Complex Roles of Insect Cytochrome P450s in Chemical Adaptation

Qi-Ren Chen[1], Timothy W. Moural[1], Fang Zhu[1,2]

Supplementary data:

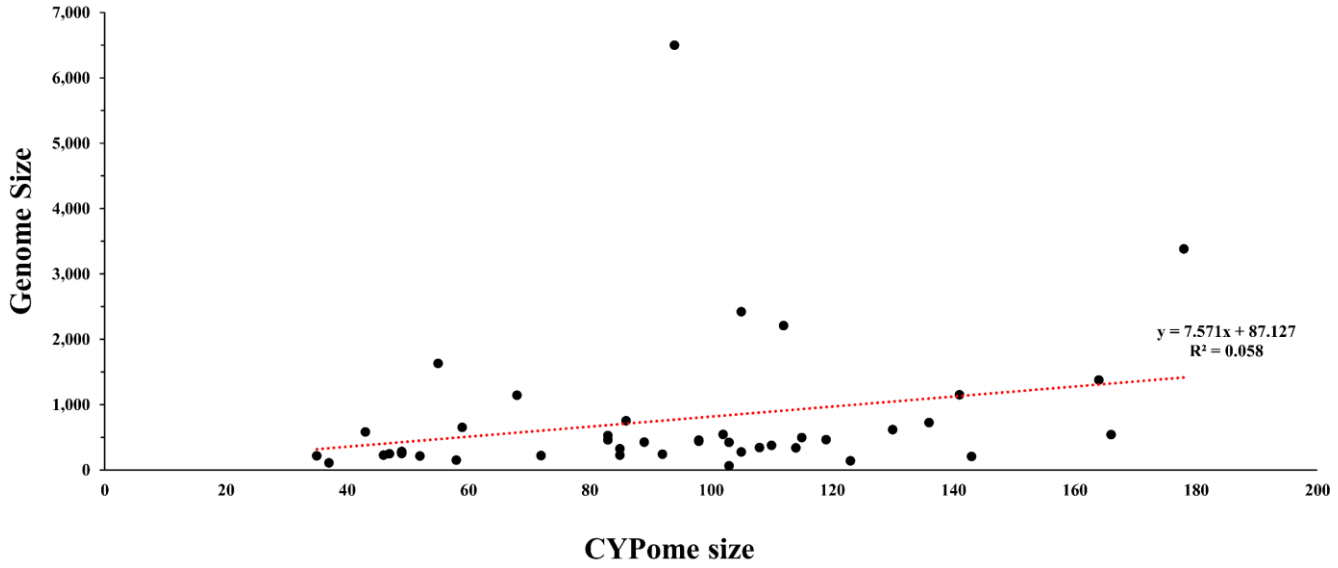

Figure S1. Lack of correlation between genome size and cytochrome P450 (CYP) gene number across insect species. Data are derived from 50 species with genome information available listed in Table S1, excluding transcriptome-based datasets. Each point represents one species, and the dashed line denotes the linear regression fit, illustrating that variation in CYPome size is largely decoupled from genome size.

Table S1. Numbers of CYP families and genes in each clan across diverse insect species.

Order	Scientific Name	Genome size (Mb)	Clan 2	Mito Clan	Clan 3	Clan 4	Total	Reference
Coleoptera (6)	*Brassicogethes aeneus*	62	7	9	50	37	**103**	King *et al.*, 2023 [1] (Table S7)
	Dendroctonus ponderosae	225	7	9	47	22	**85**	Keeling *et al.*, 2013[2]; Keeling *et al.*, 2022 [3]
	Diabrotica virgifera virgifera	2,420	9	13	58	25	**105**	Coates *et al.*, 2023 [4] (Fig. 4)
	Harmonia axyridis	423	10	9	42	28	**89**	Chen *et al.*, 2021 [5]
	Leptinotarsa decemlineata	--	2	7	61	28	**98**	Zhu *et al.*, 2016 [6] (Transcriptomes)
	Tribolium castenaum	204	8	9	79	47	**143**	Zhu *et al.*, 2013[7]; Richards *et al.*, 2008 [8]
Subaverage**			8	10	55	32	105	
Stdv**			1	2	15	10	23	
Diptera (11)	*Aedes aegypti*	1,376	11	10	84	59	**164**	Reddy *et al.*, 2012 [9] (Table 2a); Nene *et al.*, 2007 [10]
	Anopheles gambiae	273	10	9	40	46	**105**	Strode *et al.*, 2008[11]; Nene *et al.*, 2007 [10]
	Anopheles sinensis	2,208	9	9	53	41	**112**	Yan *et al.*, 2018[12]; Zhou *et al.*, 2014 [13]
	Bactrocera dorsalis	542	7	15	45	35	**102**	Jiang *et al.*, 2022 [14] (Table S4 and S13)
	Bactrocera latifrons	463	9	22	49	39	**119**	Jiang *et al.*, 2022 [14] (Table S4 and S13)
	Bactrocera oleae	455	8	18	44	28	**98**	Jiang *et al.*, 2022 [14] (Table S13); Hansen *et al.*, 2026 [15]
	Ceratitis capitata	436	7	17	51	23	**98**	Jiang *et al.*, 2022 [14] (Table S4 and S13)
	Culex quinquefasciatus	540	13	10	77	66	**166**	Reddy *et al.*, 2012 [9] (Table 2a); Zhou *et al.*, 2014 [13]
	Drosophila melanogaster	138	11	19	54	39	**123**	Jiang *et al.*, 2022 [14] (Table S4 and S13)
	Musca domestica	750	4	13	39	30	**86**	Li *et al.*, 2023[16]; Jiang *et al.*, 2022 [14] (Table S4)
	Zeugodacus cucurbitae	375	7	21	43	39	**110**	Jiang *et al.*, 2022 [14] (Table S4 and S13)
Subaverage**			9	15	53	41	117	
Stdv**			3	5	15	13	26	
Hemiptera (12)	*Acyrthosiphon pisum*	526	10	8	33	32	**83**	Ramsey *et al.*, 2010[17]; Mathers *et al.*, 2021 [18]
	Arma custos	--	5	7	48	31	**91**	Li *et al.*, 2023 [19] (Transcriptome)
	Bemisia tabaci MEAM1	615	10	7	57	56	**130**	Chen *et al.*, 2016 [20] (Table S13);
	Cimex lectularius	650	6	6	36	11	**59**	Benoit *et al.*, 2016 [21] (Table S22)
	Cyrtorhinus lividipennis	--	5	4	27	21	**57**	Li *et al.*, 2023 [19] (Transcriptome)

	Halyomorpha halys	1,150	6	6	84	45	**141**	Sparks *et al*., 2020 [22]
	Murgantia histrionica	--	7	6	43	30	**86**	Li *et al.*, 2023 [19] (Transcriptome)
	Nilaparvata lugens	1,140	10	12	19	27	**68**	Lao *et al.*, 2015[23]; Xue *et al*., 2014 [24]
	Orius laevigatus	151	6	5	34	13	**58**	Bailey *et al.*, 2022 [25]
	Pseudoregma bambucicola	582	6	7	13	17	**43**	Lu *et al*., 2023 [26] (Table S2); Zhang *et al*., 2024 [27]
	Rhodnius prolixus	--	7	8	55	49	**119**	Li *et al.*, 2023 [19] (Transcriptome)
	Triatoma infestans	--	1	6	65	22	**94**	Li *et al.*, 2023 [19] (Transcriptome)
Subaverage**			8	7	39	29	83	
Stdv**			2	2	24	17	38	
Hymenoptera (8)	*Apis mellifera*	224	8	6	28	4	**46**	Claudianos *et al.*, 2006 [28] (Table 1); Wallberg *et al*., 2019 [29]
	Apis florea	214	6	5	21	3	**35**	Beadle *et al*., 2019 [30] (Table S5); Tan *et al*., 2021 [31]
	Bombus_impatiens	247	7	6	30	4	**47**	Beadle *et al*., 2019 [30] (Table S5); Sadd *et al*., 2015 [32]
	Bombus terrestris	249	7	6	32	4	**49**	Beadle *et al*., 2019 [30] (Table S5); Sadd *et al*., 2015 [32]
	Megachile rotundata	281	7	6	32	4	**49**	Hayward *et al.*, 2019 [33] (Table S1); Shi *et al*., 2025 [34]
	Nasonia vitripennis	238	7	7	49	29	**92**	Sadd *et al*., 2015 [32] (Table 3); Smith *et al*., 2011 [35] (Table S3)
	Osmia bicornis	213	8	6	33	5	**52**	Beadle *et al.*, PLoS Genetics, 2019 [30] (Table S5);
	Pogonomyrmex Barbatus	220	7	7	40	18	**72**	Sadd *et al*., 2015 [32] (Table 3); Smith *et al*., 2011 [35] (Table S3)
Subaverage**			7	6	33	9	55	
Stdv**			1	1	8	9	18	
Lepidoptera (8)	*Bombyx mori*	460	7	11	31	34	**83**	Kawamoto *et al.*, 2019 [36]
	Cnaphalocrocis medinalis	--	5	6	16	9	**36**	Zhang *et al.*, 2018 [37] (Table 3, Transcriptome)
	Cydia pomonella	723	8	14	67	47	**136**	Wan *et al*., 2019, (Table 14)
	Danaus plexippus	--	8	12	36	30	**86**	Zhang *et al.*, 2018 [37] (Table 3, Transcriptome)
	Helicoverpa armigera	337	8	10	46	50	**114**	Pearce *et al.*, 2017 [38] (Table 2)
	Helicoverpa zea	341	8	10	42	48	**108**	Pearce *et al.*, 2017 [38] (Table 2)
	Manduca sexta	419	8	16	45	34	**103**	Kanost *et al.*, 2016 [39] (Table S15)
	Plutella xylostella	323	10	13	26	36	**85**	Yu *et al*., 2015[40]; Boyes *et al*., 2023 [41] ; You *et al*., 2013 [42]
Subaverage**			8	12	43	42	104	

Stdv**			1	2	14	8	20	
Blattodea (1)	*Periplaneta americana*	3,380	23	13	79	62	**178**	Li *et al.*, 2018 [43] (Fig. 2)
Odonata (1)	*Calopteryx splendens*	1,630	20	9	18	8	**55***	Ioannidis *et al*., 2017 [44] (Table S1)
Orthoptera (1)	*Locusta migratoria*	6,500	9	9	54	21	**94**	Wang *et al*., 2014 [45] (Fig. S31)
Psocodea (1)	*Pediculus humanus*	108	8	8	12	9	**37**	Lee *et al.*, 2010[46]; Kirkness *et al*. 2010 [47]
Siphonaptera (1)	*Ctenocephalides felis*	433-551	11	34	57	13	**115**	Feyereisen, *Curr. Res. Insect Sci*., 2022[48]; Driscoll et al., *BMC Biology*, 2020[49]
Average (42)**			9	11	45	30	94	

* Do not include Clan 20; "--" represents Transcriptome. ** The transcriptome data was excluded from calculation.

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