**Supplemental Materials:**

**S3: Scripts and Details for Analyses**

Models used in conducting analyses with their R scripts. Starting models (for model selection) and final models noted where applicable, with model selection conducted via likelihood ratio testing. If no starting model noted, the *a priori* chosen best model was used in the final analysis.

**Growth**

We assessed impacts of ALAN on growth as change in SVL and body condition using linear models including ALAN treatment, sex, initial SVL, and initial body condition as predictors. Initial SVL was centered and scaled separately for each sex. Initial body condition was scaled. Two male lizards were excluded from analyses; one died during the experiment and another experienced high weight loss and was euthanized due to poor health.

***Starting Model for Growth in SVL***

SVLChangeStarting <-lm(SVLChange~ALAN\*Sex+SVL\*Sex+ BodyConditionResidual\*Sex, data=gsc1)

Interactions that did not affect the response (as determined via likelihood ratio test) were excluded from final models.

***Final Model for Growth in SVL***

SVLChangeFinal<-lm(SVLChange~ALAN+Sex+SVL+BodyConditionResidual, data=gsc1)

***Post Hoc testing for Growth in SVL***

library(emmeans)

#Comparisons of all levels of ALAN\*Sex (4)

SVLChangeFinal.em = emmeans(SVLChangeFinal, ~ Sex\*ALAN)

cld(SVLChangeFinal.em)

pairs(SVLChangeFinal.em)

#Main effect of sex

SVLChangeFinal2.em = emmeans(SVLChangeFinal, ~ Sex)

cld(SVLChangeFinal2.em)

pairs(SVLChangeFinal2.em)

**Body Condition:**

Initial SVL was centered and scaled separately for each sex. Initial body condition was scaled.

***Starting Model:***

BodyConditionChangeStarting<-lm(BodyConditionChange~ALAN\*Sex+SVL\*Sex+BodyCondition\*Sex, data=gsc1)

***Final Model:***

BodyConditionChangeFinal<-lm(BodyConditionChange~ALAN+Sex+SVL+BodyCondition\*Sex, data=gsc1)

We tested for differences in body condition between male and female anoles at the start and end of the experiment using paired t-tests.

t.test(FemaleBCStart, FemaleBCEnd, paired = TRUE, alternative = "two.sided")

t.test(MaleBCStart, <MaleBCEnd, paired = TRUE, alternative = "two.sided")

**CORT:**

We assessed whether ALAN affected levels of CORT in plasma using a linear model with ALAN as a fixed factor and its interactions with sex, SVL, and body condition as a starting model. CORT was natural log-transformed, and SVL and body condition were scaled and centered separately for males and females.

***Starting Model for CORT:***

CORTstarting<-lm(LNCort~ALAN\*Sex+ALAN\*SVL+ ALAN\*BodyConditionResidual, data=fmc)

Interactions that did not affect the response (as determined via likelihood ratio test) were excluded from final models.

***Final Model for CORT:***

CORTfinal<-lm(LNCort~ALAN+Sex+SVL+ BodyConditionResidual, data=fmc)

**Onset of Reproduction:**

We tested whether ALAN affected onset of reproduction in females (day of laying first egg) using survival analysis as implemented in the *survival* and *flexsurv* packages. Our starting model included ALAN and its interaction with initial SVL as well as initial body condition.

***Starting Model:***

LayDateStarting<-survreg(LayDate~ALAN\*SVL+BCResid, data=ldt, dist="weibull")

The ALAN\*SVL interaction that did not affect the response (as determined via likelihood ratio test) and was excluded from the final model.

***Final Model:***

LayDateFinal<-survreg(LayDate~ALAN+SVL+BCResid, data=ldt, dist="weibull")

**Number of Eggs:**

***Model:***

Initial SVL and initial body condition were used as covariates

NofEggs<-lm(NumberofEggs~ALAN\*SVL+BodyCondition, data=ne)

**Total Egg Mass:**

***Model:***

Initial SVL and initial body condition were used as covariates

TotalEggMass<-lm(NumberofEggs~ALAN\*SVL+BodyCondition, data=ne)

**Proportion of Mothers Laying Eggs over the Course of the Experiment:**

#####Basic statistics and chi-squared tests for proportions

#####Dark: 14/16 mothers laid eggs

#####Light: 16/16 mothers laid eggs

motherlayeggs<- matrix(c(16,0,14,2),ncol=2,byrow=TRUE)

colnames(motherlayeggs) <- c("Success","Fail")

rownames(motherlayeggs) <- c("Light","Dark")

motherlayeggs <- as.table(motherlayeggs)

motherlayeggs

#####Using monte carlo simulation to calculate p-values

chisq.test(motherlayeggs, simulate.p.value = T, B = 20000)

#####X-squared = 2.1333, df = NA, p-value = 0.4873

#####One-tailed test, p=.2436

**Interval in Days between Eggs Laid:**

We tested for effects of ALAN on the interval (in days) between eggs laid using a linear mixed model implemented in the *lme4* package with ALAN, individual egg mass, Julian Day, and SVL of mother as predictors, the interaction between mother’s SVL and ALAN, and a random effect for mother. Interval between egg-laying was natural log-transformed. The first egg laid by each female was not included in this analysis as interval could not be determined for these eggs. Models were run both with and without one outlier (interval = 26 days); results were qualitatively similar, and we retained the outlier in our final model.

**Model:**

IntervalModel<-lmer(log(Interval)~MotherSVL\*ALAN+EggMass+JulianDate+(1|MomID), data=ei, REML=T)

**Egg Morphology:**

We tested for effects of ALAN on morphology of eggs using a set of models including ALAN, Julian Date, and SVL and body condition of mother as covariates.

**Egg Wet Mass:**

WetMassModel<-lmer(WetMass~ALAN+JulianDay+BodyConditionMother+SVLMother +(1|MotherID), data=wet, REML=T)

**Egg Length:**

LengthModel<-lmer(Length~ALAN+JulianDay+BodyConditionMother+SVLMother +(1|MotherID), data=wet, REML=T)

**Egg Width:**

EggWidthModel<-lmer(EggWidth~ALAN+JulianDay+BodyConditionMother+SVLMother +(1|MotherID), data=dem, REML=T)

**Egg Dry Mass:**

DryMassModel<-lmer(DryMass~ALAN+JulianDay+BodyConditionMother+SVLMother +(1|MotherID), data=dem, REML=T)

**Egg Content Mass:**

ContentMassModel<-lmer(ContentMass~ALAN+JulianDay+BodyConditionMother+SVLMother +(1|MotherID), data= dem, REML=T)

**Egg Water Content:**

WaterContentModel<-lmer(WaterContent~ALAN+JulianDay+BodyConditionMother+SVLMother +(1|MotherID), data= dem, REML=T)

**Mother SVL When Producing First Egg:**

We assessed whether SVL of females when producing their first egg differed with ALAN exposure

***Model:***

FirstEggSVL<-lm(MotherSVL~ALAN, data=dem1st)

**First Eggs Produced by Mothers:**

We assessed whether the first eggs produced by each mother differed in their morphology (wet mass, length, width, dry mass, or water content) with ALAN exposure of mother. These models used covariates that were significant predictors of each response variable in analyses using full datasets. For two females whose first clutches contained two eggs, measurements of the two eggs were averaged.

**Egg Wet Mass:**

FirstWetMass<-lm(wetMass~ALAN+MotherSVL, data=dem1st)

**Egg Length:**

FirstLength<-lm(Length~ALAN+MotherBodyCondition+JulianDate, data=dem1st)

**Egg Width:**

FirstWidth<-lm(Width~ALAN, data=dem1st)

**Egg Dry Mass:**

FirstDryMass<-lm(DryMass~ALAN+MotherBodyCondition, data=dem1st)

**Egg Water Content:**

FirstWaterContent<-lm(WaterContent~ALAN+MotherBodyCondition, data=dem1st)

**Effects of ALAN on Egg Time to Hatching and Hatchling Morphology:**

We assessed whether ALAN affected the incubation time of eggs to hatching, size, and body condition of hatchlings using linear mixed models with ALAN as a fixed factor, a random effect for mother, and egg mass, mother’s SVL, and Julian day as covariates. Egg mass, mother’s SVL, and Julian Day were centered and scaled.

***Days to Hatch:***

DaystoHatch<-lmer(Days~ALAN+MotherSVL+EggMass+JulianDate+(1|MomID), data=ham, REML=T)

***Hatchling SVL:***

HatchlingSVL<-lmer(SVL~ALAN+MotherSVL+EggMass+JulianDate+(1|MomID), data=ham, REML=T)

***Hatchling Body Condition:***

HatchlingBodyCondition <-lmer(BodyCondition~ALAN+MotherSVL+EggMass+JulianDate+(1|MomID), data=ham, REML=T)

**Effect of ALAN on Proportion of Mothers with Eggs Hatching Successfully:**

We assessed whether the proportion of mothers for which all eggs hatched successfully varied with ALAN exposure using a one-tailed chi-squared test with p-value determined via Monte Carlo simulation (20,000 replicates).

#####Creating table of mother success

mothersuccess <- matrix(c(8,0,7,4),ncol=2,byrow=TRUE)

colnames(mothersuccess) <- c("Success","Fail")

rownames(mothersuccess) <- c("Dark","Light")

mothersuccess <- as.table(mothersuccess)

mothersuccess

chisq.test(mothersuccess, simulate.p.value = T, B = 20000)

#####X-squared = 3.6848, df = NA, p-value = 0.1042

#####One-tailed test, p=.0526