0.077]
Treatment G	0.021 [-0.037 ; 0.083]
$B_L : G_L$	0.778 [0.684 ; 0.845]
$B_L : G_H$	0.801 [0.712 ; 0.867]
$B_H : G_L$	0.797 [0.714 ; 0.859]
$B_H : G_H$	0.817 [0.728 ; 0.879]
Distribution parameters	
phi	1.656 [1.308 ; 2.172]
pi	0.980 [0.969 ; 0.988]

Table S20: Model summary for the variation in preferred prey for blue tits combined using the same model structure and estimation as specified in as specified in Table S17, exempt adjusted fixed effect for significant differences in bird categories for each order.

$ProportionPreferredPrey \sim$ *ZIH-Beta*(μ, ϕ, π)	
Fixed effects	
Intercept	0.779 [0.761 ; 0.796]
Treatment B	0.007 [-0.600 ; 0.650]
Treatment G	0.240 [-0.461 ; 1.005]
Size subplot	-0.523 [-0.904 ; -0.159]
Double box	0.109 [-0.623 ; 0.856]
Nestling	0.731 [0.334 ; 1.139]
Date	-0.033 [-0.075 ; 0.008]
Year 2024	-0.528 [-1.280 ; 0.262]
Treatment B x Treatment G	-0.252 [-1.209 ; 0.679]
Random effects	
Brood ID	0.034 [0.000 ; 0.297]
Subplot	0.055 [0.000 ; 0.570]
Subplot year	0.051 [0.000 ; 0.424]
Nestlings repeat	2.070 [1.384 ; 2.968]
Residual	0.048 [0.034 ; 0.063]
Repeatability	
Brood ID	0.015 [0.000 ; 0.120]
Subplot	0.024 [0.000 ; 0.201]
Subplot year	0.022 [0.000 ; 0.161]
Nestlings repeat	0.884 [0.688 ; 0.968]
Residual	0.020 [0.011 ; 0.036]
Mean effects	
Treatment B	-0.017 [-0.103 ; 0.069]
Treatment G	0.014 [-0.071 ; 0.104]
$B_L : G_L$	0.814 [0.679 ; 0.894]
$B_L : G_H$	0.848 [0.721 ; 0.920]
$B_H : G_L$	0.815 [0.690 ; 0.894]
$B_H : G_H$	0.813 [0.658 ; 0.906]
Distribution parameters	
phi	2.663 [1.852 ; 4.025]
pi	0.977 [0.960 ; 0.989]

Table S21: Model summary for the variation in preferred prey for great tits combined using the same model structure and estimation as specified in as specified in Table S18, exempt adjusted fixed effect for significant differences in bird categories for each order.

$ProportionPreferredPrey \sim$ *ZIH-Beta*(μ, ϕ, π)	
Fixed effects	
Intercept	0.659 [0.641 ; 0.677]
Treatment B	0.090 [-0.591 ; 0.785]
Treatment G	0.382 [-0.304 ; 1.054]
Size subplot	-0.231 [-0.539 ; 0.095]
Double box	0.125 [-0.551 ; 0.826]
Nestling	1.212 [0.806 ; 1.619]
Date	-0.100 [-0.136 ; -0.065]
Year 2024	-1.794 [-2.489 ; -1.087]
Treatment B x Treatment G	-0.292 [-1.202 ; 0.653]
Random effects	
Brood ID	0.035 [0.000 ; 0.311]
Subplot	0.023 [0.000 ; 0.318]
Subplot year	0.050 [0.000 ; 0.411]
Nestlings repeat	2.660 [1.865 ; 3.597]
Residual	0.066 [0.053 ; 0.081]
Repeatability	
Brood ID	0.012 [0.000 ; 0.105]
Subplot	0.008 [0.000 ; 0.098]
Subplot year	0.017 [0.000 ; 0.126]
Nestlings repeat	0.916 [0.774 ; 0.972]
Residual	0.022 [0.014 ; 0.037]
Mean effects	
Treatment B	-0.011 [-0.116 ; 0.098]
Treatment G	0.046 [-0.064 ; 0.156]
$B_L : G_L$	0.684 [0.553 ; 0.790]
$B_L : G_H$	0.760 [0.641 ; 0.847]
$B_H : G_L$	0.704 [0.556 ; 0.817]
$B_H : G_H$	0.722 [0.578 ; 0.831]
Distribution parameters	
phi	3.878 [2.622 ; 5.670]
pi	0.919 [0.891 ; 0.941]

Table S22: Bivariate model summary for the mean exploration behaviour per individual and the proportion of preferred prey in blue and great tit adults combined. In the first equation the response variable is the exploration score (Gaussian, $exploration \sim \mathcal{N}(\mu, \sigma)$) with posterior median and 2.5 to 97.5 credible intervals. Fixed effect are the number of the exploration test an individual has taken over his lifetime (trial 1 to 3), time the test was taken after sunrise (centred) and the species (blue and great tit). All fixed effects (except the intercept) are expressed as y-standardised beta-coefficients for comparability (in standard deviation units). Random effects are the individual, a combination of Subplot and year and the residual variance. For the second equation the response variable is the proportion of preferred prey combined for both species (zero-inflated Beta-hurdle). Fitted is the mean exploration behaviour of the individual taken from the first equation as the best linear unbiased predictor (BLUP), the fixed effects of competitive treatment of blue tits (Treatment B), great tits (Treatment G), sample date, year, species (blue and great tit) and the interaction of each species-specific treatment with the exploration behaviour, the interaction of both competitive treatments and the interaction of exploration behaviour with both competitive treatments. As random effects fitted are individual ID, the combination of Subplot and year and the residual. Intercept and repeatabilities are shown as proportions on the original scale. Mean effects are calculated for the summarised effects for each species-specific treatment (blue and great tit treatment effect) and their four combinations (B_L : G_L, B_L : G_H, B_H : G_L, B_H : G_H). Distribution specific parameters phi (ϕ; precision parameter of beta distributions) and pi (π; hurdle pass probability (non-zero)) are shown. Fixed and random effects are shown on logit scale, intercept, mean effects are shown on original scale. Number of observations for exploration = 534 and observations of proportion of preferred prey = 352.

$Exploration \sim \mathcal{N}(\mu, \sigma)$	
Fixed effects	
Intercept	50.953 [47.429 ; 54.473]
Trial 1	5.834 [2.227 ; 9.466]
Trial 2	5.936 [0.241 ; 11.627]
Trial 3	4.583 [-5.983 ; 14.973]
Time sunrise	0.381 [-0.368 ; 1.146]
Great tit	-5.292 [-9.138 ; -1.403]
Random effects	
Individual ID	117.195 [57.477 ; 182.181]
Subplot year	27.658 [6.254 ; 66.087]
Residual	284.468 [232.401 ; 351.035]
Repeatability	
Individual ID	0.272 [0.137 ; 0.396]
Subplot year	0.064 [0.015 ; 0.144]
Residual	0.661 [0.529 ; 0.803]
$ProportionPreferredPrey \sim$ *ZIH-Beta*(μ, ϕ, π)	
Fixed effects	
Intercept	0.763 [0.744 ; 0.781]
Exploration	-0.026 [-0.122 ; 0.074]
Treatment B	0.143 [-0.548 ; 0.795]
Treatment G	0.523 [-0.167 ; 1.176]
Date	-0.038 [-0.073 ; -0.004]
Year 2024	-0.593 [-1.301 ; 0.100]
Great tit	0.372 [-0.055 ; 0.819]
Exploration * Treatment B	0.100 [-0.022 ; 0.250]
Exploration * Treatment G	0.002 [-0.120 ; 0.116]
Treatment B * Treatment G	-0.282 [-1.140 ; 0.613]
Exploration * Treatment B * Treatment G	-0.037 [-0.176 ; 0.107]
Random effects	
Individual ID	2.280 [1.481 ; 3.309]
Subplot year	0.115 [0.001 ; 0.550]
Residual	0.049 [0.035 ; 0.065]
Repeatability	
Individual ID	0.932 [0.771 ; 0.984]
Subplot year	0.047 [0.000 ; 0.208]
Residual	0.020 [0.010 ; 0.037]
Mean effects	
Treatment B	0.003 [-0.069 ; 0.074]
Treatment G	0.050 [-0.021 ; 0.125]
B_L : G_L	0.803 [0.683 ; 0.887]
B_L : G_H	0.873 [0.779 ; 0.931]
B_H : G_L	0.825 [0.712 ; 0.900]
B_H : G_H	0.857 [0.751 ; 0.921]

Table S22: (continued)

$Exploration \sim \mathcal{N}(\mu, \sigma)$	
Mean effects Exp	
Treatment B	0.019 [-0.006 ; 0.051]
Treatment G	-0.004 [-0.031 ; 0.021]
$B_L : G_L$	0.432 [0.230 ; 0.674]
$B_L : G_H$	0.432 [0.239 ; 0.659]
$B_H : G_L$	0.457 [0.255 ; 0.687]
$B_H : G_H$	0.449 [0.257 ; 0.672]
Distribution parameters	
phi	2.773 [1.905 ; 4.305]
pi	0.976 [0.956 ; 0.988]

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Table S23: Bivariate model summary for the mean exploration behaviour per individual and the proportion of preferred prey in blue tit adults using the same model structure and estimates as specified before in Table S22. Number of observations for exploration = 235 and observations of proportion of preferred prey = 145.

$Exploration \sim \mathcal{N}(\mu, \sigma)$	
Fixed effects	
Intercept	48.445 [45.253 ; 51.695]
Trial 1	12.079 [7.771 ; 16.471]
Trial 2	12.601 [5.888 ; 19.335]
Trial 3	23.851 [11.588 ; 35.953]
Time sunrise	0.127 [-0.775 ; 0.991]
Sex	-5.112 [-10.323 ; 0.227]
Random effects	
Individual ID	125.822 [62.482 ; 200.257]
Subplot year	11.668 [0.091 ; 48.076]
Residual	181.476 [133.838 ; 248.310]
Repeatability	
Individual ID	0.392 [0.206 ; 0.547]
Subplot year	0.036 [0.000 ; 0.140]
Residual	0.564 [0.403 ; 0.754]
$ProportionPreferredPrey \sim$ *ZIH-Beta*(μ, ϕ, π)	
Fixed effects	
Intercept	0.717 [0.689 ; 0.743]
Exploration	0.011 [-0.097 ; 0.129]
Treatment B	-0.087 [-1.010 ; 0.839]
Treatment G	0.506 [-0.434 ; 1.497]
Date	-0.069 [-0.143 ; 0.005]
Year 2024	-1.153 [-2.378 ; 0.090]
Exploration * Treatment B	0.062 [-0.057 ; 0.194]
Exploration * Treatment G	-0.043 [-0.177 ; 0.074]
Treatment B * Treatment G	-0.196 [-1.365 ; 1.021]
Exploration * Treatment B * Treatment G	-0.023 [-0.175 ; 0.121]
Random effects	
Individual ID	2.714 [1.392 ; 4.543]
Subplot year	0.368 [0.003 ; 1.487]
Residual	0.049 [0.029 ; 0.076]
Repeatability	
Individual ID	0.865 [0.605 ; 0.984]
Subplot year	0.118 [0.001 ; 0.377]
Residual	0.015 [0.006 ; 0.039]
Mean effects	
Treatment B	-0.018 [-0.117 ; 0.075]
Treatment G	0.041 [-0.044 ; 0.156]
$B_L : G_L$	0.861 [0.686 ; 0.945]
$B_L : G_H$	0.911 [0.777 ; 0.968]
$B_H : G_L$	0.851 [0.671 ; 0.939]
$B_H : G_H$	0.887 [0.731 ; 0.957]
Mean effects Exp	
Treatment B	0.012 [-0.016 ; 0.042]
Treatment G	-0.013 [-0.043 ; 0.014]
$B_L : G_L$	0.532 [0.265 ; 0.788]
$B_L : G_H$	0.521 [0.265 ; 0.769]
$B_H : G_L$	0.548 [0.288 ; 0.790]
$B_H : G_H$	0.531 [0.281 ; 0.768]
Distribution parameters	
phi	3.839 [1.951 ; 7.774]
pi	0.962 [0.923 ; 0.985]

Table S24: Bivariate model summary for the mean exploration behaviour per individual and the proportion of preferred prey in great tit adults using the same model structure and estimates specified before in Table S22). Number of observations for exploration = 299 and observations of proportion of preferred prey = 207.

$Exploration \sim \mathcal{N}(\mu, \sigma)$	
Fixed effects	
Intercept	64.466 [60.755 ; 68.350]
Trial 1	-0.069 [-5.683 ; 5.451]
Trial 2	-2.139 [-11.502 ; 7.223]
Trial 3	-14.382 [-30.284 ; 1.865]
Time sunrise	0.975 [-0.176 ; 2.116]
Sex	-5.531 [-10.627 ; -0.417]
Random effects	
Individual ID	42.376 [0.328 ; 141.020]
Subplot year	38.937 [1.741 ; 118.230]
Residual	395.923 [306.508 ; 496.489]
Repeatability	
Individual ID	0.087 [0.001 ; 0.278]
Subplot year	0.080 [0.004 ; 0.220]
Residual	0.818 [0.627 ; 0.959]
$ProportionPreferredPrey \sim$ *ZIH-Beta*(μ, ϕ, π)	
Fixed effects	
Intercept	0.494 [-0.216 ; 1.171]
Exploration	-0.057 [-0.815 ; 0.701]
Treatment B	0.160 [-0.670 ; 0.961]
Treatment G	0.255 [-0.554 ; 1.027]
Date	-0.038 [-0.077 ; 0.002]
Year 2024	-0.538 [-1.328 ; 0.292]
Exploration * Treatment B	0.024 [-0.760 ; 0.739]
Exploration * Treatment G	0.021 [-0.774 ; 0.764]
Treatment B * Treatment G	-0.339 [-1.341 ; 0.719]
Exploration * Treatment B * Treatment G	-0.004 [-0.703 ; 0.781]
Random effects	
Individual ID	1.310 [0.686 ; 2.217]
Subplot year	0.239 [0.008 ; 0.858]
Residual	0.077 [0.058 ; 0.097]
Repeatability	
Individual ID	0.803 [0.545 ; 0.944]
Subplot year	0.147 [0.005 ; 0.410]
Residual	0.046 [0.023 ; 0.095]
Mean effects	
Treatment B	-0.002 [-0.140 ; 0.140]
Treatment G	0.020 [-0.125 ; 0.167]
$B_L : G_L$	0.621 [0.446 ; 0.763]
$B_L : G_H$	0.679 [0.514 ; 0.798]
$B_H : G_L$	0.657 [0.478 ; 0.797]
$B_H : G_H$	0.639 [0.476 ; 0.773]
Mean effects Exp	
Treatment B	0.005 [-0.153 ; 0.155]
Treatment G	0.004 [-0.158 ; 0.154]
$B_L : G_L$	0.404 [0.132 ; 0.794]
$B_L : G_H$	0.404 [0.110 ; 0.842]
$B_H : G_L$	0.405 [0.116 ; 0.835]
$B_H : G_H$	0.407 [0.093 ; 0.879]
Distribution parameters	
phi	2.525 [1.767 ; 3.906]
pi	0.925 [0.884 ; 0.956]

Table S25: Bivariate model summaries for the mean exploration behaviour per individual and the proportion of preferred prey in blue tit adults combined with their nestlings, separately for males and females. Fitted is the same model structure and estimates as specified before in Table S23, exempt the added fixed effect of bird category (adult, nestling). Number of observations for exploration = 119 in females, 116 in males and observations of proportion of preferred prey = 181 in females and 161 in males.

$Exploration \sim \mathcal{N}(\mu, \sigma)$	*Female*	*Male*
Fixed effects		
Intercept	51.593 [47.254 ; 55.959]	45.519 [40.795 ; 50.317]
Trial 1	10.061 [3.759 ; 16.125]	13.280 [6.909 ; 19.620]
Trial 2	12.579 [3.928 ; 21.386]	11.392 [1.591 ; 21.702]
Trial 3	17.032 [-1.843 ; 35.547]	24.317 [9.158 ; 39.010]
Time sunrise	-0.441 [-1.673 ; 0.755]	0.663 [-0.659 ; 1.947]
Random effects		
Individual ID	99.976 [25.001 ; 199.651]	139.017 [34.568 ; 274.879]
Subplot year	20.860 [0.136 ; 86.678]	5.472 [0.009 ; 54.650]
Residual	176.821 [110.702 ; 276.539]	200.642 [130.930 ; 319.569]
Repeatability		
Individual ID	0.332 [0.082 ; 0.555]	0.398 [0.102 ; 0.620]
Subplot year	0.069 [0.000 ; 0.250]	0.016 [0.000 ; 0.143]
Residual	0.582 [0.346 ; 0.854]	0.570 [0.344 ; 0.865]
$ProportionPreferredPrey \sim$ *ZIH-Beta*(μ, ϕ, π)		
Fixed effects		
Intercept	0.786 [0.760 ; 0.810]	1.512 [0.752 ; 2.248]
Exploration	0.007 [-0.149 ; 0.124]	-0.005 [-0.124 ; 0.088]
Nestling	0.734 [0.170 ; 1.325]	0.489 [-0.090 ; 1.053]
Date	-0.070 [-0.129 ; -0.012]	-0.061 [-0.119 ; -0.006]
Year 2024	-1.081 [-2.131 ; -0.035]	-0.700 [-1.741 ; 0.369]
Exploration * Nestling	-0.050 [-0.217 ; 0.095]	-0.022 [-0.139 ; 0.088]
Random effects		
Sex brood	0.081 [0.000 ; 0.672]	0.078 [0.000 ; 0.610]
Nestlings repeat	2.166 [1.095 ; 3.632]	1.696 [0.860 ; 2.914]
Subplot year	0.103 [0.000 ; 0.651]	0.123 [0.000 ; 0.884]
Residual	0.047 [0.028 ; 0.072]	0.060 [0.039 ; 0.085]
Repeatability		
Sex brood	0.033 [0.000 ; 0.253]	0.037 [0.000 ; 0.274]
Nestlings repeat	0.877 [0.637 ; 0.977]	0.831 [0.556 ; 0.963]
Subplot year	0.042 [0.000 ; 0.231]	0.061 [0.000 ; 0.333]
Residual	0.019 [0.008 ; 0.047]	0.029 [0.012 ; 0.066]
Distribution parameters		
phi	2.860 [1.579 ; 5.546]	2.151 [1.358 ; 3.708]
pi	0.975 [0.947 ; 0.991]	0.972 [0.939 ; 0.990]

Table S26: Bivariate model summaries for the mean exploration behaviour per individual and the proportion of preferred prey in great tit adults combined with their nestlings, separately for males and females. Fitted is the same model structure and estimates as specified before in Table S24, exempt the added fixed effect of bird category (adult, nestling). Number of observations for exploration = 141 in females, 158 in males and observations of proportion of preferred prey = 217 in females and 234 in males.

$Exploration \sim \mathcal{N}(\mu, \sigma)$	*Female*	*Male*
Fixed effects		
Intercept	65.857 [60.857 ; 70.745]	62.552 [57.875 ; 67.421]
Trial 1	4.451 [-3.079 ; 12.021]	-4.540 [-12.487 ; 3.191]
Trial 2	-6.182 [-21.597 ; 9.101]	0.421 [-10.761 ; 11.348]
Trial 3	-26.973 [-56.202 ; 3.903]	-9.019 [-26.041 ; 8.303]
Time sunrise	0.766 [-0.988 ; 2.532]	1.529 [-0.005 ; 3.092]
Random effects		
Individual ID	107.752 [1.157 ; 270.456]	26.504 [0.079 ; 138.085]
Subplot year	20.027 [0.061 ; 126.650]	24.903 [0.125 ; 110.588]
Residual	367.835 [237.837 ; 544.103]	394.515 [285.773 ; 518.247]
Repeatability		
Individual ID	0.214 [0.002 ; 0.474]	0.058 [0.000 ; 0.283]
Subplot year	0.040 [0.000 ; 0.225]	0.055 [0.000 ; 0.214]
Residual	0.726 [0.457 ; 0.971]	0.867 [0.626 ; 0.990]
$ProportionPreferredPrey \sim$ *ZIH-Beta*(μ, ϕ, π)		
Fixed effects		
Intercept	0.675 [0.653 ; 0.699]	0.779 [0.305 ; 1.248]
Exploration	-0.038 [-0.395 ; 0.282]	-0.001 [-1.274 ; 1.448]
Nestling	1.113 [0.546 ; 1.683]	1.272 [0.758 ; 1.784]
Date	-0.111 [-0.161 ; -0.062]	-0.099 [-0.145 ; -0.054]
Year 2024	-1.805 [-2.796 ; -0.792]	-1.428 [-2.298 ; -0.541]
Exploration * Nestling	-0.014 [-0.390 ; 0.339]	-0.038 [-1.344 ; 1.364]
Random effects		
Sex brood	0.051 [0.000 ; 0.492]	0.102 [0.000 ; 0.686]
Nestlings repeat	3.022 [1.716 ; 4.546]	2.205 [1.353 ; 3.321]
Subplot year	0.238 [0.002 ; 1.152]	0.078 [0.000 ; 0.490]
Residual	0.062 [0.044 ; 0.085]	0.061 [0.044 ; 0.079]
Repeatability		
Sex brood	0.015 [0.000 ; 0.141]	0.040 [0.000 ; 0.253]
Nestlings repeat	0.877 [0.682 ; 0.972]	0.881 [0.665 ; 0.971]
Subplot year	0.070 [0.000 ; 0.271]	0.031 [0.000 ; 0.172]
Residual	0.018 [0.009 ; 0.038]	0.024 [0.013 ; 0.044]
Distribution parameters		
phi	4.783 [2.460 ; 8.595]	3.136 [2.080 ; 4.817]
pi	0.920 [0.880 ; 0.951]	0.947 [0.913 ; 0.970]

Table S27: Bivariate model summary for the mean proportion of preferred prey of blue tit nestlings per brood and the individual nestling weight. In the first equation the response variable is the the proportion of preferred prey (zero-inflated Beta-hurdle, $ProportionPreferredPrey \sim$ *ZIH-Beta*(μ, ϕ, π)) with posterior median and 2.5 to 97.5 credible intervals. Random effects are the brood ID, the combination of nestling age and brood ID, to correct for multiple samples taken for a brood (Nestling repeat). Intercept and repeatabilities are shown as proportions on the original scale. Distribution specific parameters phi (ϕ; precision parameter of beta distributions) and pi (π; hurdle pass probability (non-zero)) are shown. Fixed and random effects are shown on logit scale, intercept is shown on original scale. For the second equation the response variable is weight (g) for each nestling (Gaussian distribution, $W \sim \mathcal{N}(\mu, \sigma)$. Fitted as fixed effects are: the mean proportion of preferred prey of the brood taken from the first equation as the best linear unbiased predictor (BLUP), the competitive treatment of blue tits (Treatment B), great tits (Treatment G), the effect of close box proximity (Double box), the sample year, the time the nestling weight was taken (Time weight), the total number of all nestlings within the brood (Brood size) and the interaction of each species-specific treatment with the proportion of preferred prey, the interaction of both competitive treatments and the interaction of proportion of preferred prey with both competitive treatments. As random effects fitted are the combination of subplot and year, brood ID and the residual. Mean effects and standardised selection gradients are calculated for the summarised effects for each species-specific treatment (blue and great tit treatment effect) and their four combinations ($B_L : G_L$, $B_L : G_H$, $B_H : G_L$, $B_H : G_H$). All effects are shown on response scale. Number of observations for the proportion of preferred prey = 178 and observations of individual weight = 724.

$ProportionPreferredPrey \sim$ *ZIH-Beta*(μ, ϕ, π)	
Fixed effects	
Intercept	0.878 [0.836 ; 0.913]
Random effects	
Brood ID	0.033 [0.000 ; 0.352]
Nestling repeat	1.722 [0.789 ; 3.180]
Residual	0.058 [0.036 ; 0.084]
Repeatability	
Brood ID VC	0.018 [0.000 ; 0.205]
Nestling repeat VC	0.945 [0.750 ; 0.983]
Residual VC	0.031 [0.012 ; 0.080]
Distribution parameters	
phi	1.871 [1.137 ; 3.575]
pi	0.974 [0.943 ; 0.991]
$Weight \sim \mathcal{N}(\mu, \sigma)$	
Fixed effects	
Intercept	11.564 [10.757 ; 12.368]
Proportion of preferred prey	0.111 [-1.917 ; 2.161]
Treatment B	0.158 [-0.537 ; 0.827]
Treatment G	-0.146 [-0.893 ; 0.547]
Double box	0.552 [-0.147 ; 1.264]
Year 2024	-0.056 [-0.574 ; 0.507]
Time weight	0.069 [-0.026 ; 0.163]
Brood size	-0.113 [-0.196 ; -0.025]
Proportion of preferred prey * Treatment B	-0.181 [-2.302 ; 2.075]
Proportion of preferred prey * Treatment G	0.387 [-2.125 ; 2.506]
Treatment B * Treatment G	-0.348 [-1.319 ; 0.656]
Proportion of preferred prey * Treatment B * Treatment G	0.090 [-2.108 ; 2.198]
Random effects	
Subplot year	0.115 [0.007 ; 0.420]
Brood ID	0.373 [0.142 ; 0.591]
Residual	0.507 [0.454 ; 0.568]
Repeatability	
Subplot year	0.117 [0.007 ; 0.336]
Brood ID	0.368 [0.172 ; 0.511]
Residual	0.504 [0.374 ; 0.666]
Mean effects	
Treatment B	-0.014 [-0.584 ; 0.543]
Treatment G	-0.322 [-0.896 ; 0.213]
$B_L : G_L$	11.564 [10.757 ; 12.368]
$B_L : G_H$	11.409 [10.545 ; 12.258]
$B_H : G_L$	11.713 [10.901 ; 12.538]
$B_H : G_H$	11.226 [10.269 ; 12.140]
Standardised selection gradient proportion of preferred prey	
Treatment B	-0.057 [-5.341 ; 5.681]
Treatment G	0.149 [-5.664 ; 5.558]
$B_L : G_L$	0.039 [-4.978 ; 5.184]
$B_L : G_H$	0.226 [-7.570 ; 7.390]
$B_H : G_L$	-0.060 [-7.017 ; 6.618]
$B_H : G_H$	0.148 [-10.114 ; 9.844]

Table S28: Bivariate model summary for the mean proportion of preferred prey of great tit nestlings per brood and the individual nestling weight, using the same model structure and estimates as specified before in Table S26. Number of observations for the proportion of preferred prey = 165 and observations of individual weight = 528.

$ProportionPreferredPrey \sim$ ZIH-Beta(μ, ϕ, π)	
Fixed effects	
Intercept	0.829 [0.766 ; 0.880]
Random effects	
Brood ID	0.186 [0.022 ; 0.794]
Nestling repeat	3.026 [1.761 ; 4.701]
Residual	0.084 [0.061 ; 0.110]
Brood ID VC	0.057 [0.006 ; 0.230]
Nestling repeat VC	0.916 [0.741 ; 0.972]
Residual VC	0.025 [0.014 ; 0.047]
Distribution parameters	
phi	2.751 [1.670 ; 4.489]
pi	0.907 [0.857 ; 0.945]
$Weight \sim \mathcal{N}(\mu, \sigma)$	
Fixed effects	
Intercept	16.550 [15.288 ; 17.751]
Proportion of preferred prey	0.346 [-3.237 ; 2.185]
Treatment B	0.230 [-0.754 ; 1.185]
Treatment G	0.304 [-0.487 ; 1.107]
Double box	-0.397 [-1.675 ; 0.933]
Year 2024	-0.581 [-1.367 ; 0.167]
Time weight	0.206 [0.098 ; 0.309]
Brood size	-0.109 [-0.283 ; 0.069]
Proportion of preferred prey * Treatment B	-1.241 [-4.083 ; 1.617]
Proportion of preferred prey * Treatment G	-0.994 [-3.513 ; 1.442]
Treatment B * Treatment G	-0.821 [-2.242 ; 0.613]
Proportion of preferred prey * Treatment B * Treatment G	-1.356 [-4.279 ; 1.894]
Random effects	
Subplot year	0.024 [0.000 ; 0.198]
Brood ID	0.202 [0.008 ; 0.432]
Residual	0.454 [0.399 ; 0.520]
Repeatability	
Subplot year	0.035 [0.000 ; 0.239]
Brood ID	0.290 [0.017 ; 0.478]
Residual	0.654 [0.470 ; 0.922]
Mean effects	
Treatment B	-0.183 [-0.974 ; 0.600]
Treatment G	-0.109 [-0.863 ; 0.658]
$B_L : G_L$	16.550 [15.288 ; 17.751]
$B_L : G_H$	16.863 [15.614 ; 18.025]
$B_H : G_L$	16.784 [15.429 ; 18.055]
$B_H : G_H$	16.257 [14.747 ; 17.716]
Standardised selection gradients proportion of preferred prey	
Treatment B	-0.259 [-1.545 ; 0.305]
Treatment G	-0.213 [-1.210 ; 0.201]
$B_L : G_L$	0.041 [-1.011 ; 0.439]
$B_L : G_H$	-0.105 [-1.347 ; 0.252]
$B_H : G_L$	-0.160 [-1.858 ; 0.470]
$B_H : G_H$	-0.485 [-2.938 ; 0.506]

Table S29: Bivariate model summary for the mean proportion of preferred prey of blue tit nestlings per brood and their total brood weight. In the first equation the response variable is the the proportion of preferred prey (zero-inflated Beta-hurdle, $ProportionPreferredPrey \sim$ *ZIH-Beta*(μ, ϕ, π)) with posterior median and 2.5 to 97.5 credible intervals. Random effects are the brood ID, the combination of nestling age and brood ID, to correct for multiple samples taken for a brood (Nestling repeat). Intercept and repeatabilities are shown as proportions on the original scale. Distribution specific parameters phi (ϕ; precision parameter of beta distributions) and pi (π; hurdle pass probability (non-zero)) are shown. Fixed and random effects are shown on logit scale, intercept is shown on original scale. For the second equation the response variable is the total brood weight (g, sum of individual nestlings weights; Gaussian distribution, $W \sim \mathcal{N}(\mu, \sigma)$. Fitted as fixed effects are: the mean proportion of preferred prey of the brood taken from the first equation as the best linear unbiased predictor (BLUP), the competitive treatment of blue tits (Treatment B), great tits (Treatment G), the effect of close box proximity (Double box), the sample year, the time the nestling weight was taken (TimeWeight), the total number of all nestlings within the brood (BroodSize) and the interaction of each species-specific treatment with the proportion of preferred prey, the interaction of both competitive treatments and the interaction of proportion of preferred prey with both competitive treatments. As random effects fitted are the combination of Subplot and year and the residual. Mean effects and standardised selection gradients are calculated for the summarised effects for each species-specific treatment (blue and great tit treatment effect) and their four combinations (B_L : G_L, B_L : G_H, B_H : G_L, B_H : G_H). All effects are shown on response scale. Number of observations for the proportion of preferred prey = 178 and observations of brood weight = 98.

$ProportionPreferredPrey \sim$ *ZIH-Beta*(μ, ϕ, π)	
Fixed effects	
Intercept	0.877 [0.836 ; 0.914]
Random effects	
Brood ID	0.013 [0.000 ; 0.180]
Nestling repeat	1.734 [0.834 ; 3.183]
Residual	0.058 [0.036 ; 0.083]
Repeatability	
Brood ID VC	0.007 [0.000 ; 0.104]
Nestling repeat VC	0.957 [0.848 ; 0.984]
Residual VC	0.032 [0.012 ; 0.079]
Distribution parameters	
phi	1.862 [1.135 ; 3.557]
pi	0.974 [0.944 ; 0.991]
$Weight \sim \mathcal{N}(\mu, \sigma)$	
Fixed effects	
Intercept	8.198 [1.829 ; 14.997]
Proportion of preferred prey	1.802 [-34.130 ; 38.538]
Treatment B	0.525 [-5.095 ; 5.347]
Treatment G	-1.602 [-7.438 ; 3.786]
Double box	5.418 [-1.212 ; 11.860]
Year 2024	-1.456 [-5.384 ; 2.473]
Time weight	0.117 [-0.602 ; 0.854]
Brood size	9.696 [9.004 ; 10.377]
Proportion of preferred prey * Treatment B	0.040 [-35.080 ; 35.604]
Proportion of preferred prey * Treatment G	7.541 [-39.200 ; 45.638]
Treatment B * Treatment G	-3.342 [-11.144 ; 5.057]
Proportion of preferred prey * Treatment B * Treatment G	2.530 [-36.858 ; 41.368]
Random effects	
Subplot year	0.010 [0.000 ; 0.055]
Residual	0.083 [0.030 ; 0.128]
Repeatability	
Subplot year	0.114 [0.001 ; 0.480]
Residual	0.886 [0.520 ; 0.999]
Mean effects	
Treatment B	-1.198 [-5.504 ; 2.763]
Treatment G	-3.248 [-7.443 ; 0.539]
B_L : G_L	8.198 [1.829 ; 14.997]
B_L : G_H	6.599 [0.183 ; 13.129]
B_H : G_L	8.660 [2.736 ; 14.732]
B_H : G_H	3.682 [-3.571 ; 11.128]
Standardised selection gradients proportion of preferred prey	
Treatment B	0.066 [-16.954 ; 18.229]
Treatment G	0.671 [-16.947 ; 18.082]
B_L : G_L	0.131 [-15.601 ; 16.943]
B_L : G_H	0.827 [-21.567 ; 23.878]
B_H : G_L	0.092 [-21.884 ; 23.663]
B_H : G_H	1.059 [-31.177 ; 34.926]

Table S30: Bivariate model summary for the mean proportion of preferred prey of great tit nestlings per brood and the total weight of the brood, using the same model structure and estimates as specified before in Table S26. Number of observations for the proportion of preferred prey = 165 and observations of fledging success = 84.

$ProportionPreferredPrey \sim$ ZIH-Beta(μ, ϕ, π)	
Fixed effects	
Intercept	0.829 [0.767 ; 0.880]
Random effects	
Brood ID	0.018 [0.000 ; 0.289]
Nestling repeat	3.162 [1.904 ; 4.864]
Residual	0.084 [0.062 ; 0.109]
Brood ID VC	0.005 [0.000 ; 0.089]
Nestling repeat VC	0.966 [0.880 ; 0.984]
Residual VC	0.025 [0.014 ; 0.048]
Distribution parameters	
phi	2.734 [1.671 ; 4.417]
pi	0.907 [0.858 ; 0.943]
$Weight \sim \mathcal{N}(\mu, \sigma)$	
Fixed effects	
Intercept	9.177 [0.831 ; 17.541]
Proportion of preferred prey	2.579 [-43.713 ; 44.581]
Treatment B	0.573 [-6.019 ; 7.195]
Treatment G	0.034 [-5.422 ; 5.605]
Double box	-3.796 [-11.420 ; 4.035]
Year 2024	-2.557 [-7.574 ; 2.536]
Time weight	1.486 [0.766 ; 2.199]
Brood size	14.467 [13.292 ; 15.602]
Proportion of preferred prey * Treatment B	-3.009 [-48.108 ; 45.378]
Proportion of preferred prey * Treatment G	-3.785 [-43.347 ; 40.684]
Treatment B * Treatment G	-2.397 [-11.689 ; 7.174]
Proportion of preferred prey * Treatment B * Treatment G	-1.627 [-50.042 ; 50.455]
Random effects	
Subplot year	0.002 [0.000 ; 0.024]
Residual	0.085 [0.032 ; 0.135]
Repeatability	
Subplot year	0.021 [0.000 ; 0.253]
Residual VC	0.979 [0.747 ; 1.000]
Mean effects	
Treatment B	-0.621 [-5.438 ; 4.221]
Treatment G	-1.112 [-5.806 ; 3.554]
$B_L : G_L$	9.177 [0.831 ; 17.541]
$B_L : G_H$	9.287 [1.293 ; 17.227]
$B_H : G_L$	9.758 [1.250 ; 18.364]
$B_H : G_H$	7.431 [-2.002 ; 16.918]
Standardised selection gradients proportion of preferred prey	
Treatment B	-0.200 [-16.037 ; 15.638]
Treatment G	-0.224 [-12.810 ; 15.931]
$B_L : G_L$	0.128 [-12.332 ; 12.961]
$B_L : G_H$	-0.143 [-16.692 ; 18.325]
$B_H : G_L$	-0.098 [-18.648 ; 19.603]
$B_H : G_H$	-0.533 [-28.728 ; 29.558]

Table S31: Bivariate model summary for the mean proportion of preferred prey of blue tit nestlings per brood and their fledging success. In the first equation the response variable is the the proportion of preferred prey (zero-inflated Beta-hurdle, $ProportionPreferredPrey \sim$ *ZIH-Beta*(μ, ϕ, π)) with posterior median and 2.5 to 97.5 credible intervals. Random effects are the brood ID, the combination of nestling age and brood ID, to correct for multiple samples taken for a brood (Nestling repeat). Intercept and repeatabilities are shown as proportions on the original scale. Distribution specific parameters phi (ϕ; precision parameter of beta distributions) and pi (π; hurdle pass probability (non-zero)) are shown. Fixed and random effects are shown on logit scale, intercept is shown on original scale. For the second equation the response variable is the fledging success for each brood (Bernoulli distribution, $W \sim$ *Bernoulli*(p)). Fitted as fixed effects are the mean proportion of preferred prey of the brood taken from the first equation as the standardised best linear unbiased predictor (BLUP), the competitive treatment of blue tits (Treatment B), great tits (Treatment G), the effect of close box proximity (Double box), the sample year and the interaction of each species-specific treatment with the proportion of preferred prey, the interaction of both competitive treatments and the interaction of proportion of preferred prey with both competitive treatments. As random effects fitted are the combination of Subplot and year, brood ID and the residual. Intercept is shown on probability scale, fixed and random effects are shown on logit scale. Mean effects and standardised selection gradients are calculated for the summarised effects for each species-specific treatment (blue and great tit treatment effect) and their four combinations ($B_L : G_L$, $B_L : G_H$, $B_H : G_L$, $B_H : G_H$). Number of observations for the proportion of preferred prey = 232 and observations of Fledging success = 140.

$ProportionPreferredPrey \sim$ *ZIH-Beta*(μ, ϕ, π)	
Fixed effects	
Intercept	0.870 [0.834 ; 0.901]
Random effects	
Brood ID	0.061 [0.000 ; 0.506]
Nestling repeat	1.505 [0.798 ; 2.472]
Residual	0.055 [0.039 ; 0.075]
Repeatability	
Brood ID	0.037 [0.000 ; 0.289]
Nestling repeat	0.925 [0.670 ; 0.977]
Residual	0.033 [0.016 ; 0.070]
Distribution parameters	
phi	1.839 [1.246 ; 2.857]
pi	0.980 [0.957 ; 0.993]
$FledgingSuccess \sim$ *Bernoulli*(p)	
Fixed effects	
Intercept	0.900 [0.737 ; 0.968]
Proportion preferred prey	0.100 [-1.224 ; 1.455]
Treatment B	0.829 [-0.589 ; 2.279]
Treatment G	-0.087 [-1.412 ; 1.399]
Double box	0.419 [-1.171 ; 2.052]
Year 2024	0.876 [-0.382 ; 2.161]
Proportion preferred prey * Treatment B	0.087 [-1.590 ; 1.696]
Proportion preferred prey * Treatment G	0.194 [-1.714 ; 2.064]
Treatment B * Treatment G	-0.139 [-1.732 ; 1.538]
Proportion preferred prey * Treatment B * Treatment G	0.198 [-1.744 ; 2.116]
Random effects	
Subplot year	0.782 [0.003 ; 4.708]
Residual	3.290 [3.290 ; 3.290]
Repeatability	
Subplot year	0.192 [0.001 ; 0.589]
Residual	0.808 [0.411 ; 0.999]
Mean effects	
Treatment B	0.046 [-0.067 ; 0.179]
Treatment G	0.012 [-0.152 ; 0.092]
$B_L : G_L$	0.900 [0.737 ; 0.968]
$B_L : G_H$	0.891 [0.684 ; 0.976]
$B_H : G_L$	0.953 [0.828 ; 0.990]
$B_H : G_H$	0.940 [0.732 ; 0.994]
Standardised selection gradients proportion preferred prey	
Treatment B	0.006 [-0.172 ; 0.182]
Treatment G	0.031 [-0.189 ; 0.215]
$B_L : G_L$	0.009 [-0.149 ; 0.171]
$B_L : G_H$	0.034 [-0.222 ; 0.260]
$B_H : G_L$	0.008 [-0.131 ; 0.158]
$B_H : G_H$	0.057 [-0.243 ; 0.273]

Table S32: Bivariate model summary for the mean proportion of preferred prey of great tit nestlings per brood and their fledging success, using the same model structure and estimates as specified before in Table S26. Number of observations for the proportion of preferred prey = 225 and observations of fledging success = 138.

$ProportionPreferredPrey \sim$ *ZIH-Beta*(μ, ϕ, π)	
Fixed effects	
Intercept	0.842 [0.791 ; 0.884]
Random effects	
Brood ID	0.165 [0.000 ; 1.219]
Nestling repeat	3.158 [1.904 ; 4.756]
Residual	0.082 [0.062 ; 0.104]
Repeatability	
Brood ID	0.048 [0.000 ; 0.325]
Nestling repeat	0.928 [0.649 ; 0.981]
Residual	0.023 [0.014 ; 0.041]
Distribution parameters	
phi	2.763 [1.747 ; 4.368]
pi	0.910 [0.869 ; 0.942]
$FledgingSuccess \sim$ *Bernoulli*(p)	
Fixed effects	
Intercept	0.850 [0.666 ; 0.943]
Proportion of preferred prey	0.184 [-1.439 ; 1.674]
Treatment B	1.269 [-0.014 ; 2.609]
Treatment G	0.009 [-1.197 ; 1.247]
Double box	-0.313 [-2.006 ; 1.462]
Year 2024	-0.981 [-2.109 ; 0.319]
Proportion of preferred prey * Treatment B	-0.119 [-1.714 ; 1.518]
Proportion of preferred prey * Treatment G	-0.139 [-1.818 ; 1.543]
Treatment B * Treatment G	0.370 [-1.170 ; 1.952]
Proportion of preferred prey * Treatment B * Treatment G	0.054 [-1.706 ; 1.775]
Random effects	
Subplot year	0.763 [0.004 ; 4.408]
Residual	3.290 [3.290 ; 3.290]
Repeatability	
Subplot year	0.188 [0.001 ; 0.573]
Residual	0.812 [0.427 ; 0.999]
Mean effects	
Treatment B	0.106 [0.015 ; 0.241]
Treatment G	0.007 [-0.102 ; 0.119]
$B_L : G_L$	0.850 [0.666 ; 0.943]
$B_L : G_H$	0.850 [0.650 ; 0.952]
$B_H : G_L$	0.952 [0.835 ; 0.988]
$B_H : G_H$	0.966 [0.865 ; 0.994]
Standardised selection gradients proportion of preferred prey	
Treatment B	-0.014 [-0.221 ; 0.189]
Treatment G	-0.013 [-0.198 ; 0.171]
$B_L : G_L$	0.026 [-0.221 ; 0.249]
$B_L : G_H$	0.000 [-0.258 ; 0.277]
$B_H : G_L$	0.002 [-0.152 ; 0.164]
$B_H : G_H$	-0.001 [-0.166 ; 0.149]

Table S33: Alphabetical list of order taxa detected in the faecal samples of the birds. N = 34.

Order	Order	Order	Order	Order
Amphipoda	Araneae	Blattodea	Chordeumatida	Coleoptera
Crassiclitellata	Diptera	Enchytraeida	Entomobryomorpha	Glomerida
Haplotaxida	Hemiptera	Hymenoptera	Isopoda	Ixodida
Julida	Lepidoptera	Lithobiomorpha	Mesostigmata	Neuroptera
Nudibranchia	Opiliones	Orthoptera	Poduromorpha	Polydesmida
Polyxenida	Psocodea	Pteropoda	Raphidioptera	Sarcoptiformes
Siphonaptera	Siphonariida	Stylommatophora	Symphypleona	Thysanoptera
Trombidiformes	Trochida			

Table S34: Alphabetical list of family taxa detected in the bird samples. N = 307.

Family	Family	Family	Family	Family
Acaridae	Achipteriidae	Acroceridae	Adelgidae	Adelidae
Agelenidae	Agromyzidae	Aleyrodidae	Amaurobiidae	Analgidae
Anaplectidae	Andrenidae	Anthocoridae	Anthomyiidae	Anthribidae
Anyphaenidae	Aphalaridae	Aphelinidae	Aphididae	Aphrophoridae
Apidae	Araneae.spc	Araneidae	Argidae	Argyresthiidae
Arionidae	Armadillidiidae	Attelabidae	Bethylidae	Bibionidae
Blattidae	Blattodea.spc	Brachychthoniidae	Braconidae	Bourletiellidae
Buprestidae	Calliphoridae	Cantharidae	Carabidae	Carabodidae
Caeciliusidae	Cecidomyiidae	Cerambycidae	Ceratopogonidae	Ceratophyllidae
Ceratozetidae	Chloropidae	Chrysomelidae	Chrysopidae	Chyromyidae
Cicadellidae	Cimberididae	Cimbicidae	Cixiidae	Cleridae
Clausiliidae	Clubionidae	Coccidae	Coccinellidae	Coleophoridae
Coleoptera.spc	Coniopterygidae	Corinnidae	Cosmopterigidae	Corylophidae
Crambidae	Crangonyctidae	Craspedosomatidae	Creseidae	Crotoniidae
Cryptophagidae	Cunaxidae	Curculionidae	Ctenidae	Cynipidae
Cymbaeremaeidae	Dictynidae	Dicyrtomidae	Digamasellidae	Diapriidae
Discidae	Dolichopodidae	Dolomedidae	Drosophilidae	Drepanidae
Dryinidae	Dysderidae	Ectobiidae	Ectopsocidae	Elateridae
Elipsocidae	Empididae	Enchytraeidae	Enidae	Encyrtidae
Ephydridae	Erebidae	Eresidae	Eriocraniidae	Eriophyidae
Erythraeidae	Eulophidae	Eupelmidae	Eupodidae	Euphthiracaridae
Eurytomidae	Evaniidae	Euzetidae	Fanniidae	Figitidae
Formicidae	Galumnidae	Gelechiidae	Geometridae	Glomeridae
Glyphipterigidae	Gnaphosidae	Gryllidae	Halictidae	Haplotaxida.incertae.sedis
Heleomyzidae	Hemerobiidae	Hemiptera.spc	Hepialidae	Hermanniidae
Hesperiidae	Histeridae	Hygromiidae	Hymenoptera.spc	Hybotidae
Hypochthoniidae	Hypogastruridae	Ichneumonidae	Incurvariidae	Ischnorhinidae
Issidae	Isotomidae	Ixodidae	Julidae	Katiannidae
Keroplatidae	Lachesillidae	Laelapidae	Lasiocampidae	Latridiidae
Lauxaniidae	Lepidoptera.spc	Leiodidae	Limacidae	Limacodidae
Limoniidae	Liacaridae	Liocranidae	Lithobiidae	Lonchaeidae
Lumbricidae	Lymexylidae	Lycaenidae	Lycosidae	Lypusidae
Mymaridae	Megastigmidae	Melicharidae	Menoponidae	Micreremidae
Miridae	Miturgidae	Mordellidae	Muscidae	Mutillidae
Mycetophilidae	Myrmeleontidae	Nabidae	Nanhermanniidae	Nanorchestidae
Neoliodidae	Nesticidae	Nitidulidae	Nolidae	Noctuidae
Notodontidae	Nothridae	Nymphalidae	Oppiidae	Orchesellidae
Oribatellidae	Oribatulidae	Oxychilidae	Pamphiliidae	Paracaeciliidae
Parasitidae	Pentatomidae	Perilampidae	Peripsocidae	Phalangiidae
Philodromidae	Philosciidae	Phlaeothripidae	Pholcidae	Phoridae
Phthiracaridae	Phytoptidae	Phytoseiidae	Pipunculidae	Pisauridae
Platygastridae	Polleniidae	Polyxenidae	Polydesmidae	Pompilidae
Proctophyllodidae	Proctotrupidae	Psocidae	Pseudococcidae	Psylloidea.incertae.sedis
Psyllidae	Psychidae	Psychodidae	Pteromalidae	Pterophoridae
Ptinidae	Punctoribatidae	Punctidae	Pygmephoridae	Pyrochroidae
Pyroglyphidae	Pyralidae	Quadroppiidae	Raphidiidae	Reduviidae
Rhagionidae	Rhinotermitidae	Scarabaeidae	Scelionidae	Scoliidae
Sciaridae	Scirtidae	Scraptiidae	Seiridae	Signiphoridae
Silphidae	Siphonariidae	Sminthuridae	Sminthurididae	Solariellidae
Sperchontidae	Staphylinidae	Stenopsocidae	Stigmaeidae	Stratiomyidae
Succineidae	Stylommatophora.spc	Syrphidae	Tachinidae	Talitridae
Tarsonemidae	Tectocepheidae	Tenebrionidae	Tenthredinidae	Termitidae
Tetragnathidae	Tetranychidae	Tetrigidae	Theridiidae	Thomisidae
Thripidae	Tipulidae	Tineidae	Tomoceridae	Tortricidae
Torymidae	Trachelipodidae	Trichoniscidae	Trigonidiidae	Trhypochthoniidae
Triozidae	Trogiidae	Trouessartiidae	Vespidae	Vitrinidae
Xylophagidae	Xyloryctidae	Ypsolophidae	Zerconidae	

Table S35: Alphabetical list of family taxa detected in the environmental frass samples. N = 194.

Family	Family	Family	Family	Family
Acaridae	Achipteriidae	Agromyzidae	Aleyrodidae	Amaurobiidae
Anisopodidae	Andrenidae	Anyphaenidae	Anthocoridae	Anthomyiidae
Anthribidae	Aphelinidae	Aphididae	Apidae	Argidae
Araneae.spc	Araneidae	Argyresthiidae	Arionidae	Belostomatidae
Bibionidae	Bourletiellidae	Braconidae	Buprestidae	Caeciliusidae
Caenidae	Cantharidae	Carabidae	Carabodidae	Cecidomyiidae
Cerambycidae	Ceratopogonidae	Chrysomelidae	Chrysididae	Chrysopidae
Chironomidae	Chromodorididae	Cicadellidae	Cleridae	Clausiliidae
Coleophoridae	Coniopterygidae	Crotoniidae	Crambidae	Cryptophagidae
Cymbaeremaeidae	Cynipidae	Dictynidae	Diapriidae	Dipseudopsidae
Diptera.spc	Diptilomiopidae	Dolichopodidae	Drepanidae	Drosophilidae
Ectobiidae	Ectopsocidae	Elateridae	Elipsocidae	Empididae
Encyrtidae	Enidae	Ephemerellidae	Ephydridae	Erebidae
Eresidae	Eriocraniidae	Eriophyidae	Erotylidae	Eucnemidae
Eulophidae	Euphthiracaridae	Eurytomidae	Evaniidae	Fanniidae
Forficulidae	Formicidae	Gelechiidae	Geometridae	Gnaphosidae
Glyphipterigidae	Gryllidae	Halictidae	Heptageniidae	Hemerobiidae
Hemiptera.spc	Hesperiidae	Histeridae	Hygromiidae	Hymenoptera.spc
Hybotidae	Hypogastruridae	Ichneumonidae	Issidae	Isotomidae
Ixodidae	Julidae	Keroplatidae	Lasiocampidae	Lauxaniidae
Limacidae	Linyphiidae	Liocranidae	Limoniidae	Lithobiidae
Lonchaeidae	Lumbricidae	Lycaenidae	Lycosidae	Lypusidae
Megastigmidae	Micreremidae	Microphysidae	Miridae	Mordellidae
Mutillidae	Mycetophilidae	Myrmeleontidae	Neoliodidae	Nesticidae
Nitidulidae	Nolidae	Notodontidae	Noctuidae	Nothridae
Nymphalidae	Oecophoridae	Orchesellidae	Oribatulidae	Pamphiliidae
Paracaeciliidae	Pentatomidae	Phalangiidae	Philodromidae	Phlaeothripidae
Phoridae	Phthiracaridae	Phytoptidae	Phytoseiidae	Pisauridae
Platygastridae	Pompilidae	Pteromalidae	Psocidae	Psylloidea.incertae.sedis
Psyllidae	Psychidae	Pterophoridae	Ptinidae	Punctidae
Pygmephoridae	Pyroglyphidae	Pyralidae	Quadroppiidae	Reduviidae
Rhagionidae	Sarcophagidae	Sarcoptiformes.spc	Scarabaeidae	Scelionidae
Sciaridae	Scraptiidae	Sminthuridae	Sminthurididae	Signiphoridae
Silphidae	Staphylinidae	Stenopsocidae	Syrphidae	Tachinidae
Tarsonemidae	Tectocepheidae	Tenebrionidae	Tenthredinidae	Termitidae
Tetranychidae	Tettigoniidae	Theridiidae	Thomisidae	Thripidae
Tineidae	Tipulidae	Tortricidae	Trichogrammatidae	Trichoniscidae
Triozidae	Trogiidae	Ypsolophidae	Zerconidae	