☑ Fact-Checked Science

PAPER CHECK · MAGNETIC FIELDS AND INSECTS

Planthopper data reproduce the paper's gene counts; changes from 45 to 50 μT are small

Xie and colleagues raised brown planthoppers, a migratory rice pest, in fields of about 45 μT and 50 μT and in a near-zero field, then compared the genes the insects were using [1 S2]; the two strengths match either end of the insects' route (our analysis). Every count in the abstract reproduces from the authors' open data [2]. The near-zero field changed thousands of genes, far beyond chance; the step from 45 to 50 μT changed a few hundred, by small amounts, and how many depends on the method (our analysis). S0 News linked the dataset [38].

By Fact-Checked Science · Published November 21, 2026

OUR ANALYSIS marks our own reasoning, and the verdicts are our assessment. Everything else comes from the numbered sources; for the paper [1], S1–S9 number the sentences of its abstract, and for the dataset [2] a locator names the file.

The gene counts reproduce; a near-zero field moved thousands of genes, 45 against 50 μT a few hundred, slightly

OUR ASSESSMENT

244
genes passed the authors' thresholds between the 45 and 50 μT fields, exactly as their data give [2 Fig. 1 file]; the middle one changed by 1.29 times (our analysis)

1st of 10
the real grouping of the samples ranks first among all 10 possible groupings in every comparison with our negative-binomial test, the best a test this small can show (our analysis)

0.26 μT
the near-zero field as measured, about 190 times weaker than the 50 μT field [2 Fig. S1 file]

THE PAPER'S CLAIMS

TRUE

"reared under ~45 μT or ~50 μT fields, approximating intensities along their migratory route, or under a near-zero magnetic field (NZMF)"

The paper's abstract, sentence 2
[1 S2]

The global field model puts the group's two sites, Zhanjiang and Nanjing, at 45.4 and 50.2 μT, and ten places on the route at 44.8–50.2 μT (our analysis) [5][9 §4.2]. The lab's fields measured 44.4 and 50.7 μT, both at one inclination of about 30°, near the southern site's [2 Fig. S1 file]. See section 2.

TRUE

"The natural-range ~5 μT comparison identified 244 DEGs and a restricted functional response."

The paper's abstract, sentence 3
[1 S3]

The authors' results give exactly 244 [2 Fig. 1 file], and with our negative-binomial test the real grouping beats every shuffled one [2 counts]. But the changes are small (a middle change of 1.29 times), there are three samples per field, and our pre-registered methods give anywhere from 6 to 529, or 97 with an exploratory prior (our analysis). See section 3.

TRUE

"'Lipid transporter activity' was the only Gene Ontology term significant after false-discovery-rate correction, whereas 'response to light stimulus' and 'flavin adenine dinucleotide binding', both containing cryptochrome1 (Cry1), were nominally enriched."

The paper's abstract, sentence 4
[1 S4]

Exactly so in the authors' tables: one term survives correction (adjusted p = 0.018), and the two terms holding *Cry1* do not (0.42 and 0.12) [2 Fig. 2 file]. The authors call those two only "nominally enriched", which is the fair word. See section 4.

TRUE

"By contrast, NZMF identified 2753–3258 DEGs"

The paper's abstract, sentence 5
[1 S5]

The near-zero field against 45 μT gives 3,258 and against 50 μT 2,753 [2 Fig. 1 file]. Our negative-binomial re-analyses find 2,481–3,589, depending on the fit, against at most 539 for any shuffled grouping, though each comparison rests on two near-zero samples (our analysis). See sections 3 and 4.

TRUE

"Cry1 knockdown disrupted the diel eclosion rhythm, demonstrating its importance for eclosion timing and limiting this phenotype as a magnetic field intensity readout after knockdown."

The paper's abstract, sentence 8
[1 S8]

Knockdown cut *Cry1* by 88–91%. Control females emerged mostly in the light, 96%, around a clear daily peak; knockdown females emerged around the clock, 63% in the light, with no significant rhythm (our analysis) [2 Fig. 4 file]. No field was varied in this test, as the authors' own wording implies. See section 5.

UNCONFIRMED

"Together, natural-range geomagnetic variation and NZMF exposure may evoke qualitatively distinct magnetobiological response states rather than quantitatively different magnetic environments."

The paper's abstract, sentence 9
[1 S9]

A hedged reading of one small experiment. With no field strengths between near zero and 45 μT, the design can't tell a different kind of response from a bigger one, and the genes the two comparisons share can't settle it either (our analysis). See section 3.

1 · THE EXPERIMENT

Planthoppers raised in three fields, then their genes counted; one of nine samples was dropped

Xie and colleagues raised brown planthoppers, *Nilaparvata lugens*, a rice pest that migrates each year across East Asia, under fields of about 45 μT and 50 μT and under a near-zero field, and compared the genes the insects were using [1 S1][1 S2]. They sequenced three samples per field; one near-zero sample failed their quality control, leaving eight [2 README].

What was measured

The nine samples were whole insects, dated March 1, 2024, at Nanjing in their public records, each read to 38.7–49.6 million pairs of sequences [3]. The authors counted reads for 20,713 genes [2 counts] and retained those with at least 6 reads in total over the eight samples kept [2 README], then compared the fields in one DESeq2 model [2 DESeq2 script][29]. A gene counts as "differentially expressed" (a DEG) if its adjusted p is below 0.05 and its change exceeds 0.25 on the $\log_2$ scale, that is, more than 19% up or 16% down [2 README].

They also tested which functions the changed genes share (Gene Ontology and KEGG enrichment), checked selected genes by RT-qPCR with three samples per field, and knocked down the gene *Cry1* to see when adult females emerged, counted every two hours under 14 hours of light and 10 of dark [2 README].

What we read

The paper itself is behind the publisher's paywall, so we read its abstract, through PubMed [1]. We read the authors' dataset in full: they published it under CC0, with their R scripts and a README [2]. Dryad's interface refused our automated client, so the site's owner downloaded it by hand from Dryad's page; every file matches Dryad's own checksums. We also read the public records of the raw reads [3].

The abstract's abbreviations: NZMF, the near-zero magnetic field; DEG, a differentially expressed gene. The dataset calls the three fields GMF45, GMF50 and NZMF [2 README].

OUR ANALYSIS

The dropped sample was far off; the near-zero comparisons rest on two samples

The excluded near-zero sample registers 15,014 genes against 16,888–17,258 for the others, and on its own it accounts for 80% of the variation among all nine samples in the 500 most variable genes [2 counts]. Kept in, it swamps everything: with our main method the counts of changed genes fall to 38–387. So the exclusion looks sound. It does mean that both near-zero comparisons set two samples against three, which the abstract doesn't say [1 S5].

2 · THE FIELDS AND THE ROUTE

45 and 50 μT are the field's strength at either end of the route; the lab held one direction

Brown planthoppers overwinter in Vietnam and southern Hainan and fly north each spring, reaching the Yangtze valley, Korea and western Japan from mid-June [7][8 Abstract]. In the group's earlier papers, 45 μT stands for Zhanjiang, near the start, and 50 μT for Nanjing, where the lab is [9 §4.2][10 Abstract].

The field's strength along the route, from the global field model (2025)

PLACE	STRENGTH	INCLINATION	CHANGE SINCE 1900
Hanoi, northern Vietnam	45.65 μT	31.8°	+2.73 μT
Haikou, Hainan	44.79 μT	29.7°	+2.48 μT
Zhanjiang, Guangdong	**45.37 μT**	**32.0°**	**+2.51 μT**
Nanning, Guangxi	46.40 μT	35.1°	+2.64 μT
Guangzhou, Guangdong	46.04 μT	35.4°	+2.39 μT
Changsha, Hunan	48.95 μT	44.1°	+2.39 μT
Wuhan, Hubei	50.12 μT	47.5°	+2.26 μT
Nanjing, Jiangsu	**50.19 μT**	**49.0°**	**+2.00 μT**
Gwangju, South Korea	50.08 μT	51.6°	+1.53 μT
Fukuoka, Japan	48.25 μT	48.7°	+1.45 μT

Our analysis: IGRF-14 at sea level for 2025.0 [5], with code checked against NOAA's published test values to within 0.05 nT [6]. The places are fixed in our rules before the run; the two highlighted are the group's sites [9 §4.2]. At the samples' collection date the values differ by about 0.03 μT.

"50 μT" FIELD
50.68 μT
average of 30 readings, give or take 0.29 μT [2 Fig. S1 file]

"45 μT" FIELD
44.37 μT
average of 30 readings, give or take 0.50 μT [2 Fig. S1 file]

NEAR-ZERO FIELD
0.26 μT
average of 30 readings, 0.13–0.46 μT [2 Fig. S1 file]

One direction for both fields

The two fields pointed the same way: inclination 30.35° and 30.46°, declination +2.25° and +2.30° [2 Fig. S1 file]. So they differed in strength only, as a test of strength should. That shared inclination is close to Zhanjiang's 32°, not Nanjing's 49°, and along the route a field of 50 μT comes with an inclination of 47–52° (our analysis) [5]. The "50 μT" condition is therefore 50 μT at a southern site's angle, a combination the insects don't meet on their route.

OUR ANALYSIS

The right span of strengths

Both lab fields sit within half a microtesla of the route's two ends, 44.8 and 50.2 μT, so "approximating intensities along their migratory route" holds [1 S2]. What the route also changes, by about 17°, is the field's angle, which the design leaves out.

The measured step

The abstract calls the comparison between the two fields "~5 μT" [1 S3]. As measured, the step was 6.3 μT: 50.68 less 44.37 [2 Fig. S1 file]. Each field sits within 0.7 μT of its nominal value, but the two departures add, so the step is 1.3 μT larger than the nominal 5 μT, and 1.5 μT larger than the 4.8 μT between Zhanjiang and Nanjing (our analysis) [5]. The likely reading is that the abstract gives the design's nominal values, as its "~" signals. No verdict changes.

3 · HOW MANY GENES CHANGED

The counts reproduce exactly; the near-zero signal is strong, the 45-to-50 μT one small

Two separately written readers of the authors' results give 244, 3,258 and 2,753 changed genes [2 Fig. 1 file], the abstract's numbers [1 S3][1 S5]. The file's own statistics recompute, and its gene list is exactly the set with at least 6 reads (our analysis).

Changed genes in the authors' results, by rule

RULE	50 AGAINST 45 μT	NEAR-ZERO AGAINST 45 μT	NEAR-ZERO AGAINST 50 μT
The authors': adjusted p < 0.05, change > 0.25 $\log_2$	244 (144 up, 100 down)	3,258 (1,708 up)	2,753 (1,426 up)
Adjusted p < 0.05, any change	386	4,020	3,505
… and more than 1.5 times	52	940	795
… and more than 2 times	18	258	221
Adjusted p < 0.10, change > 0.25 $\log_2$	312	3,611	3,123
Adjusted p < 0.10, any change (added after the review)	565	4,739	4,184
Unadjusted p < 0.05, change > 0.25 $\log_2$	908	3,963	3,571
Unadjusted p < 0.05, any change (added after the review)	1,840	5,242	4,825
Middle change among the DEGs	1.29 times	1.36 times	1.35 times

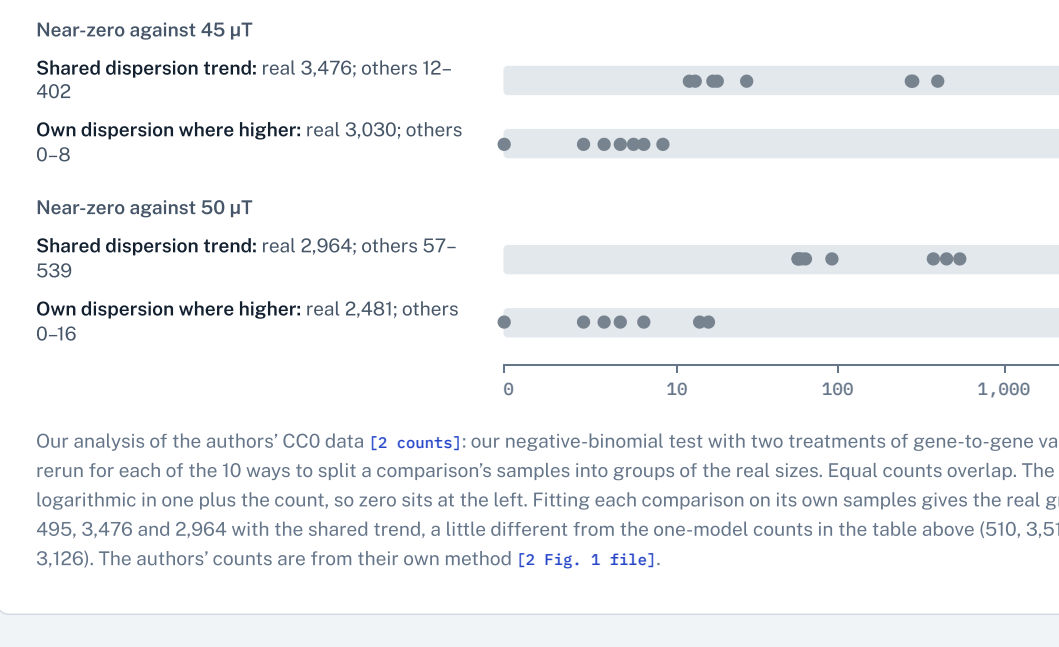
Our analysis of the authors' DESeq2 results [2 Fig. 1 file][29], under rules written before the data arrived, except the two any-change rows at adjusted p < 0.10 and unadjusted p < 0.05, which were added after an independent review and weren't pre-registered. The false-discovery adjustment is Benjamini and Hochberg's [32].

Our own re-analysis, and a test against chance

We re-derived the comparisons from the raw counts with two simpler methods we wrote ourselves: a negative-binomial test, which treats counts as counts [30], and a moderated t-test on log counts [31]. Each was fixed in advance, with variants. The counts depend on the method. For the near-zero field the negative-binomial variants land close to the authors', 2,543–3,589 in one model of all eight samples, as the authors fitted theirs, and the main one finds 99% of the authors' genes. At 45 against 50 μT they give 150–529, and the moderated t-test finds 6 with its pre-registered single prior, 97 with an exploratory prior that varies with expression.

Changed genes with the real grouping and with every other grouping of the same samples

OUR ANALYSIS



Our analysis of the authors' CC0 data [2 counts]: our negative-binomial test with two treatments of gene-to-gene variation, rerun for each of the 10 ways to split a comparison's samples into groups of the real sizes. Equal counts overlap. The scale is logarithmic in one plus the count, so zero sits at the left. Fitting each comparison on its own samples gives the real grouping 495, 3,476 and 2,964 with the shared trend, a little different from the one-model counts in the table above (510, 3,510 and 3,126). The authors' counts are from their own method [2 Fig. 1 file].

OUR ANALYSIS

Above chance, by a margin that depends on the method

With our negative-binomial test, in every comparison and under both treatments, the real grouping gives more changed genes than any of the nine others. With 10 groupings that is the strongest result possible, a chance of 1 in 10, so it can't reach the usual 1 in 20. The near-zero signal is overwhelming. At 45 against 50 μT the shuffled groupings give 116–180 "changed genes" with a shared trend and 0–9 with each gene's own variation, against 495 and 165 for the real one; the authors' 244 sits between. Leaving out any one of the six samples keeps 93–485, so no single sample drives it (exploratory).

OUR ANALYSIS

Shared genes: a pattern chance alone produces

Of the 244 genes, 123 also change in each near-zero comparison, and 98 of those 123 move the same way in "50 against 45" as in "near-zero against 45" [2 Fig. 1 file]. Both comparisons are measured against the same three 45 μT samples, so chance highs and lows in those samples push both changes the same way and make the two lists overlap. Regroupings of the samples that mix 45 and 50 μT show the same pattern: 76–92% of their shared genes move the same way, and their lists overlap 1.9–5.0 times as much as independent lists would; the real grouping, by the same method, gives 82% and 2.4 times (exploratory, added after an independent review of our draft) [2 counts]. So the shared genes can't tell a graded response from a distinct one.

4 · WHAT THE CHANGED GENES DO

At 45 against 50 μT one function survives correction; in the near-zero field, metabolism and redox stand out

Between 45 and 50 μT, of the 55 Gene Ontology terms with an unadjusted p below 0.05, only "lipid transporter activity" survives the authors' correction, which they made separately within each ontology (our analysis). It is one of the 177 molecular-function terms tested (about 750 GO terms in all) and holds 5 genes, adjusted p = 0.018 [2 Fig. 2 file]. No KEGG pathway survives [2 Fig. 2 file].

In the authors' words, and in their tables

"Nominally enriched" means a p below 0.05 before the correction for testing many terms, but not after it.

> *"'response to light stimulus' and 'flavin adenine dinucleotide binding', both containing cryptochrome1 (Cry1), were nominally enriched"*
>
> Xie et al. (2026) [1 S4]

RESPONSE TO LIGHT
OUR ANALYSIS
2 genes
cry and a long-wavelength opsin; p = 0.0047, adjusted 0.42 [2 Fig. 2 file][4]

FLAVIN ADENINE DINUCLEOTIDE BINDING
OUR ANALYSIS
5 genes
GO:0050660: *cry* and four enzymes; p = 0.0033, adjusted 0.12 [2 Fig. 2 file][4]

The near-zero comparisons: functions that survive correction

FUNCTION	SMALLEST ADJUSTED P	EXAMPLES IN THE AUTHORS' TABLES
Central carbon metabolism	5×10^{-5}	KEGG carbon metabolism; glycolysis and gluconeogenesis; pyruvate; the pentose phosphate pathway
Amino-acid metabolism	10^{-6}	Biosynthesis of amino acids; glycine, serine and threonine metabolism; many GO terms
Peroxisome	0.004	KEGG peroxisome, in both comparisons (0.034 and 0.004)
Redox	0.016	Oxidoreductase, antioxidant and peroxidase activity; response to oxidative stress

Our reading of the authors' GO and KEGG results [2 Fig. 2 file], sorted by word lists fixed in our rules before the data arrived. In all, 53 and 107 GO terms and 28 and 29 KEGG pathways survive correction in the two near-zero comparisons.

Clock genes among the changed genes

Four core clock genes, *period*, *timeless*, *cycle* and *clockwork orange*, and a cryptochrome-family gene recorded as *cry2* (NCBI's annotation calls it a (6-4)-photolyase) are among the near-zero DEGs in both comparisons, all higher in the near-zero field, by 0.27–0.69 on the $\log_2$ scale. *Clock*, *Cry1* and the *pdf* genes are not [2 Fig. 1 file][4]. The authors checked four of these five by qPCR [2 Fig. 3 file]. Clock genes change with the time of day, and the abstract doesn't say when the insects were sampled [1].

No clock term among the enriched functions

The abstract lists "clock-related genes" among what the near-zero field enriched [1 S5]. In the deposited GO and KEGG tables, no term or pathway about circadian rhythms or clocks appears for either near-zero comparison; a search of the workbook's raw text finds none [2 Fig. 2 file]. The clock genes themselves did change, as above, and the paper's figures, which we couldn't read, may present them as a group. The likely meaning is the differentially expressed clock genes rather than an enriched category, and the verdict on the count doesn't turn on it.

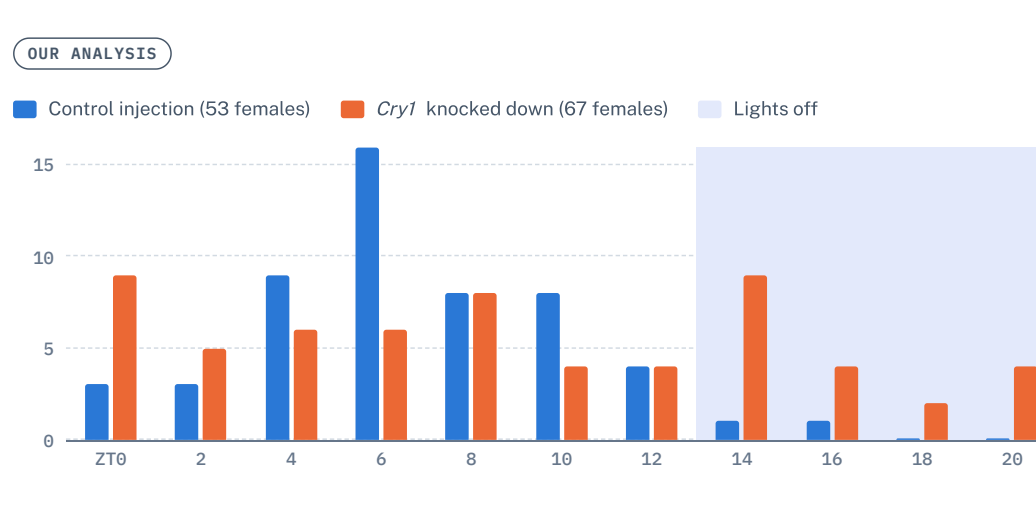
5 · CRY1 AND THE DAILY CLOCK

Knocking down *Cry1* flattened the females' daily emergence peak; the qPCR agrees with the sequencing

In the 45-to-50 μT comparison, *Cry1* is 17% lower at 50 μT, adjusted p = 0.037, just inside the authors' thresholds; the near-zero comparisons show no significant change (adjusted p 0.42 and 0.19) [2 Fig. 1 file][4]. The abstract gives that change, the gene's known light and clock roles and earlier near-zero results as its reasons for testing *Cry1* [1 S7].

When adult females emerged, by two-hour interval

OUR ANALYSIS



Our chart of the authors' CC0 counts [2 Fig. 4 file], reading each label as the start of its interval. We redrew no figure from the paper.

KNOCKDOWN OUR ANALYSIS
88–91%
less *Cry1* RNA in adults and in fifth-stage nymphs, four samples each [2 Fig. 4 file]

EMERGED IN THE LIGHT OUR ANALYSIS
96% / 63%
controls against knockdown; a test of the whole daily pattern, treating each female as independent, gives p = 0.001 [2 Fig. 4 file]

QPCR AGAINST SEQUENCING OUR ANALYSIS
20 of 20
gene comparisons change in the same direction; correlation 0.86 [2 Fig. 3 file][2 Fig. 1 file]

In other insects

Losing *Cry1* disturbs emergence elsewhere too. In monarch butterflies it "reduced the amplitude and altered the phase of adult eclosion rhythms" [27 Abstract], and silkworms without it emerged without a rhythm in constant darkness [28 Abstract]. So the planthopper result fits *Cry1*'s known place in the clock, as the abstract's "established photoreceptive and circadian functions" anticipates [1 S7].

OUR ANALYSIS

What the knockdown test does and doesn't show

Controls emerged around a clear peak near the middle of the light period; knockdown females had no significant daily rhythm (p = 0.52) [2 Fig. 4 file]. No magnetic field was varied in this test, so it shows *Cry1*'s role in timing emergence, which is what the abstract claims, not a magnetic effect [1 S8]. The qPCR changes run larger than the sequencing's: for *Cry1*, 60% lower by qPCR [2 Fig. 3 file] against 17% by sequencing [2 Fig. 1 file].

6 · THE WIDER EVIDENCE

The group has reported magnetic effects in planthoppers for a decade; how insects sense the field is still argued

The 45-against-50 μT comparison is not new to this group. In earlier work with the same design it reported changes in wing form, flight and attraction to light, and higher *Cry1* at 45 μT, by 45–74% in young females [10 Abstract][9 §2.1]; it describes that as replicating its earlier findings [9 §3].

The group's earlier near-zero results

Raised near zero, brown and small brown planthoppers developed more slowly and the adults weighed less and laid fewer eggs [11 Abstract]; adult weight fell by about 13–15% and phloem feeding by a third [13 Abstract]. In the white-backed planthopper, a different species, cryptochrome genes changed as well [12 Abstract]. A near-zero field, or reversing the field's vertical part, removed a preference in which way the insects turned to feed [15 Abstract], and magnetic particles have been found in their abdomens [14 Abstract].

The cryptochrome debate

Cryptochrome was linked to magnetic responses in fruit flies [16 Abstract][17 Abstract] and to sensing the field's inclination in monarch butterflies, in a 2021 study by this paper's last author and colleagues [18 Abstract]. Later work found that part of the fly protein, or its cofactor FAD alone, can carry a response [19 Abstract]. A large blinded study then found no magnetic effect on fly behaviour and suggested many earlier results were false positives [20 Abstract]; its authors stood by that after a published challenge [21][22]. A 2023 review of the insect work still calls how animals sense the field one of sensory biology's greatest mysteries [23 Abstract].

Other near-zero studies of insects

Fruit flies kept near zero for ten generations lost visual learning, which came back in Earth's field [25 Abstract], and a 2026 study, with two of this paper's authors, counted 202 changed genes in a fly strain near zero [26 Abstract]. A review of the literature found the size of effects unrelated to field strength or exposure [24 Abstract]. Our checks of fruit flies in a magnetic shield, bats orienting in darkness, and mint and basil in near-zero coils cover more.

OUR ANALYSIS

Where this paper fits

The paper adds gene-wide counts for this insect at the two strengths and near zero, with its data open to anyone. It doesn't settle how the insect senses the field: changed RNA levels in whole bodies can follow from sensing, or from anything else that differed between the fields' set-ups.

7 · STRENGTHS AND LIMITATIONS

Open data and careful wording; few samples, small changes and methods we couldn't read

The authors published their counts, results and scripts under CC0, with the raw reads [2][3], and their abstract separates what survived correction from what didn't [1 S4].

Few samples

Three samples per field, and two in the near-zero field. Comparisons this small can't estimate each gene's variation well, which is why the count at 45 against 50 μT moves so much with the method (our analysis).

Small changes

Half of the 244 genes changed by less than 1.29 times, and 18 by more than two times [2 Fig. 1 file]. The authors' fold-change threshold is low, though they state it [2 README].

Field and set-up

The abstract doesn't describe the apparatus. Without the methods we can't tell whether each field had its own coil, whether coils were swapped or repeated, whether a sham was used, or whether anything else differed, so a field effect can't be separated from the set-up.

Time of day

The clock genes that changed near zero also change with the hour; when the insects were sampled isn't in the abstract [1].

Abstract only

We read the paper's abstract, not its methods or figures, so the exposure length and other design details are unknown to us [1].

Two documentation points

Neither changes a verdict. The deposited script applies no p- or q-value cutoff, but the README's "Complete GO and KEGG enrichment results" holds only the terms with an unadjusted p below 0.05 (one KEGG sheet a few more), so the full lists aren't in the deposit [2 README][2 Fig. 2 file]. The workbook's sheet names and layout also differ from what the script writes, so it was arranged after export. No claim depends on the missing rows: a term with p above 0.05 can't pass the correction.

What would change these verdicts

01
The paper's methods showing that the two fields came from different apparatus with no swap or sham would leave the 45-to-50 μT count True as a count but weaken it as a field effect.

02
A repeat with more samples per field, or with strengths between near zero and 45 μT, could confirm or overturn "distinct states, not degrees".

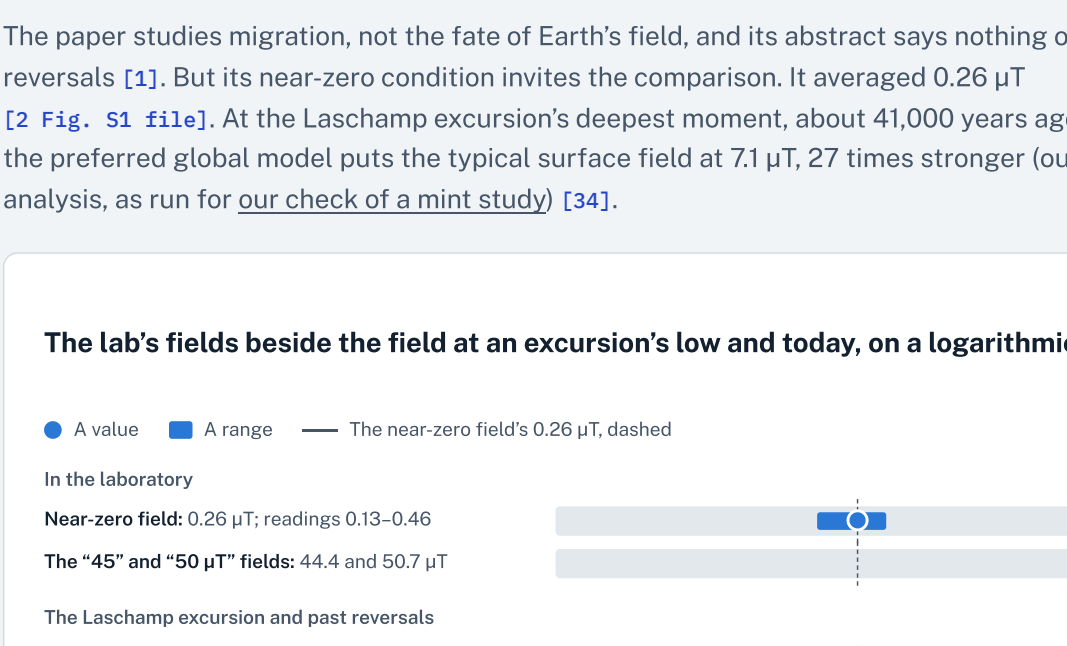
03
A test of eclosion in different fields after *Cry1* knockdown would show whether the rhythm can serve as a magnetic readout, as the authors propose.

8 · A COLLAPSING FIELD?

The near-zero field is far below what an excursion leaves at the surface, and the route's field has grown since 1900

The paper studies migration, not the fate of Earth's field, and its abstract says nothing of reversals [1]. But its near-zero condition invites the comparison. It averaged 0.26 μT [2 Fig. S1 file]. At the Laschamp excursion's deepest moment, about 41,000 years ago, the preferred global model puts the typical surface field at 7.1 μT, 27 times stronger (our analysis, as run for our check of a mint study) [34].

The lab's fields beside the field at an excursion's low and today, on a logarithmic scale



Our chart. The lab's fields: [2 Fig. S1 file]. Point minima: [33 §4.6]. The surface at the deepest moment: our run of the LSMOD.2 model on the mint page, 5th to 95th percentile by area [34]. La Palma: [35 Abstract]. Today: [6 Table 1]; the route: IGRF-14, our analysis [5].

OUR ANALYSIS

An excursion would not bring the lab's near-zero field

At the excursion's deepest moment the typical surface field was 9–60 times the lab's near-zero field, and lava from a reversal records lows of about 3.9 μT, 15 times it [34][35 Abstract]. Only the models' single lowest points dip below it [33 §4.6], and in the model, fields under 300 nT never covered more than 0.09% of Earth's surface at once, for decades at most in one place, as the mint page found [34]. At the rates a 2026 study measured, the excursion's fall took about 1,500–1,900 years (our arithmetic, as on that page) [36], a thousand or more planthopper generations, since the insects breed three or more times a season [7]. The lab switched the field within one.

Over the route, a stronger field than in 1900

Earth's dipole, the main part of its field, is about 9% weaker than in 1840 [37 p. 1], but the field over the planthoppers' route has grown: by 1.45–2.73 μT at every site since 1900, and the 45 and 50 μT lines have moved about 370–530 km south [5]. A century's change at any one place is smaller than the difference the insects already fly through between Zhanjiang and Nanjing. See our guide to the field and how fast excursions happen.

9 · REPEAT OUR NUMBERS

Our rules, scripts and derived numbers; the authors' data stay on Dryad

Each rules file was written before the data it governs were available, and the field-model rules before that script first ran. Dryad refuses scripted downloads, so the first script takes the zip you download from Dryad's page and checks every file against Dryad's checksums before anything else runs.

PY **prepare_inputs.py and run_all.py**
Checks the Dryad zip you download by hand against Dryad's own checksums, unpacks the six data files and checks them against our copies, and fetches IGRF-14 and NOAA's test values by URL; then runs every step in order · 9 KB

PY **xlsx_reader.py**
Reads the authors' spreadsheets with no extra packages · 5 KB

PY **deg_recount.py and deg_recount_check.py, with deg_recount.json**
The recount of changed genes under the authors' rule and the alternatives, by two separately written readers, section 3 · 15 KB

PY **go_terms.py and clock_genes.py, with their outputs go_terms.json and clock_genes.json**
The functions that survive correction, Cry1's identity and the clock genes, section 4 · 73 KB

PY **rederive.py, permutation.py and overlap.py, with their outputs rederive.json, permutation.json and overlap.json**
Our own re-analysis from the raw counts, every regrouping of the samples, and the overlap test with its regrouping check (exploratory, added after the review), section 3 · 71 KB

PY **field_params.py and igrf_route.py, with field_params.json and igrf_route.json**
The measured fields, and the field along the route from IGRF-14 since 1900, sections 2 and 8 · 49 KB

PY **qpcr_rnai.py, with qpcr_rnai.json**
The qPCR against the sequencing, the knockdown and the emergence rhythm, section 5 · 24 KB

PY **exploratory.py and exploratory_loo.py, with exploratory.json and exploratory_loo.json**
Checks added after the data were seen and labelled exploratory: the eight-sample spread, a t-test with a prior that varies with expression, and leaving out one sample at a time · 11 KB

TXT **RULES_deg_recount.txt, RULES_rederive.txt, RULES_permutation.txt, RULES_go_terms.txt, RULES_overlap.txt, RULES_field_params.txt, RULES_qpcr_rnai.txt and RULES_igrf_route.txt**
Our rules, each written and hashed before the data it governs were available; the field-model rules before that script first ran · 34 KB

TXT **HASHES.txt**
The SHA-256 of every file here and of our inputs, with the order of the rules and runs · 10 KB

Run it

Download the dataset from its Dryad page with "Download dataset"; Dryad answers scripts with an error. Then `python3 prepare_inputs.py <zip> <folder>` and `python3 run_all.py <folder> <out>`. Each script's header gives its own usage. The scripts need Python 3.9 or later with numpy, scipy and pandas; the field model, the clock genes and the spreadsheet reader need only the standard library.

What we don't host

The paper and its abstract, under the publisher's terms [1]; the authors' data and scripts, which Dryad serves under CC0 [2]; NOAA's coefficient files, which the script fetches [5][6]; and our three per-gene tables, about 1 MB each, which `run_all.py` writes. We host only our own rules, code and derived numbers.

Sources

Bracketed numbers refer to this list. For the paper [1], S1–S9 number the sentences of its abstract, the only part we read. For the dataset [2], a locator names its file: README; counts, the RNA-seq count matrix; Fig. 1 file, the DESeq2 results for the three comparisons; DESeq2 script, the authors' R script for that analysis; Fig. 2 file, the GO and KEGG enrichment; Fig. 3 file, the RT-qPCR; Fig. 4 file, the Cry1 knockdown and emergence counts; Fig. S1 file, the field readings. For the other sources, § gives a section, p. a page, Table a table, and Abstract that part, where only it was read. Quotations of the abstract follow the publisher's typography as deposited with Crossref; PubMed's copy has the same words. μT is the microtesla and nT the nanotesla, 1,000 nT to the μT; a DEG is a differentially expressed gene and NZMF the near-zero magnetic field, in the authors' terms. Links checked November 21, 2026.

1 Xie, W., Wang, Y., Zou, L., Qiu, H., Li, P., Krylov, V., Li, Y., Pan, W., Chen, F., and Wan, G. (2026). Geomagnetic intensity variation and deprivation elicit distinct transcriptomic responses in a migratory insect. *Insect Molecular Biology*, published online September 26, 2026. Abstract only, as given by PubMed; the paper is under the publisher's terms and wasn't read.

2 Xie, W., Wang, Y., Zou, L., Qiu, H., Li, P., Krylov, V., Li, Y., Pan, W., Chen, F., and Wan, G. (2026). Data and code from: Geomagnetic intensity variation and deprivation elicit distinct transcriptomic responses in a migratory insect. Dryad, version 7, September 15, 2026. CC0 1.0. Data, read in full; downloaded by hand by the site's owner after Dryad's interface refused our client, every file matching Dryad's checksums.

3 NCBI Sequence Read Archive (2026). BioProject PRJNA1469985: nine RNA-seq runs (SRR38815303–SRR38815311) and their BioSample records (SAMN60393961–SAMN60393969), released September 4, 2026. Records only.

4 NCBI Gene (2026). *Nilaparvata lugens* gene records: *cry* (Gene ID 111044853, also called *cry1*), *phr6-4* (Gene ID 111059678, a (6-4)-photolyase, also called *cry2*), *per*, *tim*, *Clk*, *cwo*, the *cycle* and *pdf* genes and the qPCR genes. Records read on November 20, 2026.

5 IAGA Working Group V-MOD (2024). International Geomagnetic Reference Field, 14th generation (IGRF-14): Gauss coefficients 1900–2025 and secular variation 2025–2030. Data file, NOAA National Centers for Environmental Information; the same file, by its SHA-256, as on our earlier pages.

6 Chulliat, A., Brown, W., Nair, M., Gomez Perez, N., Young, L.-Y., Watson, C., Boneh, N., Beggan, C., Meyer, B., and Paniccia, M. (2025). The US/UK World Magnetic Model for 2025–2030: Technical Report. NOAA National Centers for Environmental Information. We used its Table 1 and the model's published test values.

7 Otuka, A. (2013). Migration of rice planthoppers and their vectored re-emerging and novel rice viruses in East Asia. *Frontiers in Microbiology* 4, 309. CC BY; we read the copy in Europe PMC.

8 Hu, G., Feng, H., Otuka, A., Reynolds, D. R., Drake, V. A., and Chapman, J. W. (2025). The East Asian insect flyway: geographical and climatic factors driving migration among diverse crop pests. *Annual Review of Entomology* 70, 1–22. Abstract only.

9 Zhang, Y., Zhang, Y., Zhao, J., He, J., Xuanyuan, Z., Pan, W., Sword, G. A., Chen, F., and Wan, G. (2023). Probing transcriptional crosstalk between cryptochromes and iron-sulfur cluster assembly 1 (MagR) in the magnetoresponse of a migratory insect. *International Journal of Molecular Sciences* 24(13), 11101. CC BY 4.0; we read the copy in Europe PMC.

10 Wan, G., Liu, R., Li, C., He, J., Pan, W., Sword, G. A., Hu, G., and Chen, F. (2020). Change in geomagnetic field intensity alters migration-associated traits in a migratory insect. *Biology Letters* 16(4), 20190940. Abstract only.

11 Wan, G.-J., Jiang, S.-L., Zhao, Z.-C., Xu, J.-J., Tao, X.-R., Sword, G. A., Gao, Y.-B., Pan, W.-D., and Chen, F.-J. (2014). Bio-effects of near-zero magnetic fields on the growth, development and reproduction of small brown planthopper, *Laodelphax striatellus* and brown planthopper, *Nilaparvata lugens*. *Journal of Insect Physiology* 68, 7–15. Abstract only.

12 Wan, G.-J., Wang, W.-J., Xu, J.-J., Yang, Q.-F., Dai, M.-J., Zhang, F.-J., Sword, G. A., Pan, W.-D., and Chen, F.-J. (2015). Cryptochromes and hormone signal transduction under near-zero magnetic fields: new clues to magnetic field effects in a rice planthopper. *PLoS ONE* 10(7), e0132966. CC BY 4.0. Abstract only.

13 Wan, G.-J., Jiang, S.-L., Zhang, M., Zhao, J.-Y., Zhang, Y.-C., Pan, W.-D., Sword, G. A., and Chen, F.-J. (2021). Geomagnetic field absence reduces adult body weight of a migratory insect by disrupting feeding behavior and appetite regulation. *Insect Science* 28(1), 251–260. Abstract only.

14 Pan, W., Wan, G., Xu, J., Li, X., Liu, Y., Qi, L., and Chen, F. (2016). Evidence for the presence of biogenic magnetic particles in the nocturnal migratory brown planthopper, *Nilaparvata lugens*. *Scientific Reports* 6, 18771. CC BY 4.0. Abstract only.

15 Zhang, Y., and Pan, W. (2021). Removal or component reversal of local geomagnetic field affects foraging orientation preference in migratory insect brown planthopper *Nilaparvata lugens*. *PeerJ* 9, e12351. CC BY 4.0. Abstract only.

16 Gegear, R. J., Casselman, A., Waddell, S., and Reppert, S. M. (2008). Cryptochrome mediates light-dependent magnetosensitivity in *Drosophila*. *Nature* 454(7207), 1014–1018. Abstract only.

17 Yoshii, T., Ahmad, M., and Helfrich-Förster, C. (2009). Cryptochrome mediates light-dependent magnetosensitivity of *Drosophila*'s circadian clock. *PLoS Biology* 7(4), e1000086. CC BY. Abstract only.

18 Wan, G., Hayden, A. N., Iiams, S. E., and Merlin, C. (2021). Cryptochrome 1 mediates light-dependent inclination magnetosensing in monarch butterflies. *Nature Communications* 12, 771. CC BY 4.0. Abstract only.

19 Bradlaugh, A. A., Fedele, G., Munro, A. L., Hansen, C. N., Hares, J. M., Patel, S., Kyriacou, C. P., Jones, A. R., Rosato, E., and Baines, R. A. (2023). Essential elements of radical pair magnetosensitivity in *Drosophila*. *Nature* 615(7950), 111–116. CC BY 4.0. Abstract only.

20 Bassetto, M., Reichl, T., Kobylkov, D., Kattnig, D. R., Winklhofer, M., Hore, P. J., and Mouritsen, H. (2023). No evidence for magnetic field effects on the behaviour of *Drosophila*. *Nature* 620(7974), 595–599. CC BY 4.0. Abstract, as read for this page; our check of a fly study read more.

21 Kyriacou, C. P. (2024). Magnetic field responses in *Drosophila*. *Nature* 629(8010), E3–E5. CC BY 4.0. Record only.

22 Bassetto, M., Reichl, T., Kobylkov, D., Kattnig, D. R., Winklhofer, M., Hore, P. J., and Mouritsen, H. (2024). Bassetto et al. reply. *Nature* 629(8010), E6–E7. CC BY 4.0. Record only.

23 Merlin, C. (2023). Insect magnetoreception: a Cry for mechanistic insights. *Journal of Comparative Physiology A* 209(5), 785–792. Abstract only.

24 Binhi, V. N., and Prato, F. S. (2017). Biological effects of the hypomagnetic field: an analytical review of experiments and theories. *PLoS ONE* 12(6), e0179340. CC BY 4.0. Abstract only.

25 Zhang, B., Lu, H., Xi, W., Zhou, X., Xu, S., Zhang, K., Jiang, J., Li, Y., and Guo, A. (2004). Exposure to hypomagnetic field space for multiple generations causes amnesia in *Drosophila melanogaster*. *Neuroscience Letters* 371(2–3), 190–195. Abstract only.

26 Kang, H.-M., Li, B., Yan, S., Zhang, L.-L., Wan, G.-J., Zhang, J.-Z., and Pan, W.-D. (2026). Hypomagnetic field exposure alters iron-sulfur homeostasis and oxidative balance in a frataxin-deficient insect system. *Insects* 17(4), 373. CC BY 4.0. Abstract only, as given by Europe PMC.

27 Iiams, S. E., Wan, G., Zhang, J., Lugena, A. B., Zhang, Y., Hayden, A. N., and Merlin, C. (2024). Loss of functional cryptochrome 1 reduces robustness of 24-hour behavioral rhythms in monarch butterflies. *iScience* 27(2), 108980. CC BY-NC-ND 4.0. Abstract only.

28 Tobita, H., and Kiuchi, T. (2024). Knockout of cryptochrome 1 disrupts circadian rhythm and photoperiodic diapause induction in the silkworm, *Bombyx mori*. *Insect Biochemistry and Molecular Biology* 172, 104153. Abstract only.

29 Love, M. I., Huber, W., and Anders, S. (2014). Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biology* 15(12), 550. CC BY 4.0.

30 Anders, S., and Huber, W. (2010). Differential expression analysis for sequence count data. *Genome Biology* 11(10), R106. CC BY 2.0.

31 Smyth, G. K. (2004). Linear models and empirical Bayes methods for assessing differential expression in microarray experiments. *Statistical Applications in Genetics and Molecular Biology* 3(1), 1–25.

32 Benjamini, Y., and Hochberg, Y. (1995). Controlling the false discovery rate: a practical and powerful approach to multiple testing. *Journal of the Royal Statistical Society Series B* 57(1), 289–300.

33 Korte, M., Brown, M. C., Panovska, S., and Wardinski, I. (2019). Robust characteristics of the Laschamp and Mono Lake geomagnetic excursions: results from global field models. *Frontiers in Earth Science* 7, 86. CC BY 4.0. As read for our check of a mint study.

34 Korte, M., and Brown, M. (2019). LSMOD.2–Global paleomagnetic field model for 50–30 ka BP. GFZ Data Services (dataset). CC BY 4.0. The numbers are from our run of the model for our check of a mint study.

35 Quidelleur, X., and Valet, J.-P. (1996). Geomagnetic changes across the last reversal recorded in lava flows from La Palma, Canary Islands. *Journal of Geophysical Research: Solid Earth* 101(B6), 13755–13773. Abstract only, as read for our check of a mint study.

36 Shinu, S., Mahgoub, A. N., and Korte, M. (2026). Rates of geomagnetic field change during excursions and reversals. *Journal of Geophysical Research: Solid Earth* 131(10), e2025JB033422. CC BY 4.0. As read for our check of the paper.

37 Finlay, C. C., Aubert, J., and Gillet, N. (2016). Gyre-driven decay of the Earth's magnetic dipole. *Nature Communications* 7, 10422. CC BY 4.0.

38 SpaceWeatherNews (S0) (November 20, 2026). Solar/Pole Shift Impact: Insects, Plants, Humans | S0 News Nov.20.2026. YouTube video. Linked the source; no transcript was available, so nothing the episode said is rated here.

METHOD

How this was checked

On November 20, 2026, we checked every statement, number, quotation and citation on this page against its source: the nine sentences of the paper's abstract; the authors' complete CC0 dataset, its six data files, README and two R scripts, every file matching Dryad's own checksums; the public records of the raw reads and of the genes named; the IGRF-14 field model; and 32 other sources. Every count in the abstract reproduced exactly from the authors' files, by two separately written readers: 244, 3,258 and 2,753 changed genes, and the single Gene Ontology term that survives correction. The check also found that the two fields shared one inclination of about 30°, which the page states. A fresh reviewer then re-checked the built page against the sources and the data with separate code. That check changed no verdict. It led us to reword our reading of the genes the two comparisons share, whose pattern chance alone produces; to relabel two rows of the recount table and add two; to correct the number of terms tested, our naming of the gene recorded as cryptochrome 2 and three rounded values; and to name the test behind the panel's statistics.

The verdicts and the items tagged "Our analysis" are our own assessment, built on the cited sources. They include the field along the route from IGRF-14, our recount and re-analysis of the authors' data, the regrouping and overlap tests, and our reading of the qPCR and emergence data. The comparison with the Laschamp excursion reuses our run of the LSMOD.2 model from our check of a mint study, and the excursion's pace our arithmetic on the 2026 rates paper; no verdict restates an earlier check.

We re-ran everything the open data allow, under eight sets of rules written and hashed in advance, seven before the data were available and the field-model rules before that script first ran: the counts, the enrichment tables, a re-analysis from the raw counts with two simpler methods, every regrouping of the samples, the measured fields, the qPCR, the emergence counts and the field along the route. Two analyses departed from their rules, as the hosted files record: the enrichment sheets don't let the adjustment be recomputed, so we report the smallest number of tests they imply; and the file doesn't say whether a time label starts or ends its interval, so we read it as the start (the other reading gives 92% for the controls). Three checks added after the data were seen, and a fourth check and two further counts added after the review, are labelled as such. We couldn't read the paper beyond its abstract, so its methods, figures and apparatus are unknown to us; Dryad refused our scripts, and the site's owner downloaded the data by hand.

This page was researched and written with Claude, an AI assistant made by Anthropic, and then re-checked against its sources in a separate verification pass.

The verdicts on this page

UNCONFIRMED	Rests on a preliminary result that hasn't been confirmed.
TRUE	The evidence supports the claim.

All ten verdicts, and how we check

CORRECTIONS

Corrections and changes

If we get something wrong, we fix it and record the change below with the date. If a correction changes a verdict, the log says what the old verdict was.

Change log

NOV 21, 2026	Published on factchecked.science after a full check against the sources and an independent review of the built page. The verdicts are those of our report on the authors' data; the paper's sentence on the near-zero field is quoted for its count, and its list of functions is discussed in section 4. The review changed no verdict; it led us to reword our reading of the genes the two comparisons share, relabel two rows of the recount table and add two, correct the number of terms tested and change the first claim's label from "Field steps match the route".

Fact-Checked Science is independent. It isn't affiliated with the channels, presenters or authors whose claims it checks.

Last updated Nov 21, 2026