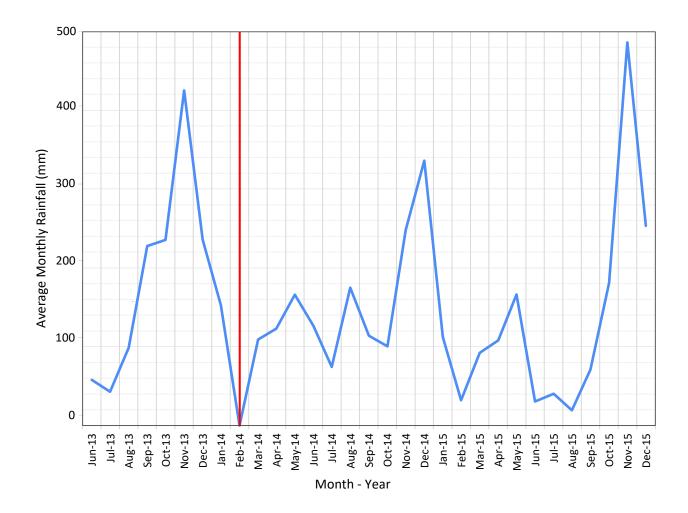
SUPPLEMENTARY MATERIAL

Higher understory vegetation complexity in oil palm plantations supports greater numbers of assassin bugs

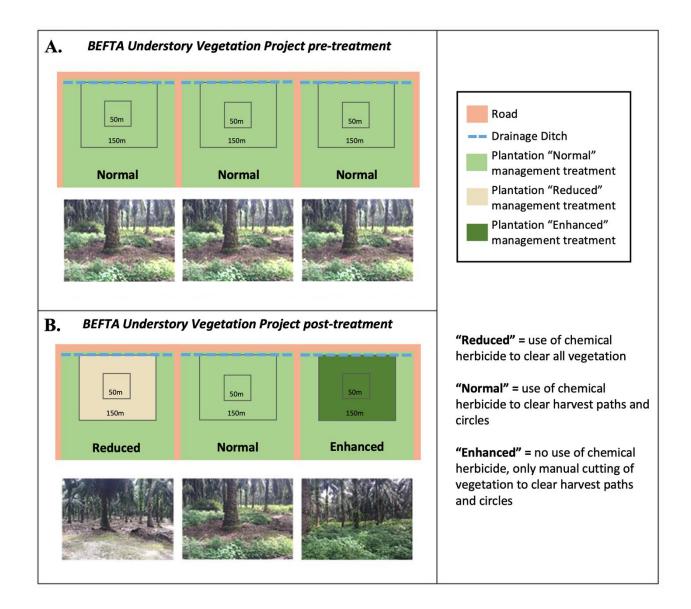
Jake Stone, Andreas Dwi Advento, Michael D. Pashkevich, Anak Agung Ketut Aryawan, Jean-Pierre Caliman, Amelia S. C. Hood, William A. Foster, Mohammad Naim, Pujianto, Dedi Purnomo, Suhardi, Ribka Sionita Tarigan, Tuani Dzulfikar Siguga Rambe, Rudy Harto Widodo, Sarah H. Luke, Jake L. Snaddon & Edgar C. Turner

Ecological Solutions and Evidence

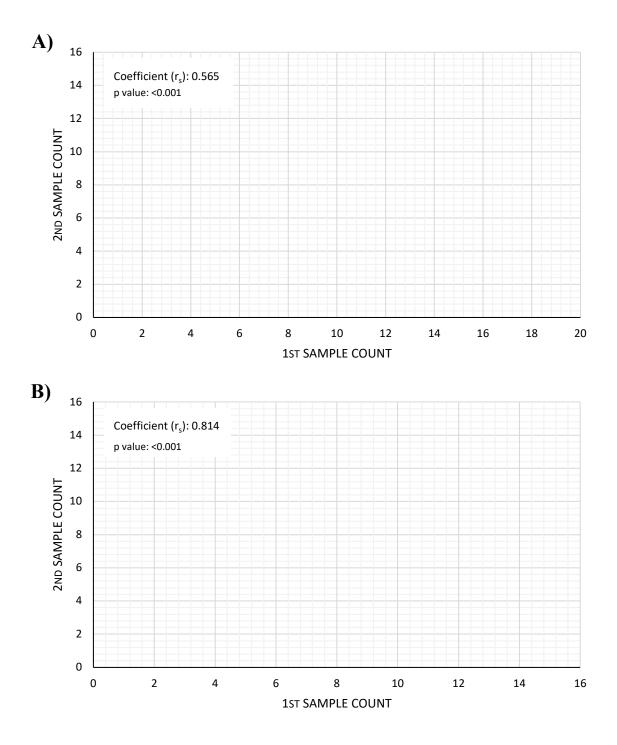
SUPPLEMENTARY FIGURES



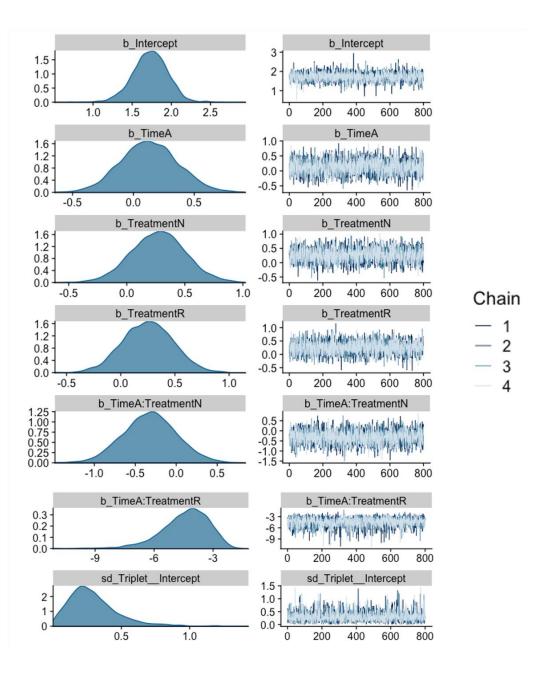
SUPPLEMENTARY FIGURE 1. Average monthly rainfall in millimetres (blue line) across the Kandista and Ujung Tanjung plantation estates, over the course of the study. Vertical green bars highlight the three sampling periods in which assassin bugs were recorded and the red line indicates when experimental treatments were implemented.



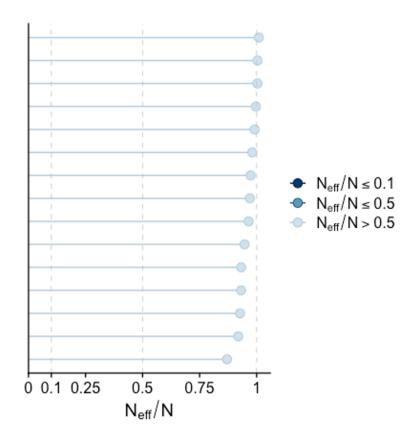
SUPPLEMENTARY FIGURE 2. Plot set up of the BEFTA Understory Vegetation Project. Each panel (**A and B**) represents a triplet of experimental plots. Each plot measures 150 x 150 m and contains a central 50 x 50 m core zone, where sampling took place. Each plot is located within the 300 m wide end of a 300 x 1000 m plantation block (note: plots and blocks are not drawn to the same scale). **Panel A** represents a single triplet pre-treatment when all plots were managed with the industry standard ("Normal") vegetation management. **Panel B** shows a single triplet post-treatment with each of the three management vegetation options represented ("Reduced", "Normal", and "Enhanced" vegetation). In each triplet the allocation of the three different treatments was assigned at random across plots. The photographs (credit: Julia Drewer) were taken two years after first treatments were implemented and give examples of what the understory vegetation looks like in each of the different treatment types. [This figure has been adapted, with the permission of original authors, from a figure included in Luke et al. (2020)].



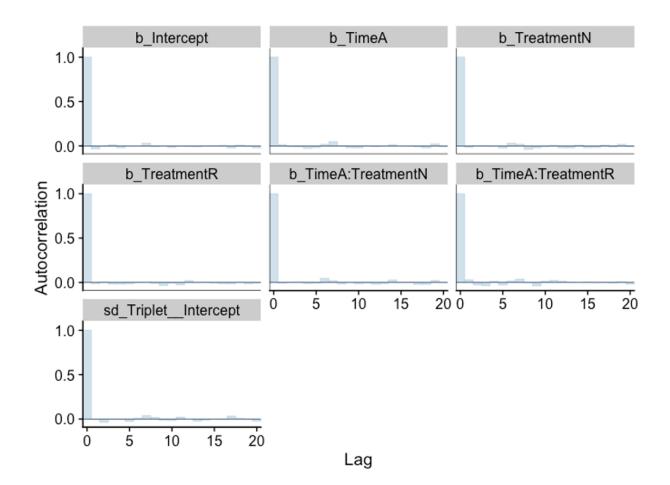
SUPPLEMENTARY FIGURE 3. Correlation plots to determine the relationship between repeat surveys of *Cosmolestes picticeps* and *Sycanus dichotomus*, with first sample count on x axis and second sample count on y axis. Blue circles correspond to counts at each of the 18 (six triplets) experimental plots; the darker the circle the greater the number of overlapping counts. Spearman's rank correlation coefficient along with the respective p value is stated in upper left-hand corner. **A**) Repeat sample counts from pre-treatment in September 2013, **B**) Repeat sample counts from post-treatment in September 2015. The stronger positive correlation in post-treatment counts (September 2015), suggests that treatment may be acting to reliably determine assassin bug numbers.



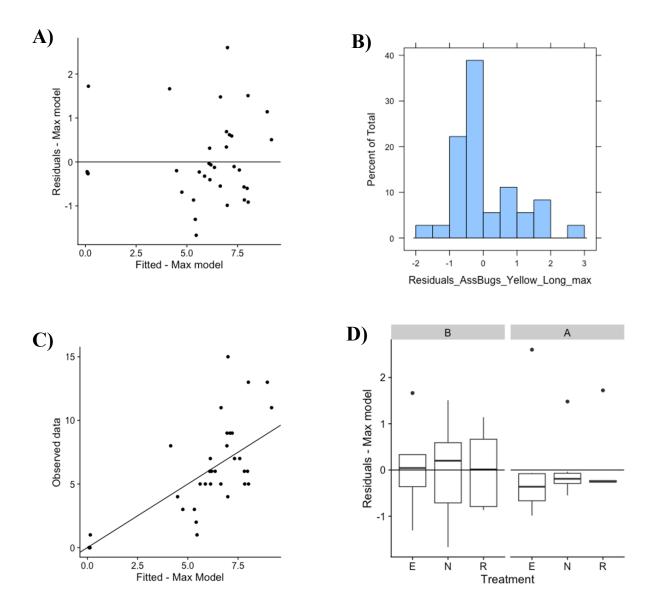
SUPPLEMENTARY FIGURE 4. Example of density (left) and trace (right) plots to determine that mixing of MCMC chains was good. Plots are shown for the max model that we fitted to analyse the long-term effects of the BEFTA-UVP treatments on numbers of *Cosmolestes picticeps* over time. The max model was: *Cosmolestes picticeps ~ Time*Treatment + (1 / Triplet)*, wherein *'Time'* is a categorical variable with two categories representing different sampling time points: after treatment in Sept 2015 'A' and before treatment in Sept 2013 'B', *'Treatment'* represents one of the three vegetation management types: Normal 'N', Reduced 'R' or Enhanced 'E' and *'Triplet'* represents six variables: 'UT₁', 'UT₂', 'UT₃', 'K₁', 'K₂', 'K₃', corresponding to the six triplets of BEFTA-UVP plots. We ran all models for 50000 iterations using four chains and a thinning rate of 10. Colours on trace plots represent the four chains we fitted.



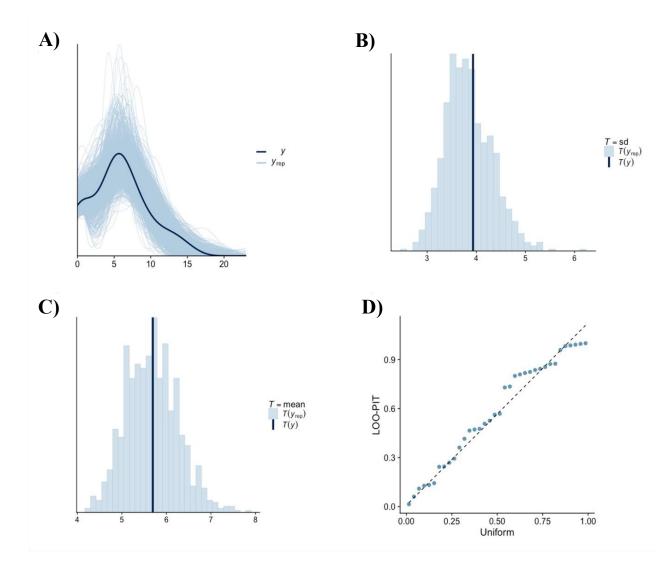
SUPPLEMENTARY FIGURE 5. Example visualisation of the "Eff. Sample" value, used to estimate the effective sample size. This value represents the number of independent samples from the posterior distribution that is needed to yield the same standard error of the posterior mean as is obtained from the dependent samples returned by the MCMC algorithm. Values of $N_{eff}/N > 0.5$ indicate that there are no issues. The plot is shown for the max model that we fitted to analyse the long-term effects of the BEFTA-UVP treatments on numbers of *Cosmolestes picticeps* over time. The max model was: *Cosmolestes picticeps* ~ *Time*Treatment* + (1 / *Triplet*), wherein '*Time*' is a categorical variable with two categories representing different sampling time points: after treatment in Sept 2015 'A' and before treatment in Sept 2013 'B', '*Treatment*' represents one of the three vegetation management types: Normal 'N', Reduced 'R' or Enhanced 'E' and '*Triplet*' represents six variables: 'UT₁', 'UT₂', 'UT₃', 'K₁', 'K₂', 'K₃', corresponding to the six triplets of BEFTA-UVP plots. We ran all models for 50000 iterations using four chains and a thinning rate of 10. Colours on trace plots represent the four chains we fitted.



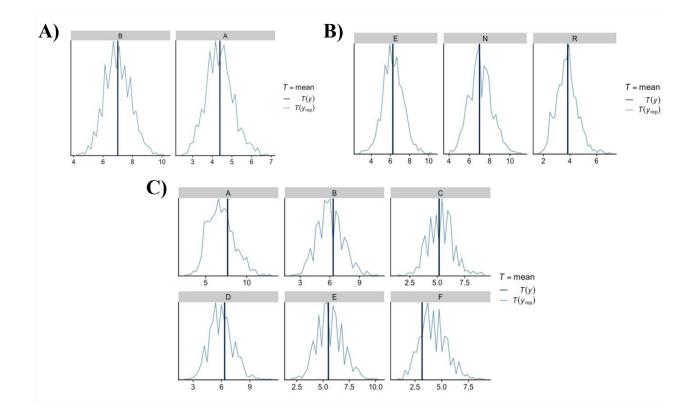
SUPPLEMENTARY FIGURE 6. Example visualisation to determine that that was no autocorrelation of the MCMC chains in our modelling. The immediate drop-off of the histograms for all parameters indicates that was no autocorrelation present. Plots are shown for the max model that we fitted to analyse the long-term effects of the BEFTA-UVP treatments on numbers of *Cosmolestes picticeps* over time. The max model was: *Cosmolestes picticeps ~ Time*Treatment + (1 / Triplet)*, wherein '*Time*' is a categorical variable with two categories representing different sampling time points: after treatment in Sept 2015 'A' and before treatment in Sept 2013 'B', '*Treatment*' represents one of the three vegetation management types: Normal 'N', Reduced 'R' or Enhanced 'E' and '*Triplet*' represents six variables: 'UT₁', 'UT₂', 'UT₃', 'K₁', 'K₂', 'K₃', corresponding to the six triplets of BEFTA-UVP plots. We ran all models for 50000 iterations using four chains and a thinning rate of 10. Colours on trace plots represent the four chains we fitted.



SUPPLEMENTARY FIGURE 7. Example diagnostic plots created during model validation. Plots include plotting model residuals versus fitted values (**A**), plotting the distribution of the model residuals (**B**), plotting the observed (i.e., raw) data versus model fitted values (**C**), and plotting the model residuals versus the fixed effects included in the model (**D**). For **A**), the cloud of points (i.e., no pattern or clustering, such as a funnel-shaped pattern) indicates no issues. For **B**), the normal distribution of the residuals indicates no issues. For **C**), that observed and fitted values generally track to each other indicates no issues. For **D**), the boxplots being clustered around the y = 0 line indicates no issues. Plots are shown for the max model that we fitted to analyse the long-term effects of the BEFTA-UVP treatments on numbers of *Cosmolestes picticeps* over time. The max model was: *Cosmolestes picticeps ~ Time*Treatment + (1 / Triplet)*, wherein '*Time*' is a categorical variable with two categories representing different sampling time points: after treatment in Sept 2013 'B', '*Treatment*' represents one of the three vegetation management types: Normal 'N', Reduced 'R' or Enhanced 'E' and '*Triplet*' represents six variables: 'UT1', 'UT2', 'UT3', 'K1', 'K2', 'K3', corresponding to the six triplets of BEFTA-UVP plots. We ran all models for 50000 iterations using four chains and a thinning rate of 10. Colours on trace plots represent the four chains we fitted.



SUPPLEMENTARY FIGURE 8. Example posterior predictive check plots created during model validation. Plots compare the distribution of our observed data (*y*) to posterior distributions from our model (y_{rep}) (**A**), the standard deviation of *y* to y_{rep} (**B**), and the mean of *y* to y_{rep} (**C**). For (**A-C**), that *y* tracks to y_{rep} indicates that there are no issues. Plot (**D**) is a qualitative check to determine that LOO-IC is an appropriate information criterion to use for model comparison. That the LOO-PIT values are approximately uniformly distributed indicates that there are no issues. Plots are shown for the max model that we fitted to analyse the long-term effects of the BEFTA-UVP treatments on numbers of *Cosmolestes picticeps* over time. The max model was: *Cosmolestes picticeps ~ Time*Treatment + (1 / Triplet)*, wherein '*Time*' is a categorical variable with two categories representing different sampling time points: after treatment in Sept 2015 'A' and before treatment in Sept 2013 'B', '*Treatment*' represents one of the three vegetation management types: Normal 'N', Reduced 'R' or Enhanced 'E' and '*Triplet*' represents six variables: 'UT₁', 'UT₂', 'UT₃', 'K₁', 'K₂', 'K₃', corresponding to the six triplets of BEFTA-UVP plots. We ran all models for 50000 iterations using four chains and a thinning rate of 10. Colours on trace plots represent the four chains we fitted.



SUPPLEMENTARY FIGURE 9. Example posterior predictive check plots created during model validation. Plots compare the mean of our observed data (T(y)) to posterior distributions from our model $(T(y_{rep}))$ for factor *Time* (**A**); T(y) to $T(y_{rep})$ for factor *Treatment* (**B**); and T(y) to $T(y_{rep})$ for factor *Triplet* (**C**). For (**A-C**), that T(y) tracks to $T(y_{rep})$ indicates that there are no issues. Plots are shown for the max model that we fitted to analyse the long-term effects of the BEFTA-UVP treatments on numbers of *Cosmolestes picticeps* over time. The max model was: *Cosmolestes picticeps* ~ *Time*Treatment* + (1 / *Triplet*), wherein '*Time*' is a categorical variable with two categories representing different sampling time points: after treatment in Sept 2015 'A' and before treatment in Sept 2013 'B', '*Treatment*' represents one of the three vegetation management types: Normal 'N', Reduced 'R' or Enhanced 'E' and '*Triplet*' represents six variables: 'UT₁', 'UT₂', 'UT₃', 'K₁', 'K₂', 'K₃', corresponding to the six triplets of BEFTA-UVP plots. We ran all models for 50000 iterations using four chains and a thinning rate of 10. Colours on trace plots represent the four chains we fitted.

SUPPLEMENTARY TABLES

SUPPLEMENTARY TABLE 1. Details of the BEFTA-UVP plots at which data were collected, includingestate name, triplet number, plot name, understory vegetation treatment (randomly allocated to the plot), and date (data provided by SMARTRI) that palms were planted within each plot.

Estate	Triplet	Plot	UV Treatment	Date Planted
Ujung Tanjung	1	C10	Reduced	1988
	1	C11	Enhanced	1988
	1	C12	Normal	1988
	2	C17	Enhanced	1989
	2	C18	Normal	1989
	2	C19	Reduced	1989
	3	D28	Enhanced	1989
	3	D29	Reduced	1989
	3	D30	Normal	1989
Kandista	4	F04	Enhanced	1992
	4	F05	Reduced	1992
	4	F06	Normal	1992
	5	G07	Enhanced	1992
	5	GO8	Normal	1992
	5	GO9	Reduced	1992
	6	G14	Reduced	1993
	6	G15	Normal	1993
	6	G16	Enhanced	1993

SUPPLEMENTARY TABLE 2. Models fitted to assess the effects of the BEFTA-UVP treatments on assassin bug numbers.

Long-term/short-term	Response variable	Model name	Model fitted
Long	Average number of <i>C. picticeps</i> per 50 x 50 m transect over two survey days	Max model	C. picticeps ~ Time*Treatment + (1 Triplet)
		Additive model	C. picticeps ~ Time + Treatment + (1 Triplet)
		Time only model	C. picticeps ~ Time + (1 Triplet)
		Treatment only model	C. picticeps ~ Treatment + (1 Triplet)
		Null model	C. picticeps ~ 1 + (1 Triplet)
Short	Average number of <i>C. picticeps</i> per 50 x 50 m transect	Max model	C. picticeps ~ Time*Treatment + (1 Triplet)
		Additive model	C. picticeps ~ Time + Treatment + (1 Triplet)
		Time only model	C. picticeps ~ Time + (1 Triplet)
		Treatment only model	C. picticeps ~ Treatment + (1 Triplet)
		Null model	C. picticeps ~ 1 + (1 Triplet)
Long	Average number of <i>S.</i> <i>dichotomus</i> per 50 x 50 m transect over two survey days	Max model	S. dichotomus ~ Time*Treatment + (1 Triplet)
		Additive model	S. dichotomus ~ Time + Treatment + (1 Triplet)
		Time only model	S. dichotomus ~ Time + (1 Triplet)
		Treatment only model	S. dichotomus ~ Treatment + (1 Triplet)
		Null model	S. dichotomus ~ 1 + (1 Triplet)
Short	Average number of <i>S.</i> <i>dichotomus</i> per 50 x 50 m transect	Max model	S. dichotomus ~ Time*Treatment + (1 Triplet)
		Additive model	S. dichotomus ~ Time + Treatment + (1 Triplet)
		Time only model	S. dichotomus ~ Time + (1 Triplet)
		Treatment only model	S. dichotomus ~ Treatment + (1 Triplet)
		Null model	S. dichotomus ~ 1 + (1 Triplet)