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The Effects of GMHT Crops on Summer Bird and Mammal Occurrence – A Power Analysis

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1. EXECUTIVE SUMMARY

1. The effects of genetically modified herbicide-tolerant (GMHT) crops on farmland biodiversity are being assessed by comparing the abundance of various taxa between conventional and GMHT halves of experimental fields in a large-scale experiment termed the Farm-Scale Evaluation (FSE).

2. A bird and mammal survey was carried out in spring and summer 2000 in order to assess the feasibility of including birds and mammals as target groups in the FSE. Specifically, this project was designed to assess the power of the FSE experimental design to detect differences in the utilisation of conventional and GMHT crops. This was achieved through a power analysis of various measures of bird and mammal occurrence for selected species, including measures of foraging activity in the crop.

3. There were 24 sugar beet sites, 12 maize sites and 12 rape sites surveyed five times between April and August, but many species were absent from several sites. Three different survey approaches were used: a territory mapping of all birds in the experimental and surrounding field boundaries; point counts of birds in fields (to record foraging events); and foraging observations of aerial feeders. Observers had no prior knowledge of how each half of a field had been treated.

4. The power analysis was based on Poisson and binomial models incorporating site, seasonal and treatment effects. Two different comparisons were made: GMHT crop before herbicide application vs. conventional crop in the same time period (i.e. early in the season) and GMHT crop after herbicide application vs. conventional crop in the same time period (i.e. late in the season).

5. Ten bird species were selected for analysis based on their abundance and detectability given the survey methods used and also to represent a range of dietary preferences. The species were Red-Legged Partridge *Alectoris rufa*, Skylark *Alauda arvensis*, Wren *Troglodytes troglodytes*, Dunnock *Prunella modularis*, Whitethroat *Sylvia communis*, Robin *Erithacus rubecula*, Blackbird *Turdus merula*, Song Thrush *T. philomelos*, Chaffinch *Fringella coelebs* and Yellowhammer *Emberiza citrinella*. For aerial feeders four species were considered: Swallow *Hirundo rustica*, Sand Martin *Riparia riparia*, House Martin *Delichon urbica* and Swift *Apus apus*.

6. Most analyses had low power to detect significant differences on a realistic scale in the data collected. The most powerful analyses involved a comparison of GMHT treated (i.e. sprayed) crop with conventionally treated crop later in the breeding season. Point counts collecting foraging data and information on bird registrations in open fields were most likely to yield analyses of high power in this data set.

7. Results for sugar beet were of relatively low power in comparison with results from maize and oilseed rape. This in part may have been because many sugar beet sites were in intensive arable areas with few, if any, trees or hedges. The geographical location of additional sites as well whether they are established as whole fields or sub-plots within fields (lacking boundaries) is therefore likely to have a big impact on future statistical power of the FSE for birds.

8. Simulated data for additional sites showed surveys of Red-Legged Partridge, Skylark, Dunnock, Whitethroat, Chaffinch and Yellowhammer in GMHT (treated) and conventional crops were predicted to achieve 95% power given the combined sample sizes for 2000 and those to be part of the FSE in 2001 - a total of 50 sugar beet, 39 maize and 37 rape sites. If it is assumed that the same number of sites is to be surveyed in 2002 as is planned for 2001 then the analyses predict that two further species, Robin and Blackbird, will also achieve 95% power.

9. In the case of mammals, only Hare *Lepus europeaus* and Rabbit *Oryctolagus cuniculus* were recorded in sufficient numbers for analysis in the mammal survey and these were of lower power relative to the bird analyses. As for birds, the most powerful analyses involved comparison of GMHT (treated) versus conventional crop treatments. Hare abundance on maize crops was the most powerful analyses and 95% power was predicted with a total of 46 sites.

10. The assumptions of all of these analyses were based on estimates derived from small sample sizes. An examination of the full set of results for all bird species combined predicted that to achieve a statistical comparison with 95% power, a difference of approximately 75% in numbers between treatments would be required for sample sizes of 40-100 sites for Poisson models. For binomial models, the odds ratio would need to be approximately three to four times greater on one treatment for 40-80 sites and 2.5 times greater for 80-100 sites to achieve 95% power.

11. In summary, the power analyses presented here indicate that a high probability of detecting significant differences in bird abundance or occurrence between treatments would be possible for six species with the additional sites proposed for 2001. Point counts recording foraging individuals on maize and rape crops in the later half of the breeding season, (i.e. after herbicides application to GMHT crops) are likely to yield the most powerful analyses. Detection of significant differences in mammal abundance was less likely.

12. There are a number of important caveats relating to these results. Crucially the findings are dependent on acceptance of the assumption that derived parameter estimates are precisely estimated and likely to remain similar when further sites are surveyed. Caution is therefore needed when interpreting these power analyses due to the small sample sizes involved. We have used a stringent level of power of 95%, but if a lower level of power were considered acceptable, the sample sizes and the magnitude of differences required to achieve this level would obviously be lower. For example, a further 26 species/crop/variable specific data sets could provide analyses of sufficient power if we considered a 75% level of power to be acceptable. However, the analysis presented in this paper provides a good baseline to direct future studies.

2. INTRODUCTION

Recent advances in recombinant DNA technology have lead to the development of genetically modified organisms. In agriculture, genetically modified herbicide-tolerant (GMHT) crops are already commercially grown in the USA and China. These differ from conventionally managed crops in that broad-spectrum herbicides (e.g. Glyphosate) can be applied, thus killing all plants save the GMHT crops. This is attractive to farmers because it is both more effective and less costly than conventional management, but also because far fewer applications are needed (e.g. the need for pre-emergence spraying is removed). However, concerns over potential environmental costs related to the introduction of GMHT crops. These include the introgression of transgenes into weedy relatives of crops and the loss of farmland biodiversity due to the complete removal of weeds from crops (Hails 2000). This study is concerned with the latter factor.

Farmland biodiversity has shown general declines over the past three decades (Krebs *et al.* 1999). Declines in birds at least are closely linked to agricultural intensification (Chamberlain *et al.* 2000). Removal of weed plants could have important implications for granivorous birds (Watkinson *et al.* 2000) and further intensification caused by the introduction of GMHT crops could potentially have severe impacts on the bird community. However, there may be potential environmental benefits of the introduction of GMHT crops in that fewer sprayings may encourage minimum tillage systems and spring sowing. Furthermore, increased productivity may mean that there is the potential for a greater proportion of land to be put into set-aside or agri-environmental schemes (Hails 2000). Later spraying may also mean that weeds are tolerated in the crop for longer periods than under conventional management.

The potential effects of GMHT crops on farmland biodiversity are currently being investigated by the Department of Environment, Transport and Regions under the Farm-Scale Evaluations (FSE) project. This considers the effects of GMHT crops compared to conventionally managed crops on a range of taxa in a large-scale field experiment. The findings of the FSE will be used to make recommendations on the likely impacts of GM crops to farmland biodiversity. These findings will influence government policy on the commercial introduction of GMHT crops. Experimental rigour is an extremely important issue and before conclusions are drawn from the FSE about environmental impacts, the feasibility of the experimental approach and the reliability of subsequent results, needs to be assessed. In this paper, we present results from a pilot study that considered the differences in bird and mammal occurrence between GMHT and conventional crops on FSE sites. A power analysis is carried out on the data in order to assess the feasibility and value of incorporating bird and mammal surveys into the main FSE programme.

3. AIMS

The aims of this study were (i) to determine the number of experimental sites likely to be required in the FSE if statistically significant differences in bird and mammal occurrence (expressed using a variety of measures) are to be detected between GMHT conventional crops; and, (ii) to identify the crop types, species and methods which are likely to provide the most powerful tests of the influence of the use of GMHT versus conventional crops on bird and mammal occurrence. As the goal of this analysis is to determine adequate sample sizes required rather than actually compare treatment types, different treatment types will not be explicitly identified in the text and no conclusions will be drawn on likely impacts of GMHT crops on bird or mammal occurrence from this study.

4. METHODS

4.1 Sites

Sites were distributed throughout England and Scotland (Fig. 1). Each site consisted of one or more experimental fields (no single site had more than one of the same crop type) that were divided equally into GMHT and conventional treatments by a bare strip. Each treatment followed recommended spraying regimes for that particular crop type. A full description of the experimental design is given in Perry *et al.* (in prep.). Three different crop types were used: sugar beet, maize and spring rape with respective sample sizes of 24, 11 and 10 (two additional rape sites and one maize site were covered but were vandalised during the course of the survey period and so were not included in the analysis).

4.2 Bird Survey

There were three different surveys undertaken: a territory mapping survey of all birds in the experimental field and surrounding field boundaries; point counts of birds in fields; and foraging observations of aerial feeders. Observers had no prior knowledge of how each half of a field had been treated, so the results should not be affected by any preconceptions they may have had.

(i) Territory mapping survey: Each site was visited five times between April and August. On each visit the location of all birds seen in the experimental field, the surrounding field boundaries and in the immediately adjacent fields and field boundaries were recorded onto maps following standard recording protocols used in the BTO's Common Birds Census (Marchant *et al.* 1990). This included birds involved in any activity apart from flying over the site, unless flight was likely to be associated with the field itself (song flights or hunting flights). Particular care was taken in recording bird locations in relation to the GM/conventional divide in the experimental field. Individual registrations that made up each territory were assigned to given habitat types (hedgerow unit, either half of experimental field).

(ii) Point counts: After the territory mapping survey had been carried out, the observers carried out a number of point counts, recording birds using the experimental field. This differs from the above not only in the actual methodology, but also as this only recorded birds that actually landed in either half of the field (singing birds and birds overhead were not included). A number of evenly spaced points were identified along the field perimeter (the same locations were used on each visit) and at each of these points the observer recorded all movements of birds to, from and within the experimental field using standard activity codes and site maps. The point count duration was five minutes and observers carried out 10 point counts per visit. These data were expressed in two ways. Firstly, the number of foraging events was recorded, where one event = a bird entering or leaving the crop. It was assumed that such birds were foraging in the crop, although it was rarely possible to observe birds feeding. Analysing the data in this way assumes that the overall use of a crop by birds is a good measure of the food available in that crop, but this takes no account of the independence of data points, i.e. an individual bird seen entering or leaving a crop 10 times during a point count would be recorded as 10 foraging events. The second data set did not take into account the use being made of the crop, but just considered the number of individual birds estimated to be foraging, whether they were seen entering/leaving the crop once or several times.

(iii) Aerial feeders: A number of experimental sites were surveyed to determine their use by foraging Hirundines and swifts in August. A viewing point was located over the crop where a 5 m wide observation transect could be identified (e.g. by using landmarks), preferably towards the centre of the treatment (i.e. GMHT or conventional) and parallel to the crop divide (so there was no chance of counting Hirundines over the other treatment). Transects were selected to be of equal length. After the normal survey had been undertaken, the observer stood at this point and counted any Hirundines actively foraging that crossed the transect in a 10 minute period, up to a height of 10 m. This was done for both treatments separately. The maximum number of birds that were within the transect at any one time during the 10 minute period was also recorded.

Data for 10 selected species were analysed for data sets (i) and (ii). Selection was based on abundance, detectability given the survey methods and also to represent a range of dietary preferences. The species were Red-Legged Partridge *Alectoris rufa*, Skylark *Alauda arvensis*, Wren *Troglodytes troglodytes*, Dunnock *Prunella modularis*, Whitethroat *Sylvia communis*, Robin *Erithacus rubecula*, Blackbird *Turdus merula*, Song Thrush *T. philomelos*, Chaffinch *Fringella coelebs* and Yellowhammer *Emberiza citrinella*. For aerial feeders four species were considered: Swallow *Hirundo rustica*, Sand Martin *Riparia riparia*, House Martin *Delichon urbica* and Swift *Apus apus*.

4.3 Mammal Survey

Throughout the duration of all bird surveys, the identity, location and number of any mammals seen within the experimental field was recorded on site maps.

5. ANALYSIS

5.1 Modelling Abundance and Presence/Absence

For birds, a number of different data sets were analysed, but they could be divided into two main groups: bird counts and bird presence. Bird counts were analysed with Poisson regression. This included most of the data collected: number of individual bird registrations per visit from territory mapping, foraging events per visit from point counts (i.e. summed over all 10 point counts), number of foraging individuals from point counts, the number of foraging passes made by aerial feeders and the number of individuals of aerial feeders present at any one time in a transect. Furthermore, bird registrations were divided into two data sets. First, the whole data set which incorporated field and boundary registrations; and second, only registrations actually recorded in the crop itself were analysed.

The three crop types were analysed separately. The effect of field treatment on bird abundance was analysed using the basic generalized linear model:

Log (*abundance*) = [intercept+site+date+treatment]

which used a log link function and assumed a Poisson error distribution. The site effect was a dummy variable that described variation caused by the location of the site (e.g. altitude, geographic location, distance from coast etc.) that may have had a significant effect on bird abundance. Including this variable maintained the paired structure of the fields in the analysis. Date was the date of a given survey visit and was expressed as a continuous variable where 1 = 1st April. Treatment was effectively GMHT or conventional, but typically, the GMHT crop was sprayed at a different time to the conventional crop. Therefore, each treatment half was recorded as sprayed or unsprayed. The models concentrated on two separate comparisons, GMHT unsprayed versus sprayed conventional (referred to as the EARLY data set), and GMHT sprayed versus sprayed conventional (LATE data set). These data sets were mutually exclusive. There were some survey visits early in the breeding season where both conventional and GMHT treatments were unsprayed. These data were not included in the analysis. Birds recorded in field boundaries were assigned to the adjacent treatment.

In addition to modelling the abundance of species, the probability of a species being present was analysed by reducing the data to a binary form (i.e. 1 = present, 0 = absent). This used a similar model to the above, but a binomial error structure was assumed and a logit link function was used with the same predictor variables. The number of mammals recorded per visit and the presence of mammals recorded per visit were analysed using Poisson and binomial models respectively as described for the bird registrations data, but this considered only mammals recorded in the experimental field and not in the adjacent boundary. A summary of all different data sets analysed is given in Table 1.

The number of sites in the models varied from species to species because all species did not occur at all sites. This has important implications when determining the power of the analysis (see below).

5.2 Power Analysis

The models generated from the above procedures were used to provide realistic parameter estimates as the basis for the power analyses. For Poisson models, estimated bird or mammal abundance was determined from the parameter estimates derived from each model. This value was then used as a mean for a randomly generated Poisson distribution with the same sample size as the original data set. The purpose of this quasi-random selection was to simulate a further identical survey, making the important assumption that the effects of the model variables in a large number of simulations would be the same. When a quasi-random data set had been generated, it was analysed using the same Poisson model. This procedure was repeated 1000 times (thus simulating 1000 identical surveys). The proportion of these simulations yielding a significant effect of treatment in addition to the effects of site and date (Type 1 analysis; SAS 1996) with the same relative ranking of treatment effects as derived from the original analysis was taken as a measure of statistical power. Power was defined as one minus the probability of accepting, falsely, a null hypothesis that two compared treatments are equal. That is, the power is the probability of the treatment that has the highest true effect being correctly identified as such in the analyses (i.e. analyses assume that the parameter estimates in the model were representative of 'real' effects). Here, as is conventional, power is expressed as a percentage.

The next step was to determine the power when the number of sites was increased. A dummy data set of additional sites was created for each simulation. Site and date parameter estimates for the sites were obtained by generating quasi-random numbers from a normal distribution with a mean equal to the mean of the actual parameter estimates from the original model for each analysis. There were three such dummy data sets containing 10, 20 and 40 sites. For each of these scenarios, a power analysis with 1000 simulations was carried out in the same way as described above. As sites with zero counts for a given species were omitted from the original analysis, the simulations ensured that no randomly-generated data sets contained sites with zero counts for particular species. The sample size for each analysis was, therefore, the original sample size plus 10, 20 and 40 extra sites. The effect of increasing sample size on the power of the analysis could then be considered by plotting power against sample size. However, the original data set omitted any sites without birds, and a proportion of any extra sites in practice are likely to have zero counts for particular species. Because all the extra sites had non-zero counts, the sample size for each species was adjusted using the proportion of actual zero counts. This is best illustrated by example. Suppose that Wren occurred on only half of all sites for a given crop. The model and parameter estimates are therefore based on only half of the total number of sites. If an extra 10 sites with Wrens were added to the original data, it was assumed that this represented half the actual sample size, i.e. it was assumed that to get data from 10 sites with Wren present, 20 sites would have to be surveyed. In estimating increases in power with respect to the number of sites, this adjusted sample size is used, so for an extra 10, 20 and 40 sites with birds, the power in this example would be plotted against an extra 20, 40 and 80 sites. Power was therefore determined not in relation to the sample size in the analysis, but to the effort required to achieve that sample size. Particularly rare species will therefore have very large adjusted sample sizes for additional sites in this analysis.

The sample size required to achieve a given power can be determined simply from figures produced by the above analysis (Fig. 2). A stringent level of 95% power is used throughout this paper. So, in the example in Figure 2, 67 sites would be needed to be 95% certain of detecting a significant difference, if the assumptions about the representativeness of the data are valid.

6. RESULTS

6.1 Model Results

With the exception of the aerial feeder data, an attempt was made to derive a model for each of the 10 species in each data set. However, in a number of cases, no valid models were produced (parameter estimates were not produced or the models had extremely large errors, implying numerical problems). This was generally due to small sample sizes, and there were also some species that were not recorded in a particular data set. A summary of all model results for species occurring on at least two sites is given in Appendix 1. The parameter estimates derived from these models are expressed as the number of birds (Poisson model) or probability of occurrence (binomial model) relative to one of the treatments (selected at random for each model). This is in order to show the magnitude of the differences found between treatments and the precision with which it is known. It is not shown in these tables which treatment had higher or lower parameter estimates, only whether a significant difference was detected. The dispersion is the deviance divided by the degrees of freedom which gives a measure of model fit which is less good the further away the value is from 1. Generally, model fits were good for the majority of species and in most data sets. There was a tendency for models to be under-dispersed (dispersion <1) when sample sizes were low. For aerial feeders, models were the poorest fitting, most being over-dispersed (>2 in all cases except maximum number of House Martins over beet crops).

It was noticeable that sample sizes and the number of models producing parameter estimates were higher in the LATE data set in the majority of species and in only one case, Skylark in rape fields, was the sample size higher in the EARLY data set. Furthermore, there were only two species (Blackbird on sugar beet and Skylark on maize) where parameter estimates were produced for foraging in the EARLY data set and these were only recorded on two sites. No further analysis of foraging events in the EARLY data set was therefore undertaken.

Only two species of mammal were recorded in sufficient numbers for analysis, Hare *Lepus europeaus* and Rabbit *Oryctolagus cuniculus* (Brown Rat *Rattus norvegicus* and Red Fox *Vulpes vulpes* were the only other mammals recorded, with one and two observations respectively). In the EARLY data set, Rabbit was recorded only on one site and so no models were derived. For Hare and Rabbit in the LATE data set, model fits were generally good, although there was a tendency for some to be over-dispersed. Model details are given in Appendix 2.

6.2 Power Analysis

The power of analyses with counts matched to the models of Appendix 1 (and identical sample sizes) is shown in Table 2. Also shown in Table 2 is the number of sites required to achieve 95% power (determined using the method described by Figure 2) for those species where fewer than 100 sites would be required. Considering the large number of analyses run (Appendix 1), there were relatively few cases where 95% power was achieved (Table 2). In most cases, this was due to very small differences in bird occurrence between treatments, although in some cases there were extreme site effects that clearly influenced the power analysis.

There were particularly few analyses achieving 95% power for the EARLY data set. Fewer species were recorded overall in this data set, and for those that were recorded in adequate numbers, analyses tended to be of low power. In the EARLY data set, the highest power and hence the lowest sample sizes required to achieve 95% power were in analyses considering registrations from both fields and field boundaries. In the LATE data set, there was little difference between analyses involving fields only and fields plus field boundary registrations. There were, however, a greater proportion of high power analyses for the foraging events data set (Table 2g) and the number of foraging individuals data set (Table 2h) compared to other data sets in this period. Generally, differences between treatments, and hence the power of the analyses, were lower in sugar beet crops than in either maize or rape crops. There was little difference in power between Poisson and binomial models.

For aerial feeders, only swallow produced predicted sample sizes of below 100 to achieve 95% power (Table 2f), but this was in each crop. However, an unusual feature of the models for sugar beet and rape and one not evident from Table 2 was that parameter estimates for foraging events and estimates for the maximum number of birds foraging showed opposing signs, i.e. there were more foraging events in one crop treatment and more individual birds in the other treatment. It is possible for this situation to occur. In both cases, the results were influenced by a large flock of swallows passing once over a given treatment. Note that this lead to over-dispersed models for Swallow (Appendix 1). These results will not be considered further.

The information provided in Table 2 can be used to identify those species and those measures of species occurrence (e.g. abundance, presence/absence, foraging events) that would provide the most powerful analyses for given sample sizes. For example, Table 3 shows those species that are predicted to achieve 95% power with total sample sizes based on the number of sites in 2000 that have been used in these analyses (24 sugar beet, 11 maize, 10 rape) plus the number of sites planned for 2001 (a further 26 beet, 28 maize and 27 rape sites). Only two species are predicted to give analyses of 95% power in the EARLY data set, Yellowhammer (on maize) and Chaffinch (on rape), and in each case this involved analysis of registrations in both fields and field boundaries (Table 3). In the LATE data set, five species were predicted to give 95% power, Red-Legged Partridge (on beet), Skylark (on maize), Dunnock (on maize and rape), Whitethroat (on maize and rape) and Yellowhammer (on maize). These LATE period analyses were based mainly on field only data (with the exception of Whitethroat on maize). Unlike the EARLY data set they were not based exclusively on registrations but also included analyses of foraging events (e.g. for Yellowhammer and Dunnock see Table 3). In contrast to those from the EARLY data set, most of these results were derived from data sets involving birds in fields only, with the exception of Whitethroat. Both Dunnock and Yellowhammer were predicted to achieve 95% power under a number of different measures of occurrence in fields (Table 3).

The results of the power analysis for mammals are shown in Table 4. Statistical power of 95% was predicted with fewer than 100 sites for Hare presence on rape in the EARLY data set and for Rabbit and Hare counts on sugar beet and maize in the LATE data set. The highest power was for Hare abundance on maize fields, where 95% power was predicted with a sample size of 46 sites. Therefore, according to Table 4, additional sites in 2001(resulting in a total for two years of 39 sites) will not increase the sample size enough to achieve 95% power in mammals, although the Hare analysis could be acceptable if a slightly lower level of power was considered.

6.3 General Relationships Between Sample Size, Parameter Estimates and Power

The above analyses give an indication of which species are likely to provide the most powerful analyses under a range of different measures and in different crops. If we pool results from all species and crop-specific analyses, we can use the randomly generated data to make general conclusions about sample sizes and average differences in bird occurrence required to achieve a given level of power. The power of an analysis to detect significant differences between treatments will be determined by the sample size of the data and the level of difference between treatments. The data simulation procedure used to generate the results in Table 2 provides a wide range of values for both of these variables. By plotting the power of an analysis against the parameter estimates (Appendix 1), we can then determine the magnitude of the difference between treatments required to achieve a given level of power for a given sample size. For the calculations of power and sample size required to achieve given levels of power in Table 2, adjusted sample sizes were used based on the proportion of sites where a given species occurred. This adjusted sample size rather than the actual sample size will be used in the following analysis.

Figure 3 shows the power (i.e. proportion of significant treatment effects out of 1000 simulated models) plotted against the relative abundance of birds where each point represents the power from individual species/crop/data type (e.g. number of registrations, foraging events) models in Appendix 1 with varying sample size. The measure of relative abundance was calculated by transforming treatment parameter estimates derived from Poisson regression and setting the lower parameter estimate to 1. Therefore, a value of 1.5 indicates that 50% more birds (or foraging events or other count variable) were found on one of the treatments. This figure uses data from the LATE data set, but combines all Poisson model results and so can be used as a general Poisson power model. Three separate, arbitrarily chosen scenarios are given based on the adjusted sample size, e.g. a species occurring on 12 out of the original 24 sugar beet sites has 10 extra sites added and the power of the analysis is estimated accordingly, but this power is plotted against the adjusted sample size of 44 (24 original sites + 20 further sites required to cover 10 sites with birds). This point would therefore be in the 40-60 sites category.

The curves added to aid visual examination of the data in Figure 3 are logistic curves (to ensure predicted power was constrained to remain between zero and 100%). For a survey with between 40 and 60 sites, 95% power would be achieved with a relative difference in abundance between treatments of 1.80. For the higher sample sizes, the difference in relative abundance needed to achieve 95% power was similar at 1.71 for 61-80 sites and 1.68 for 81-100 sites. The plots show a certain amount of scatter (Fig. 3). This occurs for three reasons. First, the power is really determined by the original sample size in the model (i.e. the number of sites with birds), which will vary (sometimes considerably) between species. Second, in some simulations, no valid statistics were produced (e.g. a given species may have produced 800, rather than 1000 simulated model results), but the power was still based on 1000 simulations. In the latter example, if 200 simulations produced significant results, the power would be expressed as 20%, but it could be argued that it should be 25%. In these cases, we have opted for lower estimate of power as this is a reflection of the quality of the data. Such cases only arose when the data were particularly sparse or sample sizes were very small and in practice most analyses had at least 900 simulations that produced results so this is a minor problem. Third, and most important, the absolute difference as well as the relative difference will have an influence on the power. For example, fields averaging 10 birds on one treatment and 20 birds on another are likely to yield greater power than fields with two and four birds respectively, yet they would both have a relative abundance of two in Figure 3. However, in these data, the majority of species were in a similar range of abundance. Only three models produced estimated counts of over 10 (Skylark on maize, Skylark on rape and Song Thrush on sugar beet). Therefore, Figure 3 should be generally applicable for situations where bird counts are less than 10.

For binomial models, there was much greater variation in estimates of absolute probability of occurrence. As we were considering binomial probabilities, we considered relative odds that incorporated absolute probability estimates. Figure 4 shows the association between power and the relative odds ratio calculated from the absolute probability estimates i.e. the odds ratio of each estimate was calculated (probability / 1-probability) and the ratio of these odds was used in Figure 4. For example, a species with an estimated probability of occurrence of 0.50 on one treatment and 0.25 on the other treatment has odds of 1 and 0.33 respectively and therefore a relative odds ratio of 3. But this value can be obtained from other pairings of probabilities, so general conclusions can be drawn from Figure 4 despite the wide range in variation of observed probabilities. For 40-60 sites an odds ratio of 3.09 would be needed to achieve 95% power, so in the above example, probabilities of 0.25 and 0.50 would be just about sufficient to achieve 95% power. For those studies in the 61 – 80 sites category a slightly higher relative odds ratio of 4.09 would be needed. With a higher sample size (81-100 sites) this value was reduced to 2.35.

7. DISCUSSION

The most powerful analyses involved the LATE data set, i.e. a comparison of GMHT treated crop with conventionally treated crop. Point counts collecting foraging data and information on bird registrations in open fields were most likely to yield analyses of high power in this LATE data set. Results for sugar beet were of relatively low power in comparison with results from maize and oilseed rape. This in part may have been because many sugar beet sites were in intensive arable areas with little or no trees or hedges. The geographical location of additional sites is therefore likely to have a big impact on future statistical power. The species where 95% power was predicted to be achieved given the combined sample sizes for 2000 and 2001 were Red-Legged Partridge, Skylark, Dunnock, Whitethroat, Chaffinch and Yellowhammer. Hare abundance on maize crops provided the most powerful analysis for mammals, and sample sizes required to achieve 95% power were only slightly greater than the planned number of additional sites for 2001. In order to achieve a power of 95%, we predict that for any Poisson model, approximately 70-80% difference in numbers between treatments would be required for sample sizes of between 40 and 100 sites. These estimates are for small bird counts (<10 per visit) and are not applicable to situations were many more birds are recorded. For binomial models, the odds ratio derived from probability of occurrence would need to be approximately three to four times greater on one treatment to achieve 95% power for a sample of 40 to 80 sites and approximately two-and-a-half times greater for 80-100 sites.

The species-specific analysis presented in this paper is reliant on the very important assumption that the observed parameter estimates (Appendix 1) will be the true parameter estimates across a range of sample sizes. These estimated parameter estimates would be expected to be more accurate as sample sizes in the original model increase. If we consider the species yielding the most powerful models in Table 3, we actually find that in all cases, the original model was based on sample sizes of five or fewer sites, with one exception, Red-Legged Partridge, which was based on 14 sites. For the majority of species, the assumption can therefore be regarded as tenuous. Data from further sites could be used to test this assumption, but due to the high proportion of sites where no birds of most individual species were recorded, this is likely to take a large effort to produce adequate sample sizes. For example, for foraging Yellowhammers on maize crops, an estimated total of 55 sites would have to be surveyed to achieve a sample size of 20 sites with birds. The combined number of maize sites for 2000 and 2001 is someway short of this total at 39.

A potential way of increasing sample sizes and therefore increasing our confidence in the representativeness of derived parameter estimates is to combine data from different crops. However, there are sound biological reasons why we should analyse crops separately. First, we know from previous studies that birds use crops in different ways and sometimes show marked preferences for particular crops (see numerous papers in Aebischer *et al.* 2000). Second, the spraying regimes differ markedly from crop to crop, both in terms of conventional management and in terms of GMHT applications. Third, different crops will obviously differ in vegetation structure and this may affect the detectability of birds.

The analyses undertaken considered a range of different measures, including bird abundance, bird presence/absence, foraging events and presence of foragers. The largest sample sizes were from bird registrations, and presence/absence of registrations, in both fields and adjacent field boundaries. For that reason, this may be considered as a good candidate for future research. However, for many species, the majority of records were in adjacent boundaries and not in fields (compare sample sizes for the two habitats in Appendix 1), so it is questionable whether the treatment could really be having any effect in these cases. Although the experimental set-up and pairing procedure should have eliminated general systematic bias in boundary characteristics across treatments, there may still have been effects of boundary characteristics for individual species. Further more complex analyses identifying these factors and incorporating them into models would be required if we were to determine the effects of these variables.

The data sets pertaining only to the fields tended to have smaller sample sizes, but they generally produced analyses of highest power (Table 3). For the foraging data sets this may be expected as this generally had more data (in terms of actual counts per site rather than the number of sites), but generally, field boundary data sets had most data. The foraging data set in particular provides some interesting results as we may expect that food abundance or availability would be the factors affected most by GMHT treatments. We may also expect less of an influence of boundary habitats with this data set. Therefore, any measure of feeding would be more likely to produce significant differences. The analysis of foraging events is reliant on the assumption that this measure can be used as an indirect measure of food availability irrespective of the independence of the data points. Presence of a foraging bird or the number of individuals foraging were more stringent measures of foraging, yet analyses involving these measures did not have appreciably lower power. Analysis of foraging passes by aerial feeders produced poorly fitting models and power analyses were obviously greatly influenced by outliers in the data.

In summary, the analyses have indicated that a high probability of detecting significant differences in bird abundance or occurrence between treatments would be possible for a small number of species in certain crops with the additional sites due to be surveyed in this coming spring/summer. A further year of fieldwork is also planned for 2002, but the number of participating sites has yet to be decided. If we assume that the same number of sites will be surveyed in 2002 as is planned for 2001, then the analyses predict that a further 23 species/crop/variable specific data sets (including two extra species, Robin and Blackbird) could provide analyses of sufficient power. Maize crops and rape crops are likely to yield the most powerful analyses and efforts should be made to concentrate fieldwork into the later half of the breeding season after GM herbicides have been applied. A point count survey recording foraging individuals is likely to be the best method both for statistical and biological reasons. Detection of significant differences in mammal abundance was less likely, although Hare abundance in maize fields was the most powerful analysis. However, the above findings are dependent on acceptance of the assumption that derived parameter estimates are likely to remain more-or-less the same when further sites are surveyed, i.e. the current (sometimes small) sample is representative of any proposed larger sample. Caution is therefore needed when interpreting these power analyses due to the small sample sizes involved.

The data can be used to make general inferences about the magnitude of parameter estimates and the number of sites needed to be surveyed to achieve a given level of power. We predict that a power of 95% could be achieved if the magnitude of the difference in bird abundance (or any other count measure) between treatments was greater than approximately 75% for Poisson models, or if the odds ratio derived from estimated probability of bird presence was approximately three to four times greater on one treatment for binomial models in samples with 40 to 80 sites and approximately two-and-a-half times greater with samples of between 81-100 sites. Throughout this study, we have used a stringent level of power of 95%, but if a lower level of power were considered acceptable, the sample sizes and the magnitude of differences required to achieve this level would be lower. For example, a further 26 species/crop/variable specific data sets could provide analyses of sufficient power if we considered a 75% level of power to be acceptable (i.e. there would be 26 more rows in Table 3). We suggest that the analysis presented in this paper should be used as a baseline to direct future studies rather than be used as a definitive statement of the power of the current GMHT trials to detect differences in bird abundance.

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Table 1. A summary of the data sets analysed in power analyses.

Analysis variable	**Sampling unit**	**Model error structure**	**EARLY or LATE**
Bird registrations	field + boundary	Poisson	Both
	field	Poisson	Both
Presence of a bird species	field + boundary	Binomial	Both
	field	Binomial	Both
Foraging events	field	Poisson	LATE
No. individual foragers	field	Poisson	LATE
Presence of a foraging species	field	Binomial	LATE
Foraging passes of aerial feeders	field	Poisson	LATE
Maximum no. individual aerial feeders	field	Poisson	LATE
Mammal registrations	field	Poisson	Both
Presence of a mammal species	field	Binomial	Both

Table 2. The power to detect significant differences in bird occurrence between treatment types for the parameter estimates given in Appendix 1 given the original sample size. The number of sites (n) required to achieve 95% power is also given. Only those species where less than 100 sites were required to achieve at least 95% power are shown. (Note that the number of sites for 2000 + those planned to be part of FSE in 2001 is 50 for sugar beet, 39 for maize and 37 for rape).

(a) EARLY data set, beet crop

Species	**Model**	**Habitat**	**Power (%)**	**n for 95% power**
Yellowhammer	Binomial	field and boundary	73.9	64
Chaffinch	Poisson	field and boundary	72.6	78

(b) EARLY data set, maize crop

Species	**Model**	**Habitat**	**Power (%)**	**n for 95% power**
Blackbird	Binomial	field only	71.4	48
Blackbird	Poisson	field only	38.6	46
Blackbird	Poisson	field and boundary	64.7	50
Yellowhammer	Poisson	field and boundary	2.6	32

(c) EARLY data set, rape crop

Species	**Model**	**Habitat**	**Power (%)**	**n for 95% power**
Red-Legged Partridge	Binomial	field only	9.0	58
Skylark	Binomial	field only	36.8	96
Skylark	Poisson	field only	6.0	73
Chaffinch	Binomial	field and boundary	77.3	25
Skylark	Binomial	field and boundary	35.6	73
Skylark	Poisson	field and boundary	8.9	74
Yellowhammer	Poisson	field and boundary	13.3	99

Table 2. Cont.

(d) LATE data set, beet crop

Species	Model	Habitat	Power (%)	n for 95% power
Red-Legged Partridge	Poisson	field only	83.9	40
Wren	Binomial	field and boundary	47.4	96
Red-Legged Partridge	Poisson	field and boundary	71.6	84

(e) LATE data set, maize crop

Species	Model	Habitat	Power (%)	n for 95% power
Chaffinch	Binomial	field only	61.0	46
Yellowhammer	Binomial	field only	91.7	28
Skylark	Poisson	field only	9.1	38
Blackbird	Binomial	field and boundary	19.8	77
Chaffinch	Binomial	field and boundary	8.6	90
Yellowhammer	Binomial	field and boundary	59.5	42
Dunnock	Poisson	field and boundary	12.9	48
Whitethroat	Poisson	field and boundary	51.5	33
Wren	Poisson	field and boundary	13.8	89
Yellowhammer	Poisson	field and boundary	45.2	78

(f) LATE data set, rape crop

Species	Model	Habitat	Power (%)	n for 95% power
Skylark	Poisson	field only	14.2	48
Chaffinch	Poisson	field only	27.6	73
Whitethroat	Poisson	field only	47.4	58
Blackbird	Binomial	field and boundary	27.8	88
Whitethroat	Binomial	field and boundary	59.5	45
Yellowhammer	Binomial	field and boundary	46.9	75
Skylark	Poisson	field and boundary	28.3	42
Whitethroat	Poisson	field and boundary	81.7	24

Table 2. Cont.

(g) LATE data set, foraging events (all crops)

Species	Crop	Model	Power (%)	n for 95% power
Blackbird	Beet	Poisson	68.6	58
Yellowhammer		Poisson	62.9	67
Chaffinch	Maize	Binomial	54.1	48
Skylark		Binomial	48.1	62
Yellowhammer		Binomial	71.5	35
Chaffinch		Poisson	37.3	46
Dunnock		Poisson	55.7	33
Robin		Poisson	21.0	97
Skylark		Poisson	84.1	50
Yellowhammer		Poisson	50.4	37
Dunnock	Rape	Binomial	38.9	86
Dunnock		Poisson	96.5	<10

(h) LATE data set, number of foraging individuals (all crops)

Species	Crop	Model	Power (%)	n for 95% power
Blackbird	Beet	Poisson	55.2	63
Chaffinch	Maize	Poisson	41.4	46
Dunnock		Poisson	45.0	90
Robin		Poisson	30.1	62
Skylark		Poisson	46.0	41
Yellowhammer		Poisson	36.0	38
Dunnock	Rape	Poisson	55.5	33

(i) LATE data set, aerial feeders (all crops)

Species	Crop	Model	Dependent variable	Power (%)	n for 95% power
Swallow	Beet	Poisson	Events	21.3	49
		Poisson	No. birds	16.8	79
Swallow	Maize	Poisson	Events	100	<10
		Poisson	No. birds	81.1	42
Swallow	Rape	Poisson	Events	18.2	53
		Poisson	No. birds	30.7	33

Table 3. Species that would achieve 95% power with extra FSE sites for the 2001 breeding season (i.e. total for 2000 + total for 2001). These assume that observed differences between GMHT and conventional treatments detected in the original models (Appendix 1) will have the same values when further sites are added. Bird presence and presence of foragers was modelled with binomial logistic regression. Other dependent variables were modelled with Poisson regression.

Crop	Combined sites 2000+2001	Data set	Species	Dependent variable	Habitat
Maize	39	EARLY	Yellowhammer	Bird registrations	Field+boundary
Rape	37		Chaffinch	Bird presence	Field+boundary
Beet	50	LATE	Red-Legged Partridge	Bird registrations	Field
Maize	39		Skylark	Bird registrations	Field
			Yellowhammer	Bird presence	Field
			Whitethroat	Bird registrations	Field+boundary
			Dunnock	Foraging events	Field
			Yellowhammer	Foraging events	Field
			Yellowhammer	Presence of foragers	Field
			Yellowhammer	No. individual foragers	Field
Rape	37		Whitethroat	Bird registrations	Field
			Dunnock	Foraging events	Field
			Dunnock	No. individual foragers	Field

Table 4. The power to detect significant differences in mammal occurrence between treatment types for the parameter estimates given in Appendix 2 given the original sample size. The number of sites (n) required to achieve 95% power is also given. Only those species where less than 100 sites were required to achieve at least 95% power are shown

Data set	**Species**	**Crop**	**Model**	**Power (%)**	**n for 95% power**
EARLY	Hare	Rape	Binomial	17.6	82
LATE	Hare	Beet	Poisson	27.6	97
	Rabbit			15.6	66
	Hare	Maize	Poisson	25.4	46
	Rabbit			16.7	78

Appendix 1 A summary of Poisson and binomial models considering the effects of GMHT and conventional crop management on bird abundance and probability of occurrence in three different crop types. Analyses from two different data sets (EARLY and LATE) are given. Within each data set, models have been run on data from fields-only and on data from fields and adjacent field boundaries. Additionally, foraging events in fields and foraging events and maximum abundance of aerial feeders in fields have been analysed for the LATE data set. The number of sites indicates the number where at least one individual of the species in question was recorded. Total number of sites surveyed was 24 for sugar beet, 11 for maize and 10 for rape. The dispersion is calculated as deviance / degrees of freedom. Parameter estimates are for the treatment effect and are given as untransformed estimates ± standard error, relative to 0. The treatment used as the reference habitat (i.e. mean = 0) was randomly assigned. Asterisks indicate a significant change in deviance when the treatment term was added to the effects of site and date, where * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$ (χ^2 test).

(a) Registrations in fields – EARLY data set

Species	Dependent variable	Data distribution	Crop	No. sites	Dispersion	Parameter estimate
Red-Legged Partridge	No. birds	Poisson	Beet	8	1.53	0.990 ± 0.672
Skylark	No. birds	Poisson	Beet	12	1.01	0.097 ± 0.366
Blackbird	No. birds	Poisson	Beet	5	2.41	0.154 ± 0.508
Yellowhammer	No. birds	Poisson	Beet	6	0.94	1.064 ± 1.144
Skylark	No. birds	Poisson	Maize	4	1.47	0.358 ± 0.636
Blackbird	No. birds	Poisson	Maize	3	0.76	1.840 ± 1.074*
Skylark	No. birds	Poisson	Rape	6	0.72	0.597 ± 0.962
Red-Legged Partridge	Presence/absence	Binomial	Beet	8	1.91	1.016 ± 0.910
Skylark	Presence/absence	Binomial	Beet	12	1.26	1.037 ± 0.933
Blackbird	Presence/absence	Binomial	Beet	5	1.60	0.476 ± 1.264
Yellowhammer	Presence/absence	Binomial	Beet	6	1.72	1.811 ± 1.432
Skylark	Presence/absence	Binomial	Maize	4	1.55	1.312 ± 1.307
Blackbird	Presence/absence	Binomial	Maize	3	1.39	3.785 ± 2.647
Skylark	Presence/absence	Binomial	Rape	6	1.17	1.486 ± 1.637

(b) Registrations in fields and boundaries – EARLY data set.

Species	**Dependent variable**	**Data distribution**	**Crop**	**No. sites**	**Dispersion**	**Parameter estimate**
Red-Legged Partridge	No. birds	Poisson	Beet	9	0.99	0.493 ± 0.549
Skylark	No. birds	Poisson	Beet	13	1.03	0.057 ± 0.351
Wren	No. birds	Poisson	Beet	7	0.92	1.027 ± 0.552*
Dunnock	No. birds	Poisson	Beet	4	0.80	0.300 ± 0.785
Whitethroat	No. birds	Poisson	Beet	3	0.52	0.449 ± 1.249
Robin	No. birds	Poisson	Beet	5	0.82	0.331 ± 0.656
Blackbird	No. birds	Poisson	Beet	8	1.29	0.415 ± 0.339
Chaffinch	No. birds	Poisson	Beet	7	1.18	0.982 ± 0.397**
Yellowhammer	No. birds	Poisson	Beet	9	0.63	1.083 ± 0.670
Skylark	No. birds	Poisson	Maize	4	0.97	0.123 ± 0.672
Whitethroat	No. birds	Poisson	Maize	2	0.31	16.220 ± 0.00
Blackbird	No. birds	Poisson	Maize	3	1.19	1.344 ± 0.616*
Chaffinch	No. birds	Poisson	Maize	4	0.96	0.496 ± 0.648
Yellowhammer	No. birds	Poisson	Maize	5	0.74	0.260 ± 0.673
Skylark	No. birds	Poisson	Rape	6	1.23	0.892 ± 0.957
Blackbird	No. birds	Poisson	Rape	2	0.67	0.649 ± 1.147
Yellowhammer	No. birds	Poisson	Rape	4	0.70	1.265 ± 1.135

Species	**Dependent variable**	**Data distribution**	**Crop**	**No. sites**	**Dispersion**	**Parameter estimate**
Red-Legged Partridge	Presence/absence	Binomial	Beet	9	1.06	0.604 ± 0.722
Skylark	Presence/absence	Binomial	Beet	13	1.31	0.505 ± 0.546
Wren	Presence/absence	Binomial	Beet	7	1.20	0.613 ± 0.687
Dunnock	Presence/absence	Binomial	Beet	4	0.99	0.114 ± 0.937
Whitethroat	Presence/absence	Binomial	Beet	3	0.74	0.507 ± 1.322
Robin	Presence/absence	Binomial	Beet	5	1.16	0.137 ± 0.770
Blackbird	Presence/absence	Binomial	Beet	8	1.31	0.504 ± 0.584
Song Thrush	Presence/absence	Binomial	Beet	2	0.54	0.071 ± 1.578
Chaffinch	Presence/absence	Binomial	Beet	7	1.29	0.848 ± 0.612
Yellowhammer	Presence/absence	Binomial	Beet	9	1.05	1.783 ± 0.809*
Skylark	Presence/absence	Binomial	Maize	4	0.94	0.016 ± 0.962
Dunnock	Presence/absence	Binomial	Maize	2	0.89	0.555 ± 1.463
Whitethroat	Presence/absence	Binomial	Maize	2	0.52	39.029 ± 0.00
Blackbird	Presence/absence	Binomial	Maize	3	1.38	0.966 ± 0.997
Chaffinch	Presence/absence	Binomial	Maize	4	1.38	1.099 ± 0.990
Yellowhammer	Presence/absence	Binomial	Maize	5	0.84	0.220 ± 0.902
Skylark	Presence/absence	Binomial	Rape	6	1.22	1.393 ± 1.095
Blackbird	Presence/absence	Binomial	Rape	2	0.86	0.599 ± 1.449
Chaffinch	Presence/absence	Binomial	Rape	3	0.59	28.365 ± 0.00*
Yellowhammer	Presence/absence	Binomial	Rape	4	1.11	1.549 ± 1.347

(c) Registrations in fields – LATE data set.

Species	Dependent variable	Data distribution	Crop	No. sites	Dispersion	Parameter estimate
Red-Legged Partridge	No. birds	Poisson	Beet	14	1.71	0.750 ± 0.262**
Skylark	No. birds	Poisson	Beet	15	1.08	0.192 ± 0.227
Wren	No. birds	Poisson	Beet	3	0.53	0.511 ± 1.033
Dunnock	No. birds	Poisson	Beet	7	0.52	0.762 ± 0.647
Blackbird	No. birds	Poisson	Beet	12	1.39	0.164 ± 0.287
Song Thrush	No. birds	Poisson	Beet	2	1.10	0.693 ± 1.225
Robin	No. birds	Poisson	Beet	2	0.37	0.693 ± 1.732
Whitethroat	No. birds	Poisson	Beet	3	1.00	0.916 ± 1.183
Yellowhammer	No. birds	Poisson	Beet	7	0.57	0.887 ± 0.635
Skylark	No. birds	Poisson	Maize	4	0.92	0.511 ± 0.730
Blackbird	No. birds	Poisson	Maize	4	1.23	0.288 ± 0.540
Chaffinch	No. birds	Poisson	Rape	3	0.92	0.847 ± 0.976
Yellowhammer	No. birds	Poisson	Maize	3	0.62	27.211 ± 0.00**
Skylark	No. birds	Poisson	Rape	5	1.68	0.288 ± 0.312
Blackbird	No. birds	Poisson	Rape	4	0.95	0.118 ± 0.687
Whitethroat	No. birds	Poisson	Rape	2	0.79	1.466 ± 0.906
Chaffinch	No. birds	Poisson	Rape	3	0.71	1.100 ± 0.817
Yellowhammer	No. birds	Poisson	Rape	4	0.88	0.134 ± 0.732
Red-Legged Partridge	Presence/absence	Binomial	Beet	14	1.18	0.814 ± 0.494
Skylark	Presence/absence	Binomial	Beet	15	1.26	0.326 ± 0.468
Wren	Presence/absence	Binomial	Beet	3	1.21	0.673 ± 1.178
Dunnock	Presence/absence	Binomial	Beet	7	0.89	1.322 ± 0.867
Blackbird	Presence/absence	Binomial	Beet	12	1.33	0.492 ± 0.500
Song Thrush	Presence/absence	Binomial	Beet	2	1.88	1.027 ± 1.482
Robin	Presence/absence	Binomial	Beet	2	1.21	1.012 ± 1.475
Whitethroat	Presence/absence	Binomial	Beet	3	1.34	0.865 ± 1.360
Yellowhammer	Presence/absence	Binomial	Beet	7	1.08	0.528 ± 0.734
Skylark	Presence/absence	Binomial	Maize	4	1.37	0.00 ± 1.050
Blackbird	Presence/absence	Binomial	Maize	4	1.35	0.365 ± 0.858
Chaffinch	Presence/absence	Binomial	Maize	3	1.37	2.248 ± 1.425
Yellowhammer	Presence/absence	Binomial	Maize	3	0.91	28.589 ± 0.00**
Skylark	Presence/absence	Binomial	Rape	5	0.31	1.386 ± 1.732
Blackbird	Presence/absence	Binomial	Rape	4	1.34	0.706 ± 0.854
Whitethroat	Presence/absence	Binomial	Rape	2	1.64	1.357 ± 1.225
Chaffinch	Presence/absence	Binomial	Rape	3	1.37	1.891 ± 1.073
Yellowhammer	Presence/absence	Binomial	Rape	4	1.01	1.016 ± 1.053

(d) Registrations in fields and boundaries – LATE data set.

Species	**Dependent variable**	**Data distribution**	**Crop**	**No. sites**	**Dispersion**	**Parameter estimate**
Red-Legged Partridge	No. birds	Poisson	Beet	14	1.30	0.600 ± 0.254*
Skylark	No. birds	Poisson	Beet	15	0.92	0.264 ± 0.228
Wren	No. birds	Poisson	Beet	14	0.77	0.593 ± 0.285*
Dunnock	No. birds	Poisson	Beet	13	0.61	0.170 ± 0.375
Whitethroat	No. birds	Poisson	Beet	11	0.63	0.577 ± 0.428
Robin	No. birds	Poisson	Beet	10	0.61	0.278 ± 0.436
Blackbird	No. birds	Poisson	Beet	15	1.08	0.124 ± 0.233
Song Thrush	No. birds	Poisson	Beet	2	0.69	0.693 ± 1.118
Chaffinch	No. birds	Poisson	Beet	12	0.68	0.155 ± 0.382
Yellowhammer	No. birds	Poisson	Beet	10	0.73	0.456 ± 0.340
Skylark	No. birds	Poisson	Maize	4	0.60	0.078 ± 0.725
Wren	No. birds	Poisson	Maize	6	0.50	0.675 ± 0.693
Dunnock	No. birds	Poisson	Maize	6	0.50	0.632 ± 0.652
Whitethroat	No. birds	Poisson	Maize	4	0.93	1.425 ± 0.767*
Robin	No. birds	Poisson	Maize	4	0.43	0.010 ± 0.932
Blackbird	No. birds	Poisson	Maize	7	0.79	0.503 ± 0.431
Chaffinch	No. birds	Poisson	Maize	7	0.63	0.251 ± 0.500
Yellowhammer	No. birds	Poisson	Maize	5	0.76	1.133 ± 0.664
Skylark	No. birds	Poisson	Rape	6	1.45	0.435 ± 0.309
Dunnock	No. birds	Poisson	Rape	2	0.67	1.086 ± 0.707
Whitethroat	No. birds	Poisson	Rape	5	0.68	1.561 ± 0.604**
Robin	No. birds	Poisson	Rape	3	0.32	0.815 ± 1.021
Blackbird	No. birds	Poisson	Rape	5	0.80	0.427 ± 0.525
Chaffinch	No. birds	Poisson	Rape	5	0.84	0.252 ± 0.487
Yellowhammer	No. birds	Poisson	Rape	5	0.94	0.145 ± 0.393

Species	**Dependent variable**	**Data distribution**	**Crop**	**No. sites**	**Dispersion**	**Parameter estimate**
Red-Legged Partridge	Presence/absence	Binomial	Beet	14	0.92	0.426 ± 0.418
Skylark	Presence/absence	Binomial	Beet	15	0.97	0.048 ± 0.380
Wren	Presence/absence	Binomial	Beet	14	0.97	0.681 ± 0.382
Dunnock	Presence/absence	Binomial	Beet	13	0.75	0.147 ± 0.443
Whitethroat	Presence/absence	Binomial	Beet	11	0.77	0.702 ± 0.507
Robin	Presence/absence	Binomial	Beet	10	0.80	0.181 ± 0.492
Blackbird	Presence/absence	Binomial	Beet	15	1.14	0.017 ± 0.327
Song Thrush	Presence/absence	Binomial	Beet	2	0.95	0.535 ± 1.314
Chaffinch	Presence/absence	Binomial	Beet	12	0.80	0.113 ± 0.465
Yellowhammer	Presence/absence	Binomial	Beet	10	1.03	0.468 ± 0.431
Skylark	Presence/absence	Binomial	Maize	4	0.76	0.576 ± 0.975
Wren	Presence/absence	Binomial	Maize	6	0.77	0.838 ± 0.741
Dunnock	Presence/absence	Binomial	Maize	6	0.71	0.006 ± 0.709
Whitethroat	Presence/absence	Binomial	Maize	4	0.73	1.659 ± 1.151
Robin	Presence/absence	Binomial	Maize	4	0.59	0.011 ± 0.976
Blackbird	Presence/absence	Binomial	Maize	7	0.99	0.590 ± 0.552
Chaffinch	Presence/absence	Binomial	Maize	7	0.83	0.253 ± 0.595
Yellowhammer	Presence/absence	Binomial	Maize	5	0.86	1.576 ± 0.858*
Skylark	Presence/absence	Binomial	Rape	6	0.89	0.280 ± 0.664
Wren	Presence/absence	Binomial	Rape	2	0.52	1.340 ± 1.591
Dunnock	Presence/absence	Binomial	Rape	2	0.98	1.542 ± 1.028
Whitethroat	Presence/absence	Binomial	Rape	5	0.93	1.418 ± 0.723
Robin	Presence/absence	Binomial	Rape	3	0.57	0.619 ± 1.160
Blackbird	Presence/absence	Binomial	Rape	5	1.08	0.800 ± 0.660
Chaffinch	Presence/absence	Binomial	Rape	5	1.14	0.378 ± 0.596
Yellowhammer	Presence/absence	Binomial	Rape	5	1.19	0.988 ± 0.578

(e) Foraging birds – LATE data set

Species	**Dependent variable**	**Data distribution**	**Crop**	**No. sites**	**Dispersion**	**Parameter estimate**
Skylark	Presence of foraging	Binomial	Beet	5	1.52	0.262 ± 0.725
Dunnock	Presence of foraging	Binomial	Beet	5	1.19	0.00 ± 0.791
Whitethroat	Presence of foraging	Binomial	Beet	3	0.91	0.00 ± 1.262
Robin	Presence of foraging	Binomial	Beet	3	1.25	1.138 ± 1.117
Blackbird	Presence of foraging	Binomial	Beet	6	1.30	1.016 ± 0.738
Chaffinch	Presence of foraging	Binomial	Beet	3	1.22	1.036 ± 1.056
Yellowhammer	Presence of foraging	Binomial	Beet	5	1.25	1.048 ± 0.865
Skylark	Foraging events	Poisson	Beet	5	3.23	0.091 ± 0.302
Dunnock	Foraging events	Poisson	Beet	5	1.54	0.095 ± 0.437
Whitethroat	Foraging events	Poisson	Beet	3	1.78	0.00 ± 0.471
Robin	Foraging events	Poisson	Beet	3	1.26	0.182 ± 0.606
Blackbird	Foraging events	Poisson	Beet	6	3.01	0.644 ± 0.270*
Yellowhammer	Foraging events	Poisson	Beet	5	1.47	0.916 ± 0.418*
Skylark	Presence of foraging	Binomial	Maize	2	1.40	2.056 ± 1.632
Dunnock	Presence of foraging	Binomial	Maize	5	1.14	0.703 ± 0.855
Robin	Presence of foraging	Binomial	Maize	2	0.77	1.334 ± 1.730
Blackbird	Presence of foraging	Binomial	Maize	4	1.41	0.636 ± 0.807
Song Thrush	Presence of foraging	Binomial	Maize	2	0.95	1.096 ± 1.543
Chaffinch	Presence of foraging	Binomial	Maize	3	1.11	1.919 ± 1.286
Yellowhammer	Presence of foraging	Binomial	Maize	4	1.11	2.461 ± 1.383*
Skylark	Foraging events	Poisson	Maize	2	1.45	2.303 ± 1.049
Dunnock	Foraging events	Poisson	Maize	5	1.89	0.811 ± 0.425
Robin	Foraging events	Poisson	Maize	2	0.92	0.916 ± 0.837
Blackbird	Foraging events	Poisson	Maize	4	3.14	0.00 ± 0.254
Song Thrush	Foraging events	Poisson	Maize	2	0.77	0.000 ± 1.000
Chaffinch	Foraging events	Poisson	Maize	4	0.84	0.981 ± 0.677
Yellowhammer	Foraging events	Poisson	Maize	4	0.93	1.946 ± 1.069*
Skylark	Presence of foraging	Binomial	Rape	3	1.46	0.00 ± 0.978
Dunnock	Presence of foraging	Binomial	Rape	2	1.14	1.695 ± 1.419
Whitethroat	Presence of foraging	Binomial	Rape	2	0.46	0.00 ± 2.000
Yellowhammer	Presence of foraging	Binomial	Rape	2	1.09	0.958 ± 1.433
Skylark	Foraging events	Poisson	Rape	3	3.05	0.105 ± 0.460
Dunnock	Foraging events	Poisson	Rape	2	1.19	2.079 ± 1.061*
Whitethroat	Foraging events	Poisson	Rape	2	1.15	0.105 ± 0.460
Yellowhammer	Foraging events	Poisson	Rape	2	2.19	0.00 ± 0.633

(e) Cont.

Species	**Dependent variable**	**Data distribution**	**Crop**	**No. sites**	**Dispersion**	**Parameter estimate**
Skylark	Max. no. birds	Poisson	Beet	5	1.87	0.143 ± 0.379
Dunnock	Max. no. birds	Poisson	Beet	5	1.25	0.118 ± 0.486
Whitethroat	Max. no. birds	Poisson	Beet	3	1.30	0.154 ± 0.556
Robin	Max. no. birds	Poisson	Beet	3	0.92	0.288 ± 0.764
Blackbird	Max. no. birds	Poisson	Beet	6	2.01	0.734 ± 0.351*
Chaffinch	Max. no. birds	Poisson	Beet	3	1.26	0.000 ± 0.707
Yellowhammer	Max. no. birds	Poisson	Beet	5	1.14	0.773 ± 0.494
Skylark	Max. no. birds	Poisson	Maize	2	1.01	1.792 ± 1.080*
Dunnock	Max. no. birds	Poisson	Maize	5	1.64	0.847 ± 0.488
Robin	Max. no. birds	Poisson	Maize	2	0.64	1.609 ± 1.095
Blackbird	Max. no. birds	Poisson	Maize	4	1.91	0.140 ± 0.306
Song Thrush	Max. no. birds	Poisson	Maize	2	0.77	0.000 ± 1.000
Chaffinch	Max. no. birds	Poisson	Maize	4	0.80	1.253 ± 0.802
Yellowhammer	Max. no. birds	Poisson	Maize	4	0.80	1.792 ± 1.080*
Skylark	Max. no. birds	Poisson	Rape	2	2.29	0.134 ± 0.518
Dunnock	Max. no. birds	Poisson	Rape	2	1.18	1.792 ± 1.080*
Whitethroat	Max. no. birds	Poisson	Rape	3	1.11	0.223 ± 0.474
Yellowhammer	Max. no. birds	Poisson	Rape	2	1.84	0.511 ± 0.730

(f) Aerial feeders – LATE data set

Species	**Dependent variable**	**Data distribution**	**Crop**	**No. sites**	**Dispersion**	**Parameter estimate**
Swallow	No. foraging events	Poisson	Beet	6	4.22	0.337 ± 0.293
House Martin	No. foraging events	Poisson	Beet	2	3.41	0.406 ± 0.646
Swallow	Max. no. birds	Poisson	Beet	6	2.8	0.375 ± 0.392
House Martin	Max. no. birds	Poisson	Beet	2	1.76	0.406 ± 0.913
Swallow	No. foraging events	Poisson	Maize	5	5.69	1.555 ± 0.284***
Swallow	Max. no. birds	Poisson	Maize	5	2.14	1.204 ± 0.466**
Swallow	No. foraging events	Poisson	Rape	4	9.11	0.289 ± 0.227
Swallow	Max. no. birds	Poisson	Rape	4	3.69	0.470 ± 0.329

Appendix 2 A summary of Poisson and binomial models considering the effects of GMHT and conventional crop management on mammal abundance and probability of occurrence in three different crop types. Analyses from two different data sets (EARLY and LATE) are given. The number of sites indicates the number where at least one individual of the species in question was recorded. Total number of sites surveyed was 24 for sugar beet, 11 for maize and 10 for rape. The dispersion is calculated as deviance / degrees of freedom. Parameter estimates are for the treatment effect and are given as untransformed estimates ± standard error, relative to 0. The treatment used as the reference habitat (i.e. mean = 0) was randomly assigned. Asterisks indicate a significant change in deviance when the treatment term was added to the effects of site and date, where * $P < 0.05$ (χ^2 test).

(a) EARLY

Species	**Data distribution**	**Crop**	**No. sites**	**Dispersion**	**Parameter estimate**
Hare	Poisson	Beet	9	2.41	0.199 ± 0.406
	Binomial		9	1.96	0.137 ± 0.935
	Poisson	Maize	2	1.20	0.693 ± 1.225
	Binomial		2	2.01	2.020 ± 2.246
	Poisson	Rape	3	4.73	0.352 ± 0.916
	Binomial		3	1.42	1.817 ± 2.363

(b) LATE

Species	**Data distribution**	**Crop**	**No. sites**	**Dispersion**	**Parameter estimate**
Rabbit	Poisson	Beet	6	1.40	1.042 ± 0.475*
Hare	Poisson		11	1.72	0.442 ± 0.247
Rabbit	Binomial		6	1.58	0.544 ± 0.743
Hare	Binomial		11	1.37	0.747 ± 0.556
Rabbit	Poisson	Maize	3	1.19	0.560 ± 0.627
Hare	Poisson		3	1.31	0.847 ± 0.690
Rabbit	Binomial		3	1.44	0.638 ± 1.145
Hare	Binomial		3	1.88	0.543 ± 1.049
Hare	Poisson	Rape	3	0.80	0.134 ± 0.518
Hare	Binomial		3	0.81	1.086 ± 1.549