

The insect-focused classification of fruit syndromes in tropical rainforests: an inter-continental comparison

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SUPPLEMENTARY INFORMATION

SUPPLEMENTARY- TABLES

TABLE S1. Syndrome categories for the entomology system. Codes refer to Table 1. Data are based on the rearing of ca 56,000 insects from seeds originating from Panama, Thailand and Papua New Guinea.

Syndrome	Insect taxa typically reared	Life history interpretation
E-A1.1	Lycaenidae	Female oviposits a single egg in fleshy fruit; large pulp-feeding larva
E-A1.2	Scolytinae, Tephritidae, Blastobasidae, Cosmopterigidae, Tortricidae	Female oviposits multiple eggs in fleshy fruit; high numbers of pulp-feeders and seed-eaters reared
E-A2.1	Baridinae	Female oviposits one or a few eggs; specialized pulp-feeders/seed-eaters often reared
E-A2.2	Sesiidae, Curculionidae	Female oviposits one or a few eggs; specialized seed-eaters often reared
E-B1	Nitidulidae, Drosophilidae, Stratiomyidae, Crambidae	Multiple oviposition events probable in fast-rotting fruits; scavengers and fungal-feeders often reared
E-B2	Anobiidae, Bruchinae, Curculionidae, Drosophiliade, Stratiomyidae,	Multiple oviposition events probable in high-resource fruits attacked before dispersal;
	Blastobasidae, Gelechiidae, Pyralidae, Tineidae	High numbers of insects reared, particularly Lepidoptera
E-C1	None specifically	Few insects reared as resources are limited
E-C2	Anthribidae	Larvae may feed on seeds and capsule before dispersal

TABLE S2. Salient characteristics of study sites, and plant, seed and insect variables measured across sites. Means are reported with se in brackets and p values refer to Kruskal-Wallis tests. Plot data are from Anderson-Teixeira *et al.* (2014) and Basset *et al.* (2018).

Variable	BCI	KHC	WAN	p
Site physiognomy and structure:				
Coordinates	9.15°N, 79.85°W	7.54°N, 99.80°E	5.24°S, 145.08°E	-
Elevation (m)	120-160	120-330	90-180	-
Annual average rainfall (mm)	2551	2665	3366	-
Annual average daily maximum air temperature (°C)	26.3	27.1	26.5	-
Average length of the dry season (days)	136	120	141	-
Total plant species in plot/% of spp. with fruits collected	499/99	802/45	748/45	-
% of plant spp. as trees/shrub/palm/liana/herb species	40/31/2/25/2	80/1/7/11/1	92/2/4/2/0	-
Plant samples:				
Years of collection	2010-2013	2013-2015	2013-2015	-
Total number of seeds or fruits collected	208,508	39,252	122,976	-
Total weight of samples (kg)	380.2	343.2	439.9	-
Mean sample fresh weight (g)	40.6 (0.5)	174.3 (5.9)	116.2 (1.9)	<0.001
Average fruit fresh weight (g)	25.6 (5.0)	18.3 (3.1)	11.4 (1.3)	<0.001
Average seed length (mm)	39.7 (2.4)	28.0 (1.1)	22.3 (0.9)	<0.01

47 TABLE S3. Plant families surveyed at the three study sites. **Denotes eight focal plant
 48 families with wide distributions and ***indicates two plant families present only at a single
 49 site.

Plant Family	Study plot / number of plant species				Comments
	BCI	KHC	WAN	Total	
Acanthaceae	3			3	
Achariaceae		1	1	2	
Anacardiaceae	5	5	7	17	
Annonaceae	11	33	16	60	BCI, KHC, WAN **
Apiaceae		1		1	
Apocynaceae	13	3	6	22	
Araceae	7	1	2	10	
Araliaceae	2	1	3	6	
Arecaceae	13	25	8	46	BCI, KHC, WAN **
Aristolochiaceae	2		1	3	
Asparagaceae		1	2	3	
Asteraceae	1			1	
Bignoniaceae	22			22	BCI***
Bixaceae	1			1	
Boraginaceae	4			4	
Brassicaceae			2	2	
Bromeliaceae	1			1	
Burseraceae	6	2	5	13	
Cactaceae	1			1	
Cannabaceae		1	2	3	
Capparaceae	1			1	
Caricaceae	2			2	
Celastraceae	7	3	6	16	
Chrysobalanaceae	4	1	1	6	
Clusiaceae	12	10	2	24	BCI***
Combretaceae	8	3	6	17	
Connaraceae	5	2		7	
Convolvulaceae	1	1		2	
Cucurbitaceae	4	1	2	7	
Dichapetalaceae	1		1	2	
Dilleniaceae	8	2		10	
Dioscoreaceae		1		1	
Dipterocarpaceae		7	1	8	
Ebenaceae	1	12	4	17	KHC***
Elaeocarpaceae	1		6	7	
Erythroxylaceae		1		1	
Escalloniaceae		1		1	

Euphorbiaceae	14	15	16	45	BCI, KHC, WAN **
Eupomatiaceae			1	1	
Fabaceae	70	13	15	98	BCI, KHC, WAN **
Fagaceae		7		7	
Gentianaceae		1		1	
Gnetaceae	1	1	6	8	
Heliconiaceae	1			1	
Icacinaceae			2	2	
Irvingiaceae		1		1	
Lamiaceae		2	7	9	
Lauraceae	9	4	13	26	BCI, KHC, WAN **
Lecythidaceae	2	2	5	9	
Loganiaceae	4	1	3	8	
Lythraceae	2	2	1	5	
Magnoliaceae		1		1	
Malpighiaceae	16			16	
Malvaceae	18	11	6	35	
Marantaceae	1	1	2	4	
Marcgraviaceae	1			1	
Melastomataceae	10	2	1	13	
Meliaceae	7	22	33	62	BCI, KHC, WAN **
Menispermaceae	5		2	7	
Monimiaceae	3		1	4	
Moraceae	20	20	32	72	
Musaceae		1		1	
Myristicaceae	3	4	19	26	WAN***
Myrtaceae	12	6	11	29	WAN***
Nyctaginaceae	2		1	3	
Ochnaceae	1			1	
Olacaceae	3			3	
Oleaceae			1	1	
Opiliaceae		1		1	
Oxalidaceae		1		1	
Pandaceae			1	1	
Pandanaceae		1	3	4	
Passifloraceae	3			3	
Pentaphylacaceae			1	1	
Phyllanthaceae		18	3	21	KHC***
Picramniaceae	1			1	
Piperaceae	1			1	
Pittosporaceae			1	1	
Poaceae	2	1		3	
Polygalaceae	1	2	1	4	
Polygonaceae	5			5	
Primulaceae	4	4	1	9	
Proteaceae			1	1	

Putranjivaceae		2	1	3	
Rhamnaceae	4	1		5	
Rhizophoraceae	1		1	2	
Rosaceae			1	1	
Rubiaceae	37	27	23	87	BCI, KHC, WAN **
Rutaceae	4	2	1	7	
Salicaceae	13	2	4	19	
Sapindaceae	26	6	16	48	BCI, KHC, WAN **
Sapotaceae	7	3	2	12	
Simaroubaceae	2	2	1	5	
Smilacaceae	3	1	1	5	
Solanaceae	10			10	
Staphyleaceae	1			1	
Stemonuraceae			2	2	
Theaceae			1	1	
Thymelaeaceae		1	1	2	
Toricelliaceae		1		1	
Ulmaceae	5			5	
Unidentified		46		46	
Urticaceae	4		1	5	
Verbenaceae	3			3	
Violaceae	3	1		4	
Vitaceae	3	1	4	8	
Vochysiaceae	1			1	
Zingiberaceae	1		1	2	
Total	497	360	335	1,192	

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TABLE S4. Test of significance of the predictors in CCA affecting the seed syndromes, using plant genera as samples and forward selection of variables. For a diagram showing the first two canonical axes see Fig. 4. P(adj) was used with $\alpha < 0.05$ for tests of significance. In the case of PCO phylogenetic axes, only the five most significant axes were retained (of 18 that were significant) to balance the variation partitioning analysis and avoid overestimating the effects of phylogeny and deep nodes (i.e. we retained a number of PCO that generated a similar DF and mean square to that for significant colours).

Forward Selection Results (matrix: 514 genera times 8 syndromes)					66
a) effect of sites					
Name	% explained (not adj.)	Contribution %	pseudo-F	P(adj)	
BCI	2.2	64.8	11.6	0.001	
KHC	1.2	35.2	6.4	0.001	
b) effect of colors					
Name	% explained (not adj.)	Contribution %	pseudo-F	P(adj)	
Brown	3.97	46.41	21.7	0.002	
Green	1.25	14.66	6.9	0.00333	
Black	0.65	7.62	3.6	0.0125	
Red	0.56	6.54	3.1	0.0125	
Orange	0.6	6.98	3.3	0.01	
c) effect of plant genera phylogeny					
Name	% explained (not adj.)	Contribution %	pseudo-F	P(adj)	
PCO.6	3.75	16.4	20.4	0.00375	
PCO.11	2.62	11.47	14.7	0.005	
PCO.2	2.21	9.68	12.6	0.00375	
PCO.5	1.9	8.32	11.1	0.00429	
PCO.10	1.75	7.65	10.4	0.00375	

TABLE S5. Test of significance of the predictors in CCA affecting the seed syndromes using plant families as samples and forward selection. For a diagram of the first two canonical axes see Fig. S3. P(adj) was used with $\alpha < 0.05$ for tests of significance.

Forward Selection Results: (matrix: 107 families times 8 syndromes)					
a) effect of sites					
Name	% explained (not adj.)	Contribution %	pseudo-F	P(adj)	
BCI	6.8	75.5	7.6	0.0015	
KHC	2.2	24.5	2.5	0.028	
b) effect of colors					
Name	% explained (not adj.)	Contribution %	pseudo-F	P(adj)	
Brown	14.4	52.9	17.7	0.005	
Green	4.2	15.3	5.3	0.005	
c) effect of plant families phylogeny					
Name	% explained (not adj.)	Contribution %	pseudo-F	P(adj)	
PCO.30	14.6	31.3	18	0.015	
PCO.10	5.3	11.2	6.8	0.01	
PCO.3	4.2	9.1	5.8	0.01	
PCO.1	2.8	6.1	4	0.03	

SUPPLEMENTARY - FIGURES

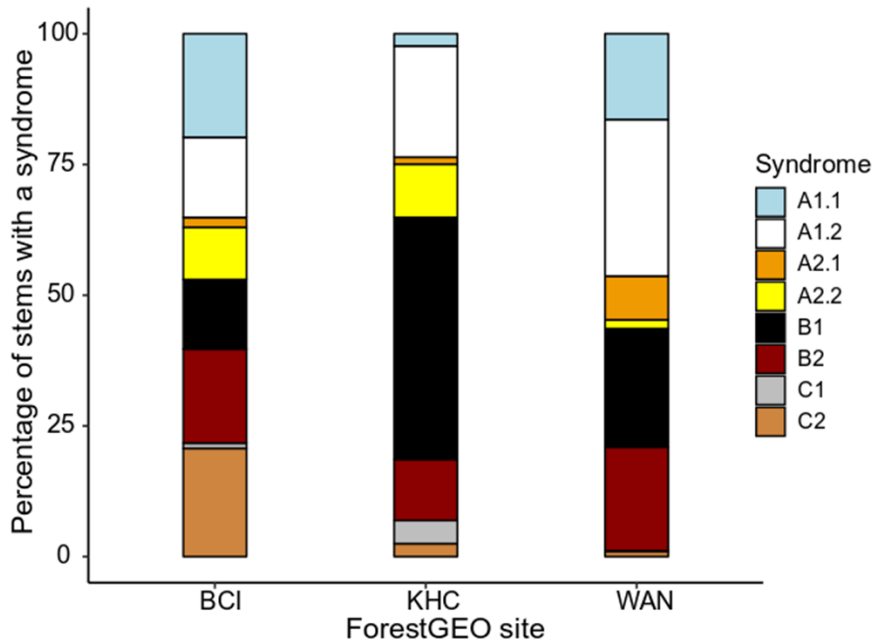


FIGURE S1. Percentage of stems represented by individual fruit syndromes at each of the three ForestGEO sites. BCI=Barro Colorado Island, Panama; KHC=Khao Chong, Thailand; WAN=Wanang, Papua New Guinea.

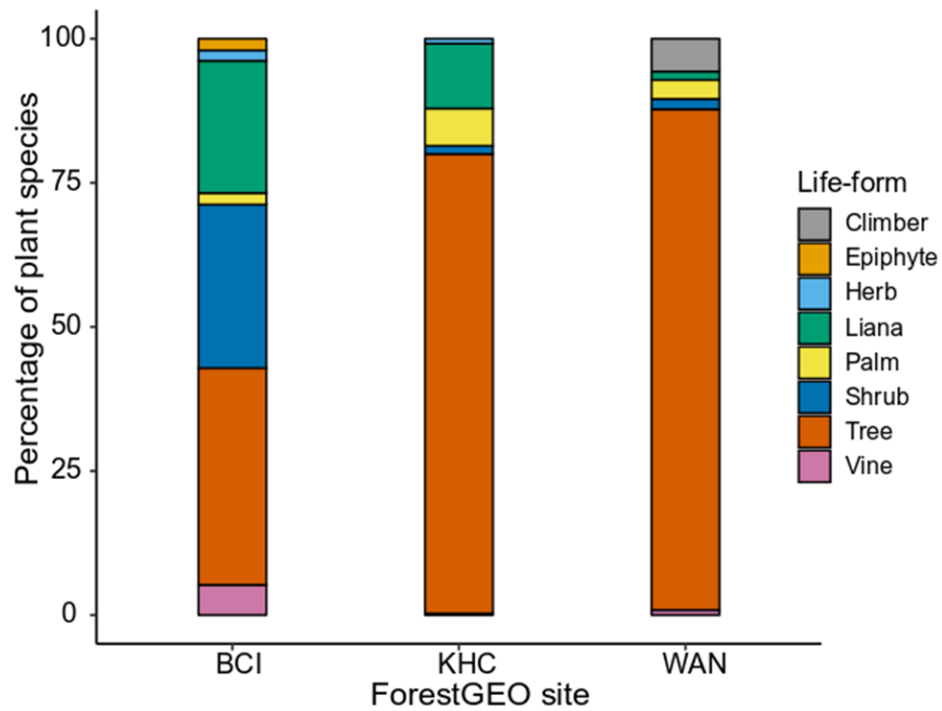


FIGURE S2. Percentage of plant species from each plant life form at the three ForestGEO study sites. BCI=Barro Colorado Island, Panama; KHC=Khao Chong, Thailand; WAN=Wanang, Papua New Guinea.

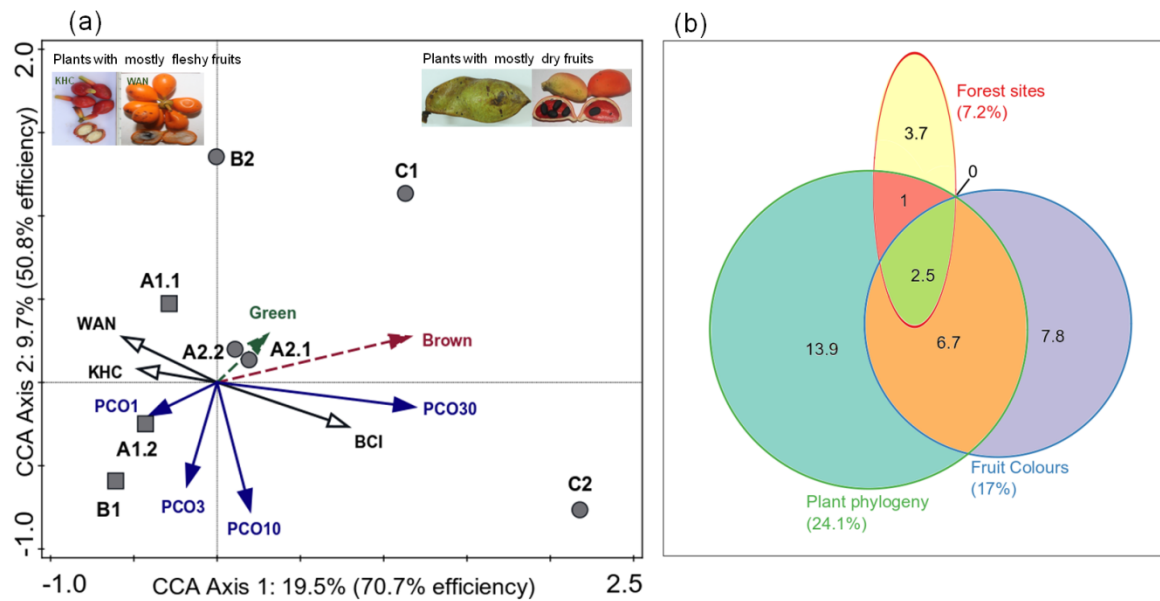


Figure S3. CCA ordination of fruit syndrome distribution based on plant families, fruit colour, forest site (BCI, KHC, WAN) and plant phylogeny (represented by PCO vectors) as explanatory variables (a), and Venn diagram visualizing the proportions of overall adjusted variability explained by each set of variables and their combinations (b). Centroids of individual seed syndromes (a) are represented by circles for the dry fruits and squares for the fleshy fruits. CCA used forward selection of the individual predictors (999 randomizations, $p_{adj} < 0.05$) and variation partitioning among the three sets of variables (see Table S5 for details).