Functional Ecology

Table S3: Models used to draw conclusions in this study. Models are shown after removal of nonsignificant interactions. All models are Linear Mixed Effects Models (LMMs). We report accompanying ANOVA tables produced with the R package LmerTest, using Type III sums of squares with Satterthwaite approximation for degrees of freedom.

Model Purpose	**Model Type**	**Final Model Structure**	**ANOVA Table**	**Random Effects (standard deviation)**
To test the effects of CO$_2$ treatment on plant cardenolide concentrations	LMM	sqrt(foliar cardenolides) ~ CO$_2$ * species	CO$_2$: $F_{1,106}$=1.69, p=0.197; **Species: $F_{3,106}$=71.72, p<0.0001*****; **CO$_2$*species: $F_{3,106}$=3.05, p=0.0320***	chamber: 1.94x10^{-16}, 1.39x10^{-8}
To test the effects of CO$_2$ treatment and host-plant species on monarch cardenolide concentrations	LMM	sqrt(monarch cardenolides) ~ species + CO$_2$ + infection + CO$_2$*species	**species: $F_{3,221}$=213.05, p<0.0001*****; CO$_2$: $F_{1,41}$=0.15, p=0.702; infection: $F_{1,232}$=0.67, p=0.414; CO$_2$*species: $F_{3,214}$=1.60, p=0.191; **species*infection: $F_{3,228}$=2.71, p=0.0462***	chamber: 4.892x10^{-3}, 6.994x10^{-2}; lineage: 1.160x10^{-2}, 2.708x10^{-1}
To test whether CO$_2$ treatment or infection altered the relationship between foliar and wing cardenolides	LMM	sqrt(monarch cardenolides) ~ CO$_2$ + plant cardenolides + infection + plant cardenolides*CO$_2$	**plant cardenolides: $F_{1,107}$=92.31 p<0.0001**; CO$_2$: $F_{1,108}$=0.29, p=0.589; infection: $F_{1,106}$=0.00, p=09958; **plant cardenolides*CO$_2$: $F_{1,109}$=5.54, p=0.020**	chamber: 0.00, 0.00; lineage: 0.0125, 0.119
To test for differences between resistant monarchs and control monarchs in the sequestration of cardenolides	LMM	sqrt(monarch cardenolides) ~ infection	infection: $F_{1,190}$=0.90, p=0.345	chamber: 0.00 ,0.00; lineage: 0.00 ,0.00
To test for differences between female monarchs and male monarchs in the sequestration of cardenolides	LMM	sqrt(monarch cardenolides) ~ sex	sex: $F_{1,250}$=0.24, p=0.624	chamber: 0.00 ,0.00; lineage: 0.00 ,0.00
To test for differences between resistant monarchs and control monarchs in monarch wing shape	LMM	PCA-Shape ~ infection	infection: $F_{1,181}$=1.90, p=0.170	chamber: 5.42x10^{-19}, 7.36x10^{-10}; lineage: 5.21x10^{-5}, 7.22x10^{-3}
To test for differences between resistant monarchs and control monarchs in monarch wing size	LMM	PCA-Size ~ infection	infection: $F_{1,166}$=0.35, p=0.552	chamber: 5.64x10^{2}, 2.38x10^{1}; lineage: 2.62x10^{-11}, 5.12x10^{-6}

Phytochemical changes in milkweed induced by elevated CO$_2$ alter wing morphology but not toxin sequestration in monarch butterflies

Decker, L. E., Soule, A. J., de Roode, J. C., and Hunter, M. D.

To test for the influence of our treatments on monarch wing shape	LMM	PCA-Shape ~ species+ infection + sex + CO_2*infection + species* CO_2 + species*infection + CO_2*sex + species*sex + infection*sex + species* CO_2*sex + species*infection*sex	**species: $F_{3,212}=3.78$, p=0.011***; **CO_2: $F_{1,214}=15.82$, p<0.0001*****; infection: $F_{1,212}=0.90$, p=0.355; **sex: $F_{1,213}=15.50$, p=0.0001*****; **CO_2*infection: $F_{1,212}=9.46$, p=0.002*****; species* CO_2: $F_{3,213}=0.792$, p=0.500; **species*infection: $F_{3,212}=4.54$, p=0.004*****; CO_2*sex: $F_{1,213}=0.01$, p=0.929; species*sex: $F_{3,212}=0.42$, p=0.737; infection*sex: $F_{1,213}=0.82$, p=0.366; species* CO_2*sex: $F_{3,213}=1.40$, p=0.244; **species*infection*sex: $F_{3,213}=2.96$, p=0.033***	chamber: 0.00, 0.00; lineage: 0.00008, 0.009
To test for the influence of our treatments on monarch wing size	LMM	PCA-Size ~ species + CO_2 + infection + sex	species: $F_{3,202}=2.09$, p=0.102; CO_2: $F_{1,31}=0.31$, p=0.579; infection: $F_{1,226}=2.42$, p=0.121; sex: $F_{1,231}=3.47$, p=0.064	chamber: 1.456×10^{2}, 12.06; lineage: 4.633×10^{-11}, 6.807×10^{-6}
To test for the influence of our treatments on monarch wing loading	LMM	Wing loading ~ species + CO_2 + infection + sex	**species: $F_{3,15}=4.77$, p=0.0153***; CO_2: $F_{1,11}=3.01$, p=0.112; infection: $F_{1,15}=3.80$, p=0.070; **sex: $F_{1,15}=17.13$, p=0.0008*****	chamber: 3.351×10^{-12}, 1.830×10^{-6}; lineage: 3.657×10^{-10}, 1.912×10^{-5}
To test for the influence of our treatments on monarch specific wing area	LMM	log(Wing Density) ~ species + CO_2 + infection + sex	**species: $F_{3,199}=2.66$, p=0.049***, CO_2: $F_{1,31}=0.02$, p=0.897; **infection: $F_{1,221}=20.65$, p<0.0001*****; **sex: $F_{1,228}=15.74$, p<0.0001*****	chamber: 0.0006, 0.0236; lineage: 0.0005, 0.0219