Larger hybrid clutch size could drive regional displacement of native *Iguana* populations across the Lesser Antilles

Matthijs P. van den Burg[1,2,*], Sarah A. van der Horn[3], P-A Åhlen[4], Lara Jansen[5], Kai Wulf[6], and Adolphe O. Debrot[5,*]

[1] IUCN SSC Iguana Specialist Group, Gland, Switzerland

[2] Burg Biologica, The Hague, The Netherlands

[3] Nature and Environmental Policy team, Public Entity Saba, Saba, Caribbean Netherlands

[4] Swedish Association for Hunting and Wildlife Management, Nyköping, Sweden

[5] Marine Animal Ecology group, Wageningen University and Research, P.O. Box 338, 6700AH Wageningen, The Netherlands

[6] Saba Conservation Foundation, Saba, Caribbean Netherlands

* Corresponding authors: thijs.burg@gmail.com, dolfi.debrot@wur.nl

Abstract

Hybridization is among the main threats posed by invasive alien species (IAS) and can lead to extinction of endangered species. Here we focus on insular native populations of *Iguana* in the Lesser Antilles that are threatened by hybridization with non-native green iguanas (NNGI) through genetic swamping and eventual extinction. Whilst much effort is put towards preventing NNGI incursions and these subsequent processes, their underlying mechanims are poorly understood. We collected data on snout-vent length (SVL), tail length (TL) and clutch size during an eradication program of hybrid and non-native iguanas on the island of Saba. First, we genetically assessed the status (native/hybrid/non-native) of all individuals from Saba. Subsequently, we combined these data with total length (SVL+TL) data from NNGI on St. Martin (source of NNGI on Saba), and SVL and clutch size from native insular and mainland *Iguana* populations. We found that hybrids on Saba produce significantly larger clutches than native Saba iguanas with a similar SVL, and even larger than one mainland population. However, comparisons of total length between native and hybrid Saba iguanas and NNGI from St. Martin indicate that native iguanas are only significantly smaller than NNGI, not compared to hybrids. Our results suggest that declines in native *Iguana* populations are at least partially driven by genetic swamping, through larger clutch sizes of NNGI as well as larger clutch sizes of hybrid iguanas compared to native iguanas. To optimize long-term conservation maintaining intraspecific genetic diversity is critical and we thus urge rapid identification and protection of remaining native iguanas within populations heavily impacted by hybridization with NNGI (e.g., Grenada, Guadeloupe, and Martinique).

Keywords: Competition, Displacement, Hybridization, Iguana iguana, Lesser Antilles.

Introduction

Global biodiversity is threatened significantly by invasive alien species (IAS) that negatively impact native species through a range of processes like resource competition, introduction of diseases, predation, and hybridization (e.g., Allendorf et al. 2001; Strubbe and Matthysen 2009). Hybridization and introgression with IAS (i.e. anthropogenic hybridization; Allendorf et al. 2001) can have different diminishing impacts on native species (e.g., loss of genetic diversity, wasted reproductive effort, see Allendorf et al. 2001), and has even led to local extirpations (Rhymer & Simberloff 1996; Todesco et al. 2016). Conservationists are especially challenged when hybridization occurs between a rare species and closely-related IAS because this process can go undetected for a number of reasons including inherent low population sizes and morphological and behavioural similarities between species (e.g., Vanhaecke et al. 2012; Hata et al. 2019). Consequently, understanding the processes driving hybridization between IAS and rare species is essential to optimize both IAS management strategies and conservation plans and practices.

Native iguanas within the genus *Iguana* were once present across islands in the Caribbean Lesser Antilles, but have been either extirpated from numerous islands or have dramatically decreased in population size due to a range of direct and indirect anthropogenic causes (Knapp et al. 2014, 2021; Vuillaume et al. 2015; van den Burg et al. 2018a; Breuil et al. 2019). Within this insular region the current most severe threat to remaining native *Iguana* populations is the region-wide presence of non-native green iguanas (NNGI) (Breuil et al. 2019; Knapp et al. 2021; van den Burg et al. 2023). Their initial arrival on Les Saints dates to the 1860's (Vuillaume et al. 2015), while more recently, natural (hurricanes, Censky et al. 1998) and unnatural (e.g., as stowaways in cargo containers) intra-regional translocations have occurred resulting in the establishment of non-native populations (van den Burg et al. 2018b, 2020).

Impacted native iguanas include *Iguana delicatissima* Laurenti, 1768 (from Anguilla to Martinique, except Saba and Montserrat) and members of the *Iguana iguana* species complex

(Linnaeus, 1758) (sensu Iguana Taxonomy Working Group, 2016). Considering the entire complex, these populations are part of one of the four major mtDNA clades (named IIb in Stephen et al. 2013; and *I. iguana* in van den Burg et al. 2021). Following a number of recent manuscripts on the taxonomy of these insular Lesser Antillean *I. iguana* populations (Breuil et al. 2019, 2020, 2022), currently the subspecies of *I. iguana insularis* (St. Vincent and the Grenadines and Grenada) and *I. iguana sanctaluciae* (St. Lucia) are recognized, but not the species *I. melanoderma* (also not recognized as subspecies; Saba and Montserrat) (Iguana Taxonomy Working Group, 2022). Additionally, the Iguana Taxonomy Working Group (2022) currently recognizes *I. iguana iguana* and *I. iguana rhinolopha*; see geographic limitation for *I. i. rhinolopha* in van den Burg et al. (2021).

Non-native green iguanas within the Lesser Antilles have a diverse origin, which have been traced through genetic assessments of NNGIs from several islands using geographic referenced datasets from the native range (see Stephen et al. 2013 and van den Burg et al. 2021a for clade references). These studies indicate origins from all four mtDNA clades, especially from Central America (clade III; see by Stephen et al. 2013 for clade codes) and northwestern South America (clade IIa), with only few non-native populations including eastern South America (clade IIb) and the Curaçao clade (clade I) (Vuillaume et al. 2015; van den Burg et al. 2018b, 2023, 2024; Pounder et al. 2020). However, a complete overview is still lacking, as several islands lack assessments or include only limited analyzed samples.

The arrival of NNGIs to Lesser Antillean islands has repeatedly led to anthropogenic hybridization and introgression with native *Iguana* populations (Day and Thorpe 1996; Vuillaume et al. 2015; van den Burg et al. 2018a; Breuil et al. 2019). Since this process leads to genetic swamping, including complete admixture without selection against hybrids with eventual extinction of the native population (Allendorf et al. 2001), much effort is being invested, through morphological (Breuil 2013; van den Burg et al. 2023, 2024) and genetic methods (Day and Thorpe 1996; Valette et al. 2013; Pounder et al. 2020; van den Burg et al. 2021a; van Kuijk et al. 2025), to rapidly identify and

remove NNGIs. However, the mechanisms behind genetic swamping have received less research attention and are mostly limited to anecdotal data from *I. delicatissima* populations invaded by NNGIs. Vuillaume et al. (2015) indicate that hybrid and introgressed iguanas are "bigger and longer" than *I. delicatissima* and non-native males are more "powerful," but without providing data. Using morphometric data, van den Burg et al. (2024) showed that NNGI on St. Maarten/Martin attain larger overall size compared to *I. delicatissima* on St. Eustatius, which also holds for native green iguanas from Saba (*I. i. iguana*; van den Burg et al. in review), but a broader geographic study should confirm this further as there is variation in both parental species (Day and Thorpe 1996; Bock et al. 2018). Whether native X non-native hybrids also attain larger overall size compared to native iguanas has remained unassessed. Additionally, Vuillaume et al. (2015) suggested that the difference in reproductive timing between native and non-native iguanas could be beneficial for earlier sexual activity and survivorship of the latter. Considering clutch size, *I. delicatissima* lays fewer eggs than (most of the) populations in the *I. iguana* species complex (Knapp et al. 2016; Bock et al. 2018). However, there is only a single published record of clutch size for an F1 *I. delicatissima* x *I. iguana* that suggests a larger clutch size in hybrids compared to *I. delicatissima* (see van Wagensveld and van den Burg 2018 and references therein). To better understand the underlying mechanism(s) of the regional decline in native *Iguana* populations, we studied the difference in clutch size between native and hybrid iguanas in a native *I. i. iguana* population on the Lesser Antillean island of Saba.

Materials and Methods

On Saba, the presence of NNGIs was first identified in 2021 (van den Burg et al. 2025), which catalyzed a program to map their spread and remove as many non-native individuals as possible. Efforts within this program were sporadic during 2022 and 2023, but became more structural with a major NNGI removal effort during the reproductive season between December 2024 and March 2025. During these efforts we surveyed for and culled pure non-native and hybrid iguanas following morphological assignment based predominantly on the presence (native assignment)/absence (non-

native or hybrid assignment) of the melanistic lateral spot between the eye and the tympanum (van den Burg et al. 2025), but also using the relative length of the head and dorsal spines and presence of enlarged nasal scales (van den Burg et al. 2023; van den Burg et al. unpublished data). We also opportunistically captured native iguanas to collect morphological data, which were thereafter released at their capture location. Additionally, we culled few native females given they were part of a harem that included a large non-native dominant male and the high probability that mating had already taken place. Prior to December 2024, iguanas were either culled using an air rifle or through euthanasia after noose/hand captures, whilst most iguanas were shot using either a .22 or high-caliber rifles during the 2024-2025 effort; .223, .243 and 6.5X55 with soft point ammunition for longer distances. At longer distances, and given windy conditions on Saba, accurate bullet placement was aided using the Vortex Fury HD 5000 AB distance measuring feature and the Fury HD Vortex application, and all shots preluded a thorough assessment of backstop presence and orientation. These efforts allowed us to collect data on snout-vent length (SVL), tail length (TL), and clutch size, except for those bodies that could not be retrieved or when these variables were affected by bullet impact. From each captured or retrieved iguana we also sampled blood or tissue, which were stored in Longmire buffer (Longmire et al. 1992) or ethanol respectively. We performed necropsies on all females to determine reproductive state and count the number of enlarged follicles or eggs to score clutch size. Lastly, prior to 2024, we collected data opportunistically from a single native female in 2021 (van den Burg et al. 2025). Fieldwork permits were obtained through the Public Entity Saba (permits BC663.21, BC515.2023, and BC428.2024), and we worked following recommendations from the IUCN SSC Iguana Specialist Group (IUCN SSC Iguana Specialist Group 2017) and euthanasia guidelines from the American veterinary Medical Association.

We constructed two datasets to assess differences in total size (SVL + TL from animals with complete and unbroken tails) and clutch size among different groups. We assessed differences in total size among native iguanas from Saba, NNGIs from St. Maarten (van den Burg et al. in review), and genetically confirmed hybrid iguanas from Saba (for genetics see below). Hereafter we retrieved

residuals from a SVL-tail length regression, and compared the means of these SVL-corrected tail length differences using an analysis of variance (ANOVA) including subsequent posthoc Tukey test to assess different results between the groups. Considering clutch size, we assessed SVL-clutch size relationships among native and non-native iguanas from Saba, as well as previously published data from an *I. i. iguana* population in Panama (Rand 1984; Miller 1987), an *I. i. rhinolopha* population Nicaragua (Fitch & Henderson 1977), one population of *I. delicatissima* (Knapp et al. 2016), and the only reported *I. delicatissima* x *I. iguana* F1 hybrid datapoint (van Wagensveld & van den Burg 2018). We first assessed differences in regression slopes for the SVL – clutch size relation among these groups (excluding the F1 hybrid record) through a linear model and pairwise comparisons of regression coefficients and least-square means. Then, for groups with equal slopes, we tested for differences in SVL-corrected clutch size using an overall ANOVA and individual *t*-tests between all combinations; *p*-values were corrected using the BY-FDR method (White et al. 2019).

We used the blood/tissue samples to assess species/hybrid status for each female iguana and all iguanas with complete SVL+tail data, following van den Burg et al. (2023, 2024). After DNA extraction using a DNeasy Kit (QIAGEN, Germany), we performed Sanger sequencing (forward and reverse) at the University of Amsterdam where laboratory methods were implemented following Malone et al. (2017) and van den Burg et al. (2018b) to amplify the mitochondrial NADH dehydrogenase subunit 4 (ND4) and the nuclear MutL homolog 3 (MLH3). Using Geneious Prime 2024.0.4 (Kearse et al. 2012), we quality-checked chromatograms and compared consensus sequences per individual to published GenBank records and unpublished sequences. Additionally, for the female iguanas only, we generated microsatellite data for 17 loci commonly used for *Iguana* (Valette et al. 2013; Vuillaume et al. 2015; van den Burg et al. 2021a) at the Qualyse laboratory in France. Generated allelic data were compared to the IguanaBase database (van den Burg et al. 2021b) using discriminant analyses of principal components (DAPC) using the *adegenet* package (Jombart 2008) in the R environment (R Core Team 2025, version 4.3.2; RStudio Team 2025, version 2023.12.1+402).

Results

For the total body size comparison, we obtained complete data on SVL and tail length from 42 individuals on Saba (25 native, 17 hybrid, see Appendix 1), and 22 non-native individuals from St. Maarten (see van den Burg et al. 2024). For clutch size comparisons, we obtained data from 15 culled gravid female iguanas during Dec 2024–March 2025, indicating that both native, hybrid and non-native iguanas are reproductively active in the same period. From these, we could not accurately assess SVL of one iguana, and for two iguanas an unknown number of eggs was destroyed and irretrievable. Therefore, including the record of the native female from 2021 (van den Burg et al. 2023, 2025), we analyzed data from 13 gravid morphologically and genetically assessed iguanas. We obtained ND4 and MLH3 sequences data from all individuals (Table 1); native ND4 and MLH3 haplotypes correspond to HM352505 and OQ556119, respectively. We also generated microsatellite allelic data from all but two samples (SAB103+104; Figure 1); samples that clustered within "*Iguana iguana* melanistic" were considered native as these include previously assessed native Saba samples (van den Burg et al. 2021a, 2023), while the other samples included alleles not observed in native Saba iguanas (Breuil et al. 2020; van den Burg et al. 2021a, 2023). Combined, these data indicated that five iguanas were native Saba iguanas (SAB45, 103, 104, 108, 114), six iguanas were native X non-native F1 hybrids (SAB80, 97, 100, 101, 102, 117), and one iguana was a F2 hybrid (SAB91). SAB88 was a non-native iguana with mixed geographic origins and was therefore not included in SVL-clutch size comparisons.

Table 1. Collected data on snout-vent length (SVL) and egg count from female iguanas on Saba, including morphological and genetic assignment for mitochondrial (mtDNA), nuclear (nDNA), and microsatellite (msat) data. Unless native, clade numbers in the assignment columns refer to mtDNA clades within the *Iguana iguana* species complex following Stephen et al. (2013). Asterisk: SAB88 was not included in further analyses since it lacked native haplotypes.

Individual	SVL (mm)	Eggs	Morphology	mtDNA	nDNA	msat
SAB45	325	29	native	native	native / native	native
SAB80	361	40	nonnative	native	native / Clade III: PV974928	nonnative
SAB88*	371	48	nonnative	Clade IIa: PV974931	Clade III: OQ556117 / Clade III: PV974930	nonnative
SAB91	311	37	hybrid	Clade III: HM352508	native / native	nonnative
SAB97	357	42	hybrid	Clade III: HM352508	native / Clade III: OQ556118	nonnative
SAB100	369	50	hybrid	native	native / Clade I: KX610637	nonnative
SAB101	379	58	nonnative	Clade III: HM352508	native / Clade III: OQ556117	nonnative
SAB102	340	45	hybrid	native	native / Clade III: PV974928	nonnative
SAB103	305	21	native	native	native / native	NA
SAB104	345	29	native	native	native / native	NA
SAB108	354	34	native	native	native / native	native
SAB114	381	44	native	native	native / native	native
SAB117	345	42	hybrid	native	native / Clade III: OQ556117	nonnative

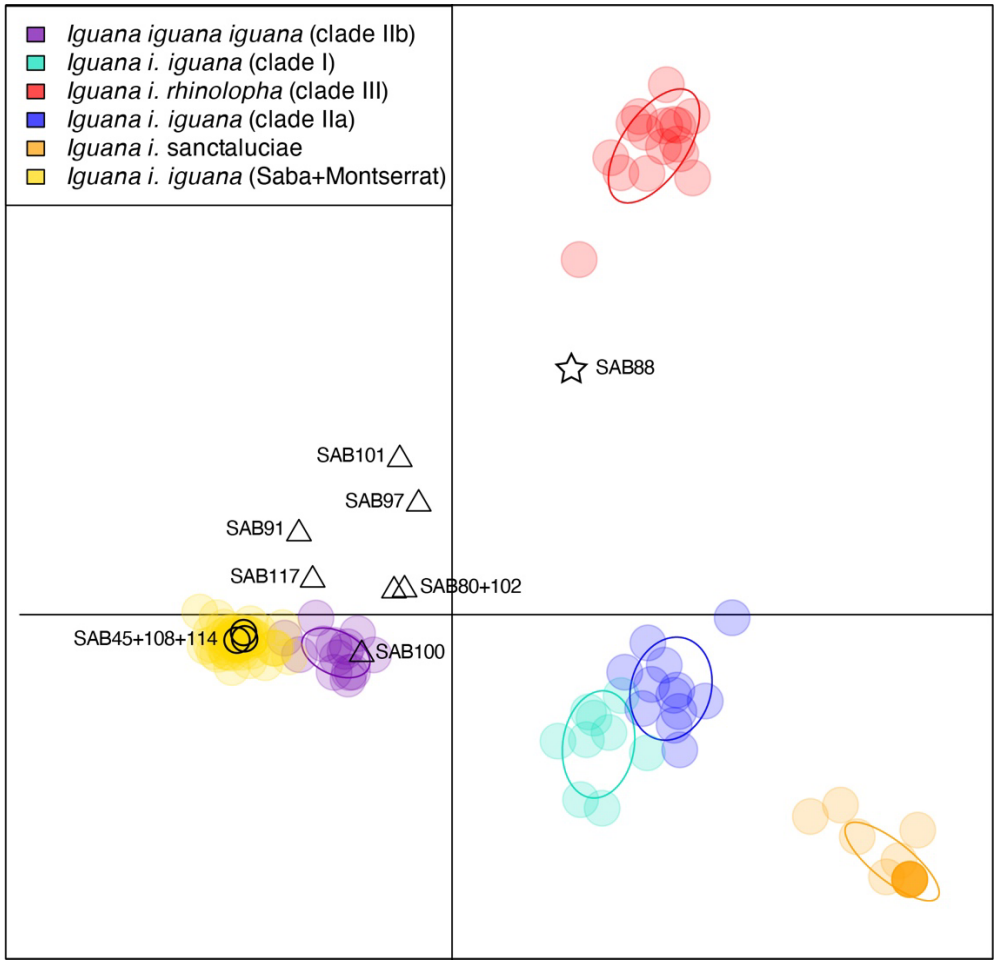

Figure 1. Discriminant analysis of a principal components scatterplot representing 17 microsatellite loci from reference IguanaBase individuals (colored circles) and 11 gravid females from Saba; three native iguanas (circles), and eight hybrid (triangles) and nonnative (star) iguanas. Clade codes follow Stephen et al. (2013).

Regression slopes differed significantly only between *I. delicatissima* – *I. i. iguana* Panama (p = 0.0003) and *I. delicatissima* – *I. i. rhinolopha* Nicaragua (p = 0.0302) (Figure 2A). Therefore, *I. delicatissima* (as well as the single *I. delicatissima* x *I. i. iguana* record) was not included in the subsequent SVL-corrected clutch size comparison. The ANOVA indicated significant differences among SVL-corrected clutch size among means of the four groups (Figure 2B), $p = 0.0011$; Saba (native), Saba (hybrid), *I. i. rhinolopha* Nicaragua, and *I. i. iguana* Panama. HY-FDR adjusted *p*-values for pairwise comparisons were significant for all but two comparisons (Table 2): Saba (native) – *I. i. rhinolopha* Nicaragua and Saba (hybrid) – *I. i. iguana* Panama.

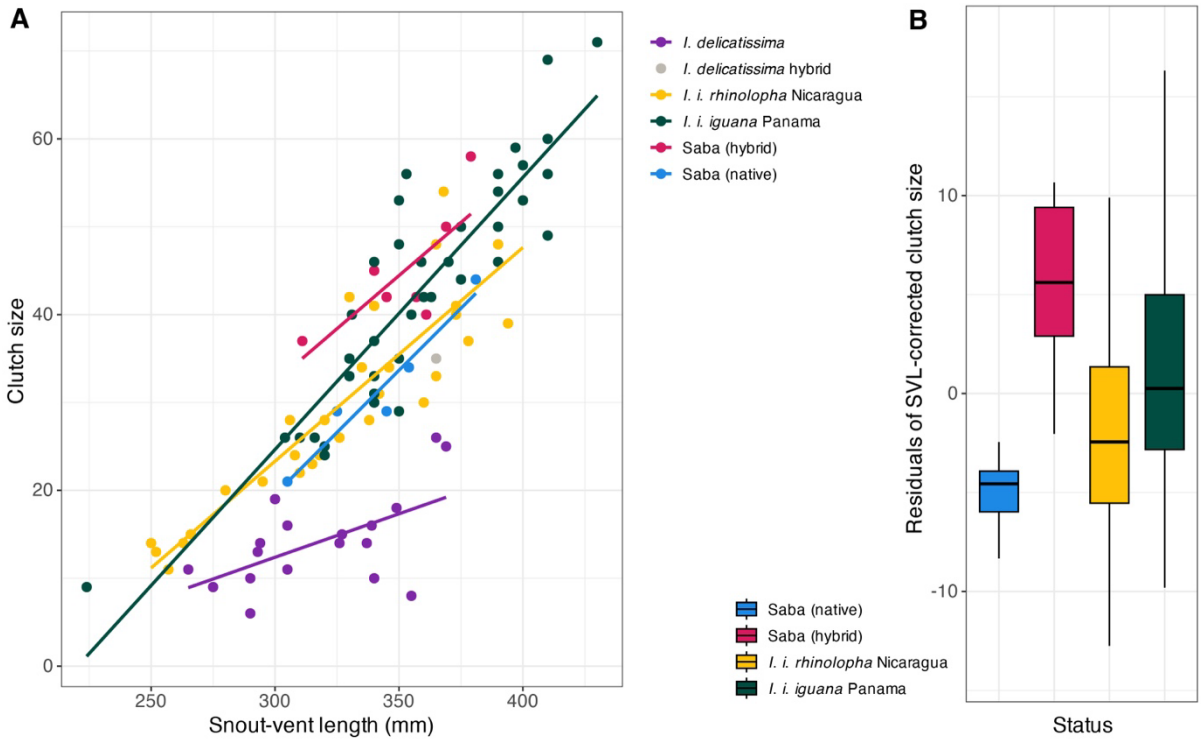

Figure 2. Relationships between snout-vent length (SVL) and clutch size among native and hybrid iguanas on Saba and different populations of *Iguana* spp., including data from Fitch & Henderson (1977), Rand (1984), Miller (1987), Knapp et al. (2016), and van Wagensveld & van den Burg (2018). **A)** SVL-clutch size regression including all groups. **B)** Boxplots of SVL-clutch size residuals among groups with regression slopes that were not significantly different. SAB88 is not included.

Table 2. Results of pairwise *t*-test for differences in SVL-corrected residuals in clutch size for female iguanas across four groups; Saba (native), Saba (nonnative), *I. i. rhinolopha* Nicaragua, and *I. i. iguana* Panama. *P*-values are HY-FDR adjusted. Non-significant results are indicated by n.s. These results exclude *I. delicatissima* and the only reported *I. delicatissima* x *I. iguana* hybrid (van Wagensveld & van den Burg 2018) as also in Figure 2A. SAB88 was also not included.

	Saba (native)	Saba (hybrid)	*I. i. rhinolopha* Nicaragua	*I. i. iguana* Panama
Saba (native)				
Saba (hybrid)	0.0017			
I. i. rhinolopha Nicaragua	0.073 (n.s.)	0.0065		
I. i. iguana Panama	0.0017	0.073 (n.s.)	0.016	

ANOVA results indicated significant differences of mean total sizes among native Saba iguanas, hybrid iguanas from Saba, and non-native iguanas from St. Maarten; $p = 0.0312$ (Figure 3). Tukey posthoc test showed only a significant difference between native Saba and non-native St. Maarten iguanas ($p = 0.0265$), and non-significant differences between Saba hybrids and the other two groups ($p > 0.29$).

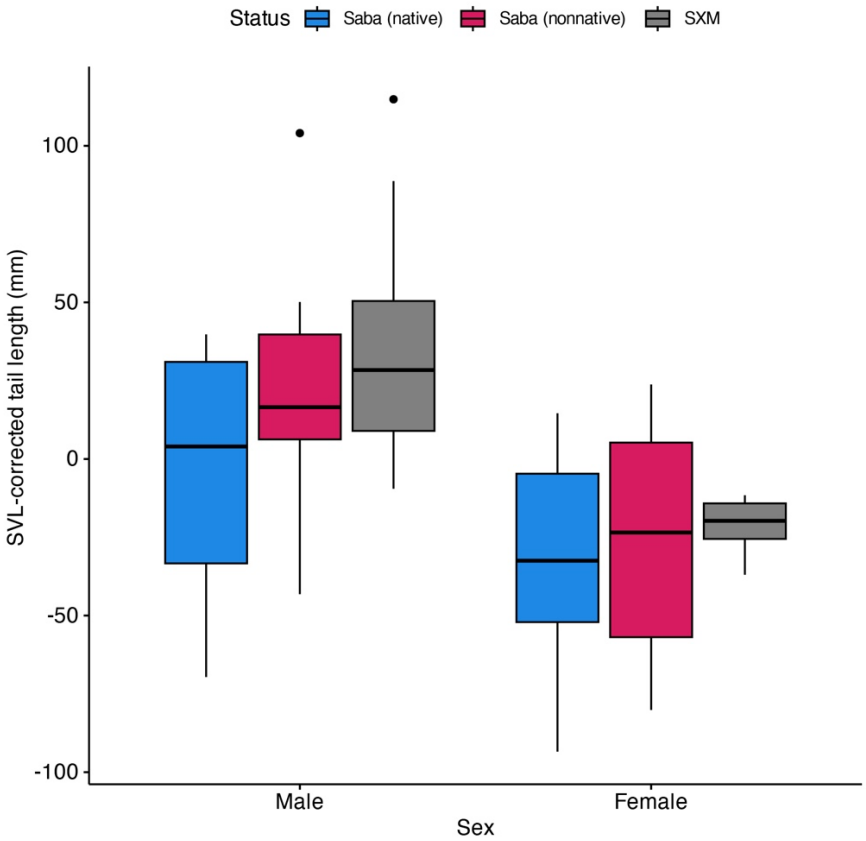

Figure 3. Boxplots showing differences between SVL-corrected tail length (overall size) between native Saba iguanas, hybrid iguanas from Saba, and non-native iguanas on St. Maarten.

Discussion

Non-native green iguanas (NNGI) are replacing native *Iguana* populations across the Lesser Antilles leading to eventual extinctions of native populations. Our data from native, hybrid, and NNGIs from Saba combined with published data provide novel insights on the underlying mechanisms of these ongoing extinctions. Our results indicate that NNGIs attain a larger overall size compared to native iguanas (see also van den Burg et al. 2024) but that hybrids are not significantly larger than native

iguanas. Larger body size has been suggested to partially drive observed replacement of native iguana populations across the region (Vuillaume et al. 2015). Contrarily, we find that hybrids produce larger clutches than native Saba iguanas with a similar snout-vent length (Figure 2). These results are an example of "hybrid-vigor" and aid to our understanding of the observed drivers of non-native/hybrid swamping of native *Iguana* populations witnessed throughout the Lesser Antilles, and emphasize the need for continuous monitoring and management strategies not only aimed at controlling NNGI populations, but also at protecting native individuals in swamped populations.

Here we provide a report on clutch size difference between native Saba iguanas, hybrid iguanas from Saba, and two mainland *Iguana* populations. Previously, only a single recorded clutch size had been published for an *Iguana* hybrid (van Wagensveld & van den Burg 2018). Our results indicate that both hybrid and non-native mainland iguanas lay larger clutches compared to native Saba iguanas. These results also highlight high variation in clutch size across *Iguana* (Figure 2), and partially follow earlier findings that island populations lay fewer eggs compared to mainland populations (Siliceo & Díaz 2010; Meiri et al. 2020). Clutch size within the *I. iguana* species complex is known to vary widely (Nosolov et al. 2012; Bock et al. 2018), and is presumably affected by local climate and environmental conditions similar to other reptiles (e.g., Diaz et al. 2012; Roitberg et al. 2013). However, this remains to be further studied in *Iguana*. Non-native iguanas on Saba are believed to originate from St. Maarten/Martin, from where genetic data indicate at least three *Iguana iguana* mitochondrial clades being present (two non-regional and one regional; van den Burg et al. 2018b). Our genetic data suggests that individuals with (partial) genetic origins from all four mitochondrial clades are present on Saba (Table 1 and Appendix 1). Currently there are no data on clutch sizes from St. Maarten/Martin, which would be interesting to better interpret the difference in clutch size between hybrid Saba iguanas and the two mainland populations. Clutch size data combined with genomic approaches could additionally shed light on genes involved in fecundity and selective pressure in (hybrid) iguanas, as well as potential novel gene complexes and local adaptation

in NNGIs populations across the Lesser Antilles as these have different non-native origins (Vuillaume et al. 2015; van den Burg et al. 2018b, 2023, 2024; Pounder et al. 2020).

Equally variable compared to clutch size is the timing of reproduction within both *I. delicatissima* and *I. iguana* that follows local annual climate patterns (van den Burg et al. 2018a; Breuil et al. 2019). On Saba, we found that reproductive timing was similar between non-native/hybrid and native iguanas, which is in contrast to some Lesser Antillean islands native to *I. delicatissima* (Breuil et al. 2019). However, since non-native iguanas from different geographic origins are present within the region and also hybridize (see Table 1; e.g., Vuillaume et al. 2015; van den Burg et al. 2023), future assessments of reproductive timing and geographic origin of non-native populations should be considered (e.g., on St. Martin), as well as potential changes in reproductive timing when hybridization results in hybrid swarms. Understanding these population characteristics could inform tailored conservation strategies to bolster native populations against the threats posed by non-native iguanas, especially when targeting gravid females (with potential hybrid clutches) at nesting sites.

Our results suggest that the observed decline in native *Iguana* populations is at least partially driven by genetic swamping, not only by a larger clutch size of pure non-native iguanas, but also through larger clutch size of hybrid iguanas compared to native iguanas (i.e., hybrid vigour). Despite numerous anthropogenic threats to iguanas on islands in the Lesser Antilles (Knapp et al. 2016; van den Burg et al. 2018c), native iguanas can live to 24 years in the wild (Warret Rodrigues et al. 2021), and thus remain present long enough after incursions and establishment of NNGIs for (genetic) identification to make it possible to safeguard their genetic lineage for conservation purposes. We emphasize that despite the low variation in mtDNA across the range of *I. delicatissima* (Martin et al. 2015), nuclear markers do indicate genetic structure among the different island populations (van den Burg et al. 2021). Since the maintenance of intraspecific genetic diversity is critical to long-term conservation of a species (e.g., Lacy 1997), identifying and capturing remaining native iguanas in

hybridized and introgressed populations is critical for native *Iguana* conservation. We therefore urge regional partners to identify remaining native *Iguana* survivors within areas that have been heavily impacted by hybridization and introgression with non-native green iguanas (e.g., Grenada, Guadeloupe, and Martinique) so that their protection can be improved.

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Appendix 1. Collected data on snout-vent length (SVL) and tail length from iguanas on Saba, including genetic assignment for mitochondrial (mtDNA; one haplotype), nuclear (nDNA; two haplotypes), and microsatellite (msat) data. Unless native, clade numbers in the assignment columns refer to mtDNA clades within the *Iguana iguana* species complex following Stephen et al. (2013). Asterisk indicate data published in van den Burg et al. (2023). Native ND4 and MLH3 haplotypes correspond to HM352505 and OQ556119, respectively.

Individual	Fate	SVL (mm)	Tail (mm)	mtDNA	nDNA
SAB01 (M)*	Alive	230	595	native	native/native
SAB03 (M)*	Alive	405	1022	native	native/native
SAB08 (M)*	Dead	345	888	Clade III: HM352508	native/Clade III: OQ556118
SAB11 (F)*	Alive	340	821	native	native/native
SAB15 (M)*	Alive	389	959	native	native/native
SAB17 (F)*	Alive	350	828	native	native/native
SAB18 (F)*	Alive	326	795	native	native/native
SAB22 (M)*	Alive	310	725	native	native/native
SAB23 (F)*	Alive	267	697	native	native/native
SAB24 (M)*	Alive	265	708	native	native/native
SAB28 (M)*	Alive	401	965	native	native/native
SAB30 (F)*	Alive	316	776	native	native/native

SAB31 (F)*	Alive	300	774	native	native/native
SAB41 (F)*	Alive	362	846	native	native/native
SAB44 (M)*	Alive	305	757	native	native/native
SAB51 (F)*	Alive	363	810	native	native/native
SAB57 (F)*	Dead	359	838	Clade III: HM352508	native/Clade III: OQ556117
SAB60 (F)	Alive	361	838	native	native/native
SAB61 (M)	Alive	391	988	native	native/native
SAB63 (M)	Dead	410	1104	Clade I: OQ556120	native/ Clade I: KX610637_a
SAB69 (M)	Dead	267	697	Clade I: OQ556120	native/ Clade I: KX610637_a
SAB70 (F)	Alive	357	902	native	native/native
SAB75 (M)	Alive	311	830	native	native/native
SAB76 (M)	Alive	371	957	native	native/native
SAB80 (F)	Dead	361	875	native	native/Clade III: PV974928
SAB82 (M)	Dead	340	896	native	native/native
SAB83 (M)	Alive	383	907	native	native/native
SAB84 (M)	Alive	327	844	native	native/native
SAB85 (M)	Dead	440	1073	Clade I: HM352499	native/Clade IIa: PV974929
SAB87 (M)	Dead	400	991	Clade III: HM352508	native/Clade III: OQ556117
SAB90 (M)	Dead	312	835	Clade III: HM352508	native/Clade III: OQ556118
SAB91 (F)	Dead	311	802	Clade III: HM352508	native/native
SAB94 (M)	Dead	315	855	native	native/Clade III: OQ556117
SAB97 (F)	Dead	357	811	Clade III: HM352508	native/Clade III: OQ556118
SAB100 (F)	Dead	369	921	native	native/Clade I: OQ556119
SAB102 (F)	Dead	340	880	native	native/Clade III: PV974928
SAB105 (F)	Dead	255	659	Clade III: HM352508	native/native
SAB112 (M)	Dead	271	675	native	native/native
SAB114 (F)	Dead	381	955	native	native/native
SAB115 (M)	Dead	189	503	Clade III: HM352508	native/native
SAB116 (F)	Dead	259	633	Clade III: HM352508	native/Clade III: OQ556117
SAB117 (F)	Dead	345	843	native	native/Clade III: OQ556117

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