

Supplementary Information for

The demise of caterpillar fungus in the Himalayan region due to climate change and overharvesting

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Supplementary Information Text

Supplementary Methods

Systematic literature review

We conducted a systematic review of the literature on caterpillar fungus (1). To identify papers for inclusion, on March 6, 2017, we searched Web of Knowledge for the terms "*Ophiocordyceps sinensis*" and "*Cordyceps sinensis*" (its former Latin name) and filtered out research categories not related to environmental or social topics, which eliminated most of the pharmacological studies that otherwise dominated the search results. This produced 54 papers for "*Ophiocordyceps sinensis*" and 200 papers for "*Cordyceps sinensis*." We scanned titles and abstracts to further eliminate papers about its artificial cultivation, medical studies, and other species of *Cordyceps*. We then supplemented this with searches on Google Scholar, the China National Knowledge Infrastructure database, the Digital Library of the Commons, and with content alerts from Google Scholar for these search terms, which continued to update results through December 31, 2017. Additional publications were the result of "snowball sampling" from the references cited in other papers. In total, these searches produced 396 papers, books, reports, theses, and presentations that contained information about the caterpillar fungus social-ecological system, published between 1723‒2017, and written in English, French, German, Chinese, or Japanese. Publications in English and French were read by the first author, and publications in other languages were translated by native or fluent speakers.

Of the 396 publications, we identified 73 that reported trends in its production. To focus on sources of LEK, we filtered out studies that were based on model results or harvest amounts without supporting LEK $(n = 12)$, and those that were author assertions, including sources that did not clearly differentiate whether a statement was LEK or the author's own interpretation (*n* = 13). We also excluded studies that did not describe any methods for obtaining LEK $(n = 14)$, that only repeated results from earlier studies ($n = 4$), or that were too unclear to interpret confidently ($n = 1$). This left 29 studies with information about LEK of caterpillar fungus production trends and their causes.

Local ecological knowledge

We conducted interviews about local ecological knowledge (LEK) of caterpillar fungus production trends during the 2017 harvest season in collection areas in Rebgong county, Qinghai and in Damshung county, Tibet; in caterpillar fungus markets in Xining and Rongbo, Qinghai, Lhasa and Damshung, Tibet, and Chengdu, Sichuan; and in person or by phone with others identified through our network of collaborators and respondents. All interviews were conducted in the local dialect of Tibetan by a native speaker except one in Mandarin and three in English with interviewees who were also fluent in those languages. Of the 49 interviewees, 12 were female (24.5%) and 37 were male (75.5%), and all were ethnically Tibetan. On average, they had been involved in the caterpillar fungus trade for a mean of 16.9 years and median of 18 years (st. dev. = 10.2 years; 4 people did not give responses about their involvement time). Twenty-two people (45%) had been involved with it for 20 years or longer, while only 11 people (22%) had less than a decade of experience. Three men had started collecting it as early as the 1970s. For interviews that occurred outside of collection areas, we recorded the location of the collection area to which they were referring.

In addition to our 49 interviews, we included 10 studies with clearly stated sample sizes and quantitative LEK responses ($N = 768$ interviewees), 6 studies with clearly stated sample sizes but only qualitative LEK information that may not have been from their full sample of interviewees ($N = 3919$), and 13 studies with only qualitative LEK information and no stated sample size. For these studies and our interviews, we used a combination of a priori and emergent codes to classify LEK of changes in caterpillar fungus production and their causes (Table S3). A priori codes included responses about trends and causes that we anticipated encountering and/or wanted to examine from the outset (*e.g.*, "increasing," "decreasing," "climate change," "overexploitation," "competition"). Emergent codes arose as we began to read the LEK responses and found other frequently mentioned themes that did not fit easily into our a priori categories (e.g., "fluctuating," "unsustainable," "weather" distinct from broader climate trends). We ensured that two coders reached consensus on code designations for each study before proceeding with analysis. We assigned confidence weightings to all LEK data as follows. For our interviews, we

weighted responses by the number of respondents within each county (see sample sizes in Table S4). For data from the literature, quantitative studies with clearly stated sample sizes (all of which were larger than the largest number of people we interviewed per county) were assigned the largest weighting from our interviews (i.e., 16), and all others for which the exact number of respondents was unclear were assigned the smallest weighting from our interviews (i.e., 1).

We organized LEK data spatially at the level of county (China), gewog (Bhutan), or district (Nepal and India). We define the timing of the LEK data as the latest year in which field data were collected for each study. To understand spatial trends, we consider only data collected within the past decade (2008–2017) as indicative of contemporary LEK. To understand temporal trends, we fit quasibinomial regressions to data from all years (1999–2017), but removed one study for which the year of data collection was unclear. For 4 studies that described a qualitative response across 2-3 administrative units (e.g., counties), we displayed these responses across all relevant administrative units when examining spatial trends, but used only one response per study when examining temporal trends in order to avoid weighting them disproportionately.

Few of the published studies were explicitly designed to investigate LEK of caterpillar fungus production, and many had limitations due to unclear methods or results with regard to our aims. In the case of our interviews, sample sizes for specific areas tended to be low, given our opportunistic sampling of people from diverse areas encountered at regional markets. Recognizing these caveats, we consider the broader regional picture that emerges from these data, rather than relying on them as strong evidence for the changes occurring in any particular location.

Species distribution modeling

We obtained caterpillar fungus presence points for the species distribution models by extracting caterpillar fungus location data from all publications in our review that included spatial information for occurrence points or collection areas. Each point underwent a quality control check to ensure accuracy of the input data. From each publication, we either used coordinates reported, asked authors to provide

location details, or digitized figures with maps. Administrative boundaries, village locations, roads, rivers, and graticules served as reference points for georectifying the maps. We calculated the root mean square error (RMSE) between reference points and digitized figures. Fine-scale locational errors have been found to have minimal effect on model performance, particularly for presence-background approaches such as ours (described below) (2, 3). Still, precise georecification can provide slight improvements when modeling more specialized species and when using predictor variables derived from empirical data such as elevation (as opposed to modeled surfaces) (4, 5). After removing 2 publications for which precise georectification was not possible $(RMSE > 1000 \text{ m})$, the mean RMSE across all digitized figures was 293 m (but dropped to 278 m if only considering publications with data used in the final models, after performing all quality control steps described in more detail below). If maps showed collection area boundaries instead of point locations, we reduced uncertainty caused by digitization error by first creating an inverse buffer within the collection area equal to the RMSE distance for that figure. Then, we subtracted the buffer area from the original collection boundary and generated a random point within the remaining area.

To prevent inclusion of erroneous caterpillar fungus locations in our models, we inspected all presence points using high-resolution imagery in Google Earth. Of the 561 points intended to denote collection areas, we removed 108 because they were in settlements, dense forests, lakes, or other highly improbable locations. We maintained a strict removal criterion for points within 1 km of towns to prevent apparent convenience sampling on the part of study authors from biasing our models toward lower elevations. We removed 2 duplicate points and an additional 36 that had imprecise or incorrect locations, as indicated by low precision of their coordinates, our difficulty rectifying source images from the literature (RMSE > 1 km), or if they had very different elevations from what was reported for them in the source data. These disqualification criteria removed 70 of the 218 locations (32%) reported by Yan et al. (6). Our final caterpillar fungus location dataset is available at https://purl.stanford.edu/ww909xk7776.

We restricted our analyses to elevations between 3000–5500-m a.s.l., given caterpillar fungus' reported distribution range (7, 8). Although there were a few points in Gansu and northeastern Qinghai below 3000 m that may have been credible $(2700-2860 \text{ m})$ $(9, 10)$, all others below this range did not meet the quality control criteria. Moreover, Li et al. determined that the lowest confirmed *O. sinensis* specimen was found at 3,084 m (7), which suggests that reports of lower locations should be viewed with skepticism until they can be verified. The highest location was at 5500 m in Arunachal Pradesh, India (8).

Our environmental predictor variables included elevation, MODIS Vegetation Continuous Fields, and CHELSA bioclimatic variables (Table S5). To maintain parsimony and ecological relevance, we developed a decision tree and used insights from LEK to select variables for inclusion in the model that avoided ecological redundancy and highly correlated variables (11, 12) (Fig. S4, S5). To prepare the predictor variables for use in the Software for Assisted Habitat Modeling (SAHM) (13), we masked water pixels and computed 17-year means (2000–2016) for all MODIS data of percent non-tree vegetation, nonvegetated, and tree cover. To match the spatial resolution of the elevation and MODIS data, we resampled the 19 bioclimatic predictor variables to 250-m using a nearest neighbor interpolation within SAHM. We removed all highly correlated variables from the models, but based on the importance of winter precipitation that emerged from our review of caterpillar fungus LEK, we decided to retain mean precipitation of the coldest quarter, despite its correlation with precipitation of the wettest quarter being above our 0.70 correlation cutoff $(r = 0.72)$.

As a final processing step, we removed presence points if they fell outside the bounds of the predictor layers ($n = 2$) or in the same pixel as another point ($n = 13$), leaving 400 presences. To reduce the effect of sampling bias in our presence data, we generated 400 random pseudo-absence points within a binary kernel density estimator surface with a 99% isopleth and ad hoc optimization method (14).

Then, we used the point data and environmental variables to develop habitat predictions from four models: boosted regression trees (BRT) (15), random forest (RF) (16), multivariate adaptive regression splines (MARS) (17-19), and a generalized linear model (GLM) (20). Each of these models is widely used in the species distribution modeling literature, well-documented, and able to be run in opensource R programming language. BRT is an ensemble classifier that can be understood as an additive

regression model, with the advantages of being able to fit complex nonlinear relationships, automatically handle interaction effects between predictors, and requires no prior data transformation (15). RF is a popular ensemble classifier and has been shown to be highly accurate and efficient with highdimensional, multi-source data sets (21, 22). MARS is a non-parametric technique that fits piecewise logistic regressions to build a flexible model (23). It is similar to generalized additive models, but is faster and offers improvements for models of a single species (19). GLM is the simplest and most interpretable of the four models, and its implementation in SAHM uses a bidirectional, stepwise covariate selection procedure to identify a parsimonious model (23). For MARS and GLM, we used the default settings in the SAHM package (23). For BRT, we set *n trees* = 1000 (15) and used SAHM's internal settings to determine the learning rate and other parameters (23). For RF, we set *n trees* = 500 (22) and used the tuneRF function to determine the *mTry* value that minimizes out-of-bag prediction error (24).

The primary output from each model is a continuous raster surface showing the relative likelihood of caterpillar fungus occurrence for each 250-m cell. To convert this to a discretized (binary) map as an input for further analysis, we applied a statistically-determined threshold based on maximizing the sum of sensitivity and specificity (25). We evaluated model predictions using a 10-fold crossvalidation on the discretized maps. This generated a suite of evaluation statistics, including area under the receiver operator characteristic curve (AUC) (26), percent correctly classified, sensitivity, specificity, and the true skill statistic (TSS) (27). We calculated variable importance scores for the predictor variables included in each model using a model-independent method in SAHM, whereby the change in AUC is recorded when each variable is successively permuted between the presence and background data (23). A larger change in AUC indicates a larger influence. We then converted the AUC differences into values of relative importance. Finally, we created a multivariate environmental similarity surface (MESS) map to identify areas where the models were extrapolating beyond the training data (28).

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Permafrost comparison

The 30-arcsecond modeled permafrost distribution data, which we compared to our caterpillar fungus locations and habitat predictions, are scaled from 0 to 1 and interpreted as ranging from permafrost occurring "only in very favorable conditions" (e.g., only with a sufficient combination of appropriate radiation exposure, snow drift, vegetation, ground material, etc.) to occurring "in nearly all conditions," regardless of ideal solar radiation, etc. (29). Using a threshold of 0.5, we considered areas above this level to be "likely" to have permafrost, and areas below this threshold to be "unlikely" to have it. We then calculated the proportion of presence points and habitat area located in likely permafrost area, as well as the mean geodesic distance between all presence points and their nearest areas likely to have permafrost. For the distance calculation, we excluded 69 presence points in Gansu, Sichuan, and Yunnan prefectures in China, since these prefectures had little likely permafrost according to our 0.50 threshold and other estimates of permafrost extent in China (30).

Environmental determinants of caterpillar fungus production

If collection data for multiple years were available, or if a range of values was reported, we took the mean value for each administrative unit. For Nepal and Bhutan, we only used data starting at least two years after collection became legal (in 2001 and 2004, respectively) to ensure that we were not capturing a potential "spin-up" time, when collection effort may have been lower and thus less representative of true production amounts. For China, we included data from official reports starting in 2000, due to China's longer history of legal collection. Had we limited China to data starting in 2003, to match the timing for Nepal, the final production level calculations would not have resulted in different production bin assignments, so we opted to retain more years of data for calculating means. We discarded data from years with a known impediment to collection or reporting, such as when snow hindered access to harvesting areas, years when collectors in Bhutan were allowed to sell outside the official auction system, or when official statistics underestimated collection amounts relative to field data gathered by researchers (31, 32). We did not include data that were the result of study authors'

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calculations (e.g., Winkler's estimates for large areas of Nepal and India (33)). In cases where no other data were available (i.e., Qinghai, Sichuan, and Gansu in China and Humla, Jumla, Mugu, and Kalikot in Nepal), we included collection amounts from the literature that were provided without a well-defined source, but only if the context of the publication suggested that these were from within our acceptable timeframe for each country. We treat these with more caution in our interpretation of subsequent analyses using these data.

In China, three prefectures had collection data at the county level that met our quality control criteria. For Nagchu, Chamdo, and Nyingtri, county data from specific years allowed us to calculate the proportion of caterpillar fungus in those counties relative to the total for their prefecture in that same year. We then used these proportions to calculate the average amount collected in those counties based on the multi-year prefectural mean (2000-2009).

To calculate production level for each administrative unit, we divided mean collection amounts $(kg yr⁻¹)$ by the area of habitat $(km²)$ predicted by the ensemble of our four species distribution models. Due to the uncertainty associated with the production and area estimates, we used tertiles to bin the production level data into categories of "low", "medium", and "high."

We performed ordered logistic regressions on binned production data with environmental variables selected by the majority of species distribution models as predictors. This ensured that we included factors thought to be relevant to caterpillar fungus growth, based on insights from the species distribution models and a priori information from the literature and LEK, thereby avoiding "a 'shot-gun' attempt to find significant variables" (34). For bioclimatic variables, we followed the methods described below to derive a customized climate data set and then calculated mean conditions for each pixel from 2000-2013, corresponding to the time period of the collection data. For each predictor variable, we calculated its mean across the predicted habitat area in each administrative unit. Using the polr function in the MASS package in R (35, 36), we ran regressions with a logistic link function on all combinations with three or fewer predictors, excluding highly correlated $(r > 0.70)$ and collinear (VIF > 5) variables. We limited each model to a maximum of three predictors to avoid over-fitting to our relatively small data

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set $(N = 33$ administrative units). We used Akaike information criterion scores corrected for small samples (AICc) (37) and log-likelihood tests to assess model performance and parameter significance. We present several models with similar AICc scores (ΔAICc < 2 from the model with smallest AICc) to avoid some of the bias associated with selecting a single, minimum adequate model (34), while also prioritizing model parsimony and generalizability (38).

Climate change trends

To assess changes in climatic conditions likely to affect caterpillar fungus, we conducted pixelwise linear regressions through time (1979–2013) for each climate variable (39). For this we calculated annual bioclimatic variables equivalent to those used in the species distribution models and logistic regression analyses, using monthly CHELSA precipitation and temperature data from 1979-2013 (40) and the "biovars" function in the dismo package in R (41).

We conducted all analyses in R (v. 3.4.3) and created all maps in R and ArcGIS (v. 10.5.1).

Fig. S1. Species distribution models indicate where the likelihood of caterpillar fungus occurrence is highest. Caterpillar fungus presence points $(N = 400)$ used as inputs to the models are shown in (a). Results from four models are shown: generalized linear model (b), multivariate adaptive regression splines (c), boosted regression tree (d), and random forest (e).

Fig. S2. Four species distribution models identified relationships between suitable caterpillar fungus habitat and environmental conditions. Response curves are shown for environmental variables selected by the models (a): generalized linear model (GLM), multivariate adaptive regression splines (MARS), boosted regression tree (BRT), random forest (RF). Relative importance scores for each variable are determined from a model-independent comparison of the relative influence of each predictor in each model (b). Predictor variables are: $Bio_16 = precipitation$ of the wettest quarter, $Bio_19 = precipitation$ of the coldest quarter, NonVeg = non-vegetated cover, elevation, Bio_11 = mean temperature of the coldest quarter, Bio 15 = precipitation seasonality, Bio 3 = isothermality.

Fig. S3. Caterpillar fungus habitat and production are constrained by climate. Logistic regressions predict that production increases with colder winter temperatures (Bio_11) and higher elevations (a). "NA" denotes areas with elevation or temperature values beyond the range of the data included in the model, which were based on administrative units' mean conditions from 2000-2013. Mean climatic conditions from 1979-2103 are shown for Bio_11 (b), Bio_19 (d), and Bio_16 (f). The total amount of change from 1979-2013 for Bio_11 (c), Bio_19 (e), and Bio_16 (g) is shown for pixels with significant linear trends (*p* < 0.05).

Fig. S4. Decision tree for selecting variables to retain in the species distribution model. Due to the study region's monsoon climate, BioClim variables could be grouped into highly correlated seasonal categories, with "warmest" and "wettest" time periods roughly corresponding to summer conditions, and "driest" and "coldest" corresponding to winter.

Fig. S5. Correlation matrix of all environmental variables considered as candidates for inclusion in the species distribution models, arranged to show clusters of highly correlated variables. Environmental data were extracted for each of the 400 caterpillar fungus presence points used in these models. Following the criterion used by SAHM, the maximum of Spearman, Pearson, and Kendall coefficients are displayed. Coefficients $> |0.70|$ are in white. (NonVeg = % non-vegetated cover, Bio_2 = mean diurnal temp range, Bio_4 = temp seasonality, Bio_3 = isothermality, Bio_15 = precip seasonality, Bio_5 = max temp warmest month, Bio $8 =$ mean temp wettest quarter, Bio $10 =$ mean temp warmest quarter, Tree = % tree cover, Bio 9 = mean temp driest quarter, Bio 1 = annual mean temp, Bio 6 = min temp coldest month, Bio_11 = mean temp coldest quarter, NonTreeVeg = % non-tree vegetation cover, Bio_12 = annual precip, Bio 18 = precip warmest quarter, Bio 13 = precip wettest month, Bio 16 = precip wettest quarter, Bio 19 = precip coldest quarter, Bio 14 = precip driest month, Bio 17 = precip driest quarter.)

Table S1. Species distribution model evaluation statistics on test data and total predicted habitat area are shown for four models: generalized linear model (GLM), multivariate adaptive regression splines (MARS), boosted regression tree (BRT), and random forest (RF). Total predicted habitat area refers to the area of pixels generated by binary thresholding of the continuous likelihood surface produced by each model. The percentage of habitat in extrapolated areas is the proportion of the predicted habitat that fell within areas where the model was extrapolating to environmental characteristics beyond those sampled by the presence and background point locations.

Table S2. Model comparison of environmental effects on caterpillar fungus production using ordered logistic regression. Model fit statistics are shown for the best-fitting models (ΔAICc < 2 from the model with smallest AICc). For the null (intercept-only) model, $AICc = 76.63$, $AIC = 76.51$, $BIC = 79.50$, and log likelihood $= -36.25$. *P*-values for each coefficient are from likelihood ratio chi-square tests. Coefficients' standard errors are shown in parentheses.

	Model 1	Model 2	Model 3
Bio_111	$-1.10(0.29)$ ***	$-1.01(0.27)$ ***	$-0.88(0.241)$ ***
E levation ²	$0.42(0.21)$ *	$0.45(0.21)^{*}$	
Bio_19^3	$-0.02(0.01)$		$-0.02(0.01)^{*}$
AICc	59.98	60.52	61.96
AIC	59.33	60.09	61.54
BIC	66.81	66.08	67.52
Log likelihood	-24.67	-26.04	-26.77
Deviance	49.33	52.09	53.54
Pseudo R^2	0.57	0.52	0.49
Num. obs.	33	33	33

****p* < 0.001, ***p* < 0.01, **p* < 0.05

 1 Bio_11 = mean temperature of the coldest quarter

² Elevation was rescaled (m/100) to improve model performance

 3 Bio_19 = precipitation of the coldest quarter

Table S3. Description of codes assigned to local ecological knowledge of trends in caterpillar fungus production and their causes.

Table S4. Data sources and responses for local knowledge of changes in caterpillar fungus production. For changes and their causes, percentages of the number of people who gave each response are reported if quantitative data were available; otherwise, qualitative responses are shown. Percentages for causes add to more than 100% if interviewees gave more than one response. Shaded rows denote data that were collected entirely before 2008 and are therefore not displayed in Fig. 2. If the year in which the data were collected was unclear, we give an assumed year based on the publication date or other methods described by the study authors.

* For place names we use spellings from the Tibetan and Himalayan Library (http://www.thlib.org), except in several places where a different transliteration is more commonly used. Chinese names in pinyin are given in parentheses where they differ from the Tibetan. TAR = Tibet Autonomous Region.

† Sample sizes not in parentheses reflect the number of people who specifically responded to questions about caterpillar fungus change and its causes. Sample sizes in parentheses denote studies that listed the total sample size of interviewees, but gave only a generalized response about the changes they reported; therefore, the actual number of responses may have been lower than the total sample. If studies reported generalized responses without specifying any sample size for their interviews, the cell is left blank.

‡ Proportional responses were given, but they were reported in a way that prevented attributing exact percentages to our codes. For Shrivastava et al. (45), overexploitation and degradation were reported together. For Shrestha and Bawa (67), interviewees selected multiple types of climate change, making it impossible to accurately assign a total percentage of people who observed "climate change" as a general category. Therefore, we treat these cases as qualitative responses that are equally divided between "overexploitation" and "degradation" in the former case and "climate change" and "overexploitation" in the latter, with a low-confidence weighting for each, given our uncertainty in the true proportions.

** Data collected through interviews as part of this current study.

Table S5. Candidate variables for inclusion in caterpillar fungus species distribution models. Those without a justification description were removed based on the variable selection decision tree (Fig. S4).

Table S6. Mean caterpillar fungus collection quantity and habitat area are shown by administrative unit. Habitat area is derived from the ensemble of the 4 species distribution models. The "QC" codes indicate quality control levels*. Shaded rows designate data that were not used in the logistic regression either because they were not the best available for that administrative unit, or in the case of Dingxi prefecture and Kalikot district, because the production level results were implausibly high outliers in the model. If the collection year was unclear, we give an assumed year or range based on the publication date or other methods described by the study authors.

* Quality control levels: "1" indicates preferred data, with the original source and collection year clearly stated. "2" indicates the best-available data, despite the original source and/or collection year not being clearly stated. "3" indicates data that were not used because the original source and/or collection year were not clearly stated, and level 1 data were available for that administrative unit instead. "4" indicates counties in Gansu prefecture for which collection data were given for a subset of townships within the

county; since Chinese township boundaries are not available, caterpillar fungus habitat areas could be not calculated.

† We use place name spellings from the Tibetan and Himalayan Library (http://www.thlib.org), except in several places where a different transliteration is more commonly used. Chinese names in pinyin are given in parentheses where they differ from the Tibetan. $TAR = Tibet$ Autonomous Region.

‡ 2016 caterpillar fungus auction data are from Bhutan's Department of Agricultural Marketing and Cooperatives, sent by Sonam Wangdi in an email to K. Hopping on April 16, 2017.

** A study published after the completion of our data analysis reported that 384.1 kg of caterpillar fungus was collected in Darchula district, Nepal in 2014 (107). Including this additional year of data would change the mean collection amount for Darchula to 403 kg yr⁻¹, at a density of 0.534 kg km⁻² yr⁻¹.

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