



Green turtles in the Gulf of Venezuela



Gaby Montiel-Villalobos

Kate Rodríguez-Clark

Hector Barrios-Garrido

Alberto Abreu-Grobois, Rodrigo Lazo



WIDECAST AGM Baltimore, MD February 2, 2013



Instituto Venezolano de Investigaciones Científicas



• Ecology Center.

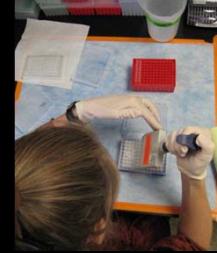


• Caracas. Research serving national needs.

My research



- Conservation biology broadly, conservation genetics specifically.
- Common thread: Venezuelan species threatened by over-exploitation.
- Turtles, alas, included.



Gaby



Overview of PhD finished last fall

The Gulf of Venezuela (GV)



Chelonia mydas in the GV

- Most important feeding area in Venezuela?
- Many turtles, many sizes.
- Wuayuú traditional use.
- Some tag recaptures.



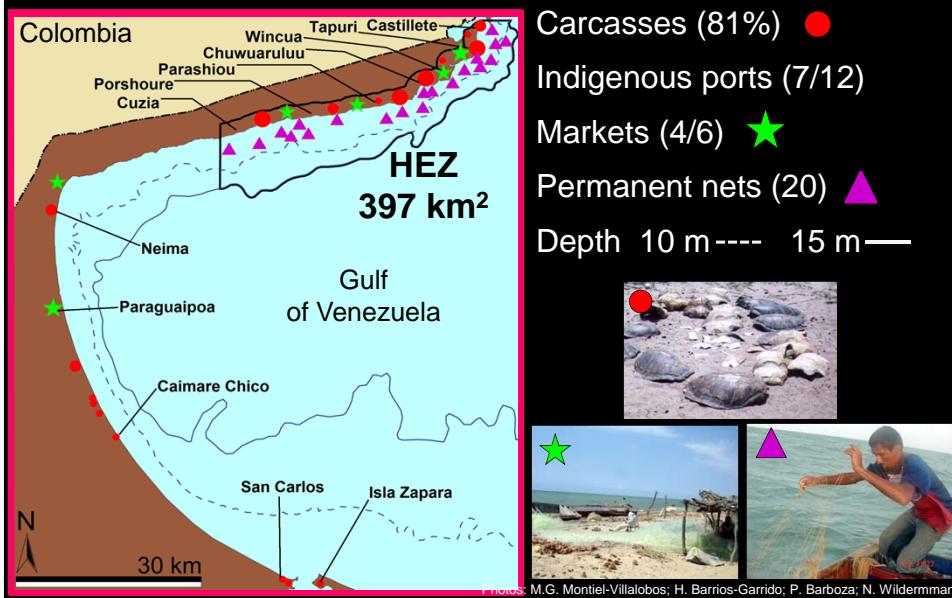
Photos: M.G. Montiel-Villalobos; H. Barrios-Garrido

© M. Montiel-Villalobos

Questions

1. Importance as a feeding area?
2. Relative turtle abundance and factors influencing it?
3. Size structure?
4. Impacts of harvest:
 - Selectivity?
 - Origins of turtles harvested?

Study area: High Extraction Zone



1. Food availability for *C. mydas*

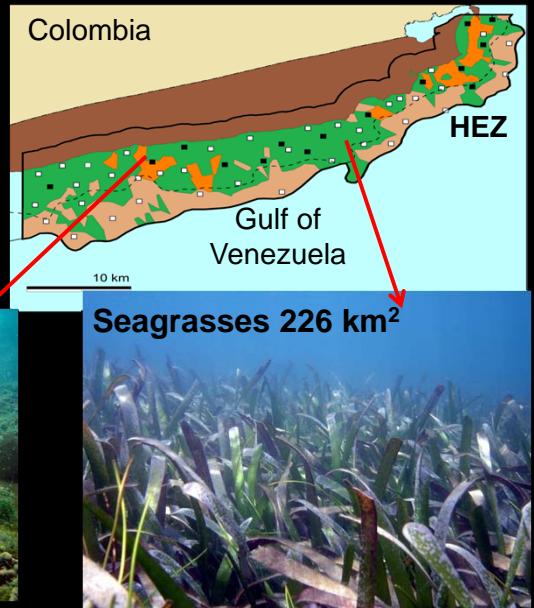
- 410 points.
- X, Y, Z, type, nets.



Sponges, algae & coral reef 38 km²

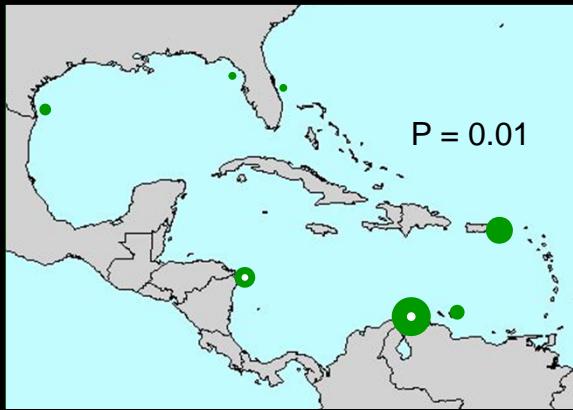


Photos: H. Barrios-Garrido, N. Espinoza



2. Index turtle abundance (CPUE)

- 52 bouts, **15.03 km-net*hr**
- CPUE = $c/(\sum l_t)$. Two estimates.
- CPUE_{total} = **1.21 ± 0.21 tu/km-net*hr**

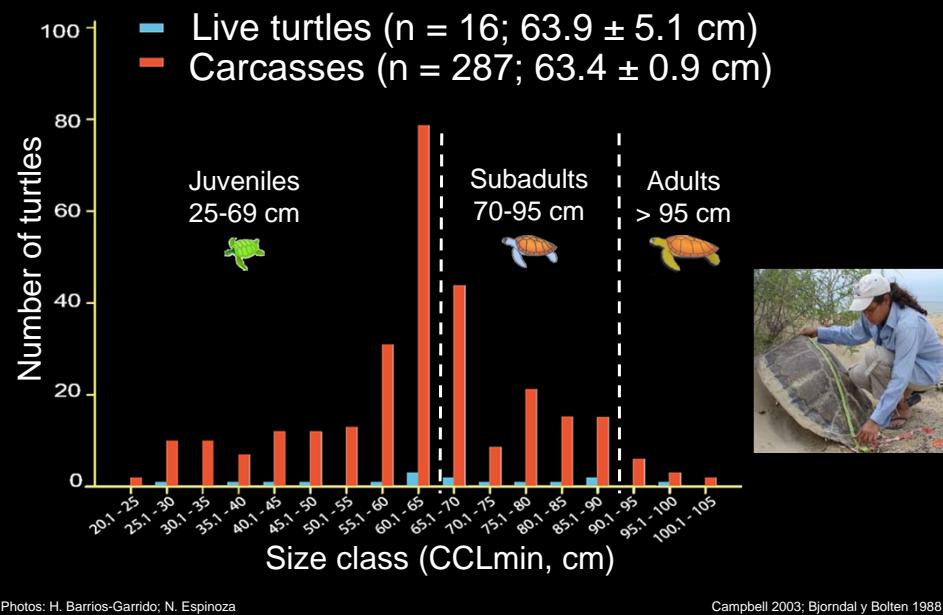


Brabeck y Nava 2009; Campbell 2003; Schmid 1998; Coyne 1994; Collazo *et al.* 1992; Mendonça y Ehrhart 1982



Photos: M. Montiel-Villalobos; H. Barrios-Garrido

3. Size class structure



4. Total annual catch & effort

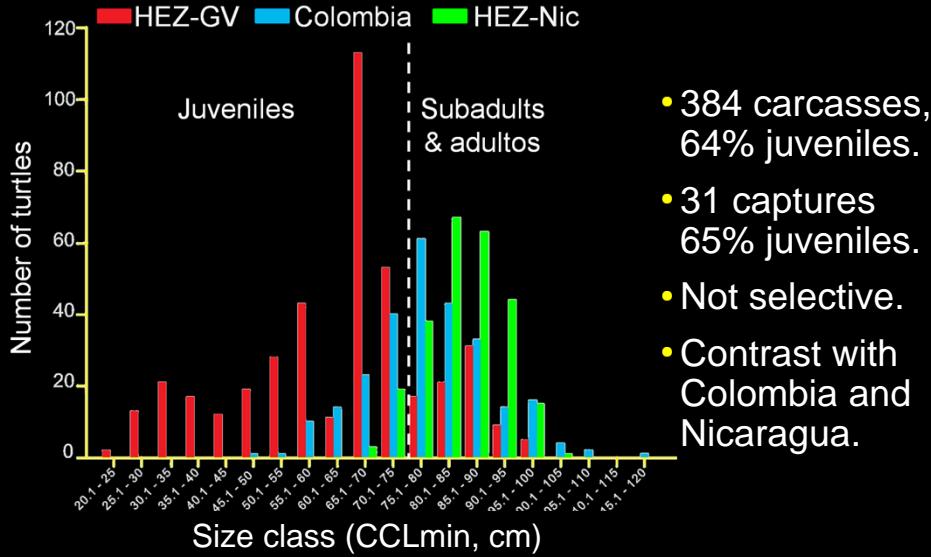
- Interviews: 37 fishers.
- Observations: 38 bouts (20 interviewees).
- # fishers = 103.
- # nets = 264 interv. vs. 142 obs.
- $CPUE_i = 0.07$ turtle/km-net*hr.
- $CPUE_o = 0.08$.

Total effort = 44,595 km-net*hr
Annual total catch 3,649 tu/y
vs. 11,000 tu/y HEZ-Nicaragua
6,000 tu/y Colombia



Photos: M.G. Montiel-Villalobos; H. Barrios-Garrido

4. Catch selectivity

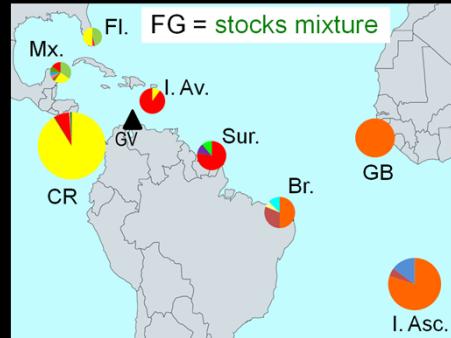


4. Geographic origins - tags

- 33 tags 1997 – 2011.
- **Adult females** from Costa Rica, Colombia and Aves Island.
- **Juveniles** from several Caribbean feeding areas.



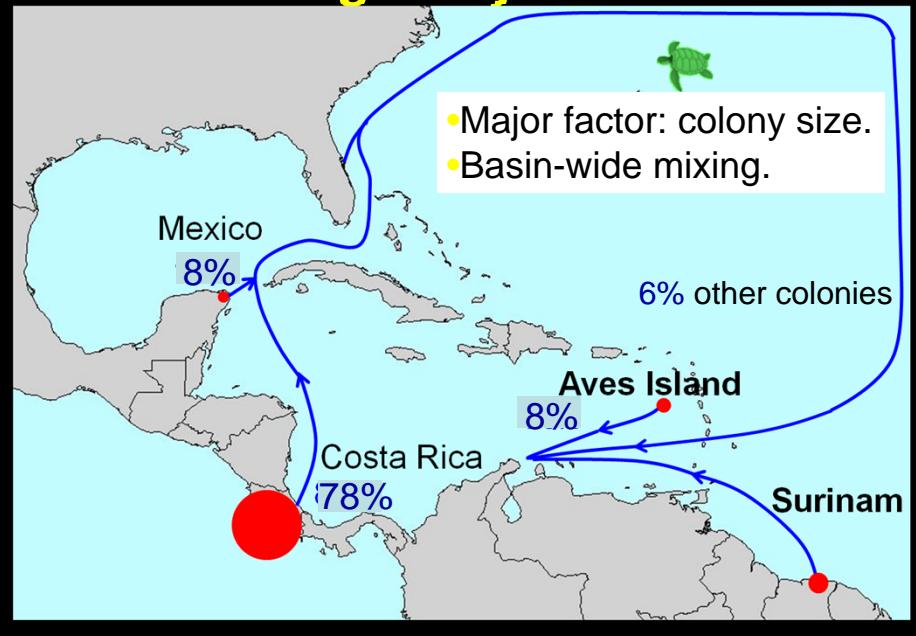
4. Geographic origins - mtDNA



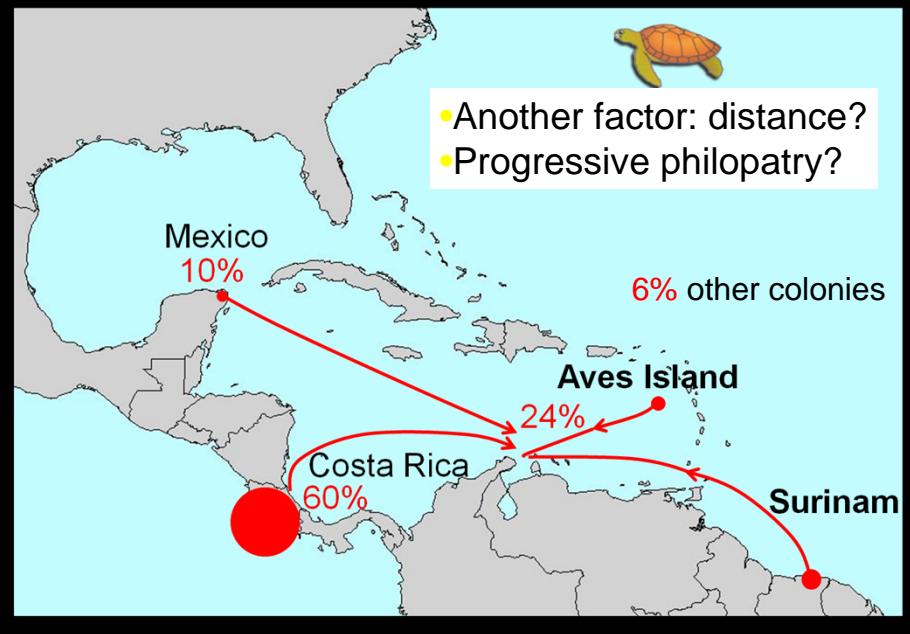
- 142 sequences. 486 bp mtDNA control region.
- 10 haplotypes (CM-A3>20% & CM-A5>60%)
- Foraging-group centric mixed stock analysis (ACCSTR).
- Juveniles vs subadults & adults (CCLmin 80 cm).

Proetti *et al.* 2012; Monzón-Argüello *et al.* 2010; Bolker *et al.* 2007; Naro-Maciel *et al.* 2007; Bass *et al.* 2006; Luke *et al.* 2004; Bass y Witzell 2000; Bass *et al.* 1998; Lahanas *et al.* 1998;

4. Origins - juveniles



4. Origins – sub/adults



Conclusions

1. Large area of food resources.
2. Among highest CPUE reported for Caribbean.
3. Unusual mix of juveniles, subadults, adults.
4. Harvest third largest in region, sustainability unknown, but:
 - No evidence for selectivity.
 - Mostly juveniles, mostly from Costa Rica.
 - Adults from Aves Island? More work.

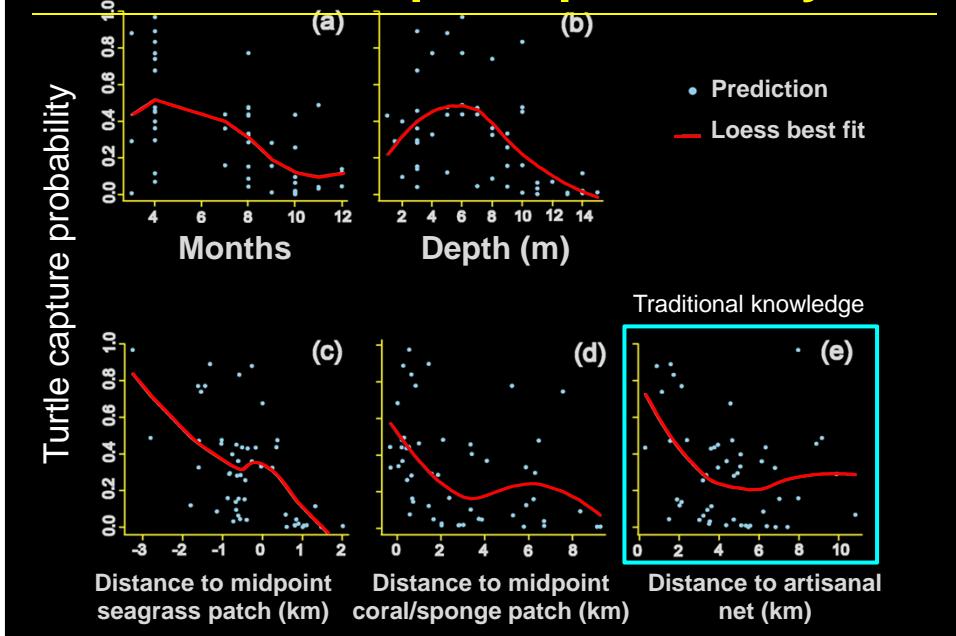
Thanks



kmrodriguezclark@gmail.com

mmontielv@gmail.com

2. Turtle capture probability



4. Catch selectivity & origin

- CCLmin (turtles caught, carcasses)



- Tags obtained opportunistically:
 - method, date & place of capture.
 - Outcome (consumed, sold, released).



Photos: H. Barrios-Garrido

Total annual catch & capture effort

37 Interviews

20

38 Fishing bouts

$$\text{CPUE}_i = C_i / (E_i * h_i)$$

C_i = captures/month

E_i = # net-km

h_i = net-h/month

$$\text{CPUE}_o = C_o / (E_o * h_o)$$

C_o = captures/fisher

E_o = net-km/fisher

h_o = net-h/fisher

$$N_{tio} = N_f * h_{total} * \text{CPUE}_o * 12$$

$$E_t = N_f * h_{total} * E_o$$



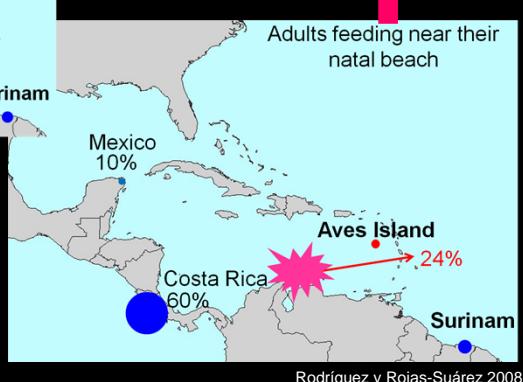
Photos: M.G. Montiel-Villalobos; H. Barrios-Garrido

Conservation



1) Caribbean context:
smaller problem?

2) Aves Island rookery:
national issue



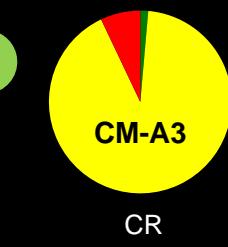
Next steps

- Sustentabilidad de la extracción en la ZME-GV: **monitorización**

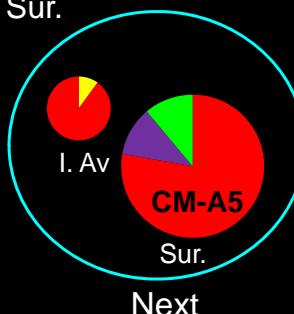
 Datos históricos

 Percepción Wayúu
No. absoluto menor
No selectividad
CPUE temp. Estable

- Análisis genéticos: genoma mitocondrial completo
- Distinción nuevos haplotipos dentro de más comunes (CM-A3 y CM-A5). Poco diferenciados: I.Av y Sur.



Now



Next