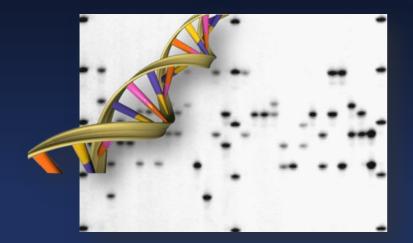
Application of genetic tagging for the management and conservation of European lobster *Homarus gammarus* stocks





#### Paulo A. Prodöhl & Deborah Bailie

#### $2003 \rightarrow \text{ongoing}$





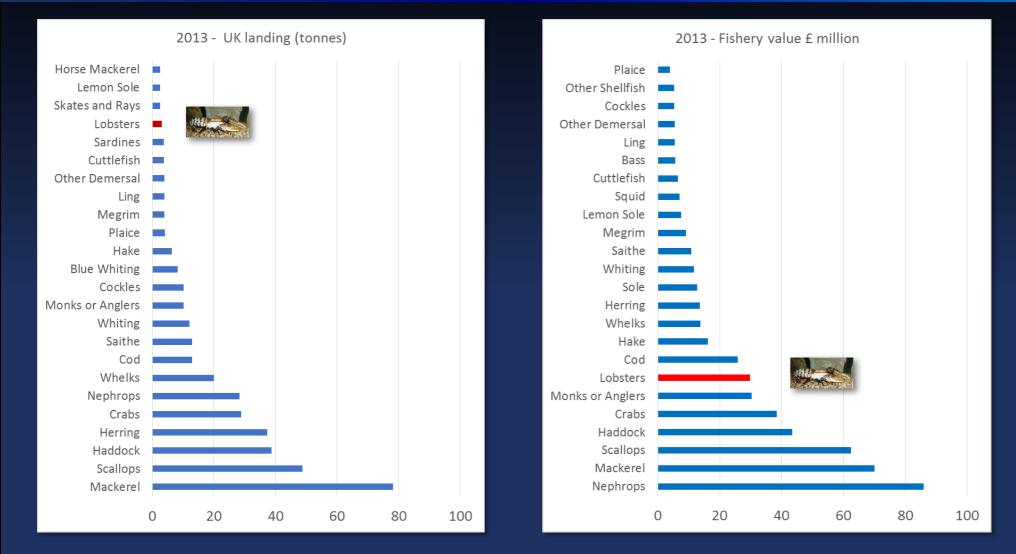


- Lobster biology, V-notching schemes & how we got started...
- DNA profiling/Genetic tagging: "the theory"
- North East Lobster Co-op (NELCO)"genetic" Vnotching scheme
- Results and implications for conservation & management



# Why lobsters?









- Homarus gammarus (European lobster)
- Long lived species 20-50 years
- Nocturnal, benthic, sedentary (home range 2-10km)
- Females spawn biannually/annually (size dependent) eggs carried ~1 year
- Pelagic phase: 2 3 weeks (high potential for dispersal)
- 1<sup>st</sup> 3 4 years lifespan cryptic
- Maturity takes 4-8 years?



- V-notching: female lobsters carrying eggs (berried) are marked with a small notch, and subsequently returned to sea (same location)
- Individuals legally protected = increased egg output
- "Potential" benefits to recruitment and long-term stock sustainability
- Existed for nearly 100 years!









- Volunteer or supported through grant aid schemes to local lobster fishermen willing to participate
- Fishermen get financial compensation to mark and release egg bearing females to the sea
- Conditional: implementation of appropriate monitoring mechanisms (good practice) to ensure that the Vnotching is being carried out properly



- Queen's University Belfast
- Participants bring egg berried lobsters ashore for Vnotching under scrutiny of a fishery officer
- Procedure means that egg carrying lobsters were often removed from local habitat and kept in cages
- Complex/expensive logistics; approach has also been linked to substantial egg loss, undue stress, and even the death of lobsters
- Fishermen in general not particularly happy!



#### How we get started - EU GEL project 1998

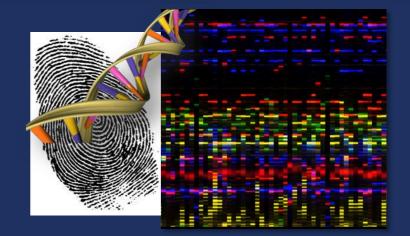




- N > 4,150 (51 sites)
- <u>Project aims</u>: genetic marker development (microsatellites), population structure; mating system; evaluation of genetic tagging (DNA profiling) – stock assessment
- In 2003 NELCO approached QUB to investigate the possibility of employing genetic tagging (DNA profiling) as suggested in GEL Website as a tool to monitor NELCO V-notching programme

Microsatellite DNA profiling/Genetic tagging

- A forensic based technique that allows for the unequivocal identification of individual to families
- No two individuals within outcrossing populations share the same microsatellite DNA profile
- Individual "DNA fingerprinting"
- Ideal tool for monitoring and assessing the impact of Vnotching on local stocks



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Microsatellite DNA profiling/Genetic tagging

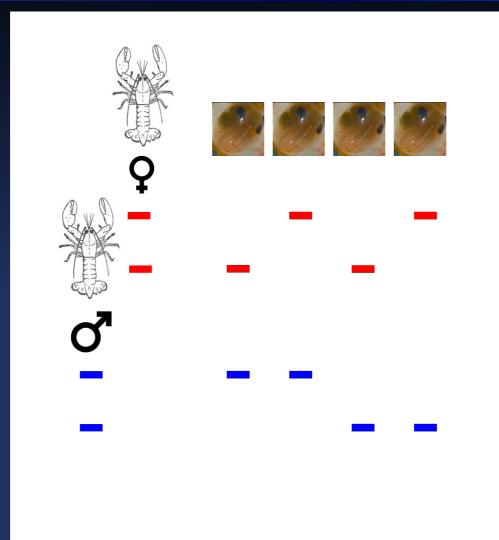
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- <u>Approach</u>: sampling/preservation of V-notch and eggs from individual females
- Examination of the maternal genetic profile (DNA extracted from the V-notch) alongside that of the offspring (DNA extracted from fertilised eggs) *enables the paternal contribution to be precisely identified*



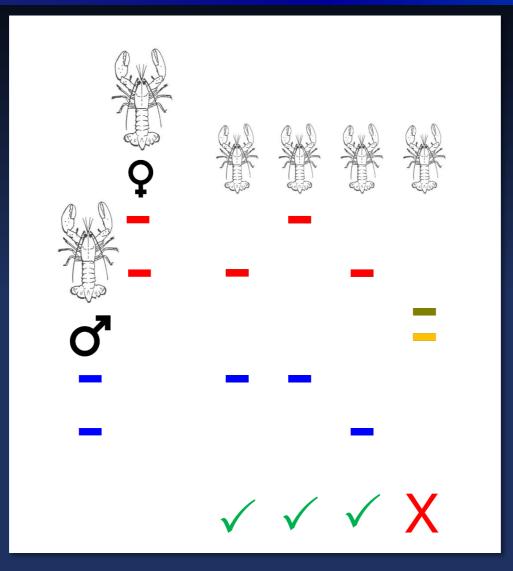
#### Identification of individuals to families





#### Identification of individuals to families







- Monitoring tool: no two individuals share the same genetic profile (eggs have to share half of the maternal genetic profile)
- <u>Fishery Applied Research</u>: if family genetic information is recorded into a database, it is then possible to subsequently test whether an unknown individual from the fishery belongs to any of the families existing in the database (i.e. *Vnotched/genetically tagged families*)
- How effective is the V- notching scheme?



## NELCO V-notching genetic programme

- First grant award to NELCO (2003): EC- Building Sustainable Prosperity Programme
- Protocol: from each berried female: V-notch + ~20 -100 eggs removed and stored
- Individuals returned to sea immediately: reduced egg loss
- V-notches & eggs sent for QUB

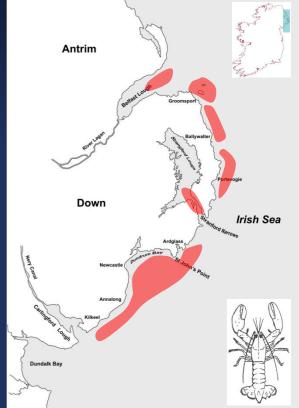




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## Summary of NELCO scheme

- Genetic screening commenced in 2003 (~40 boats)
- avg. 2,206 lobsters/year (1 for each 6 landed lobsters)
- In 2014, the NELCO database was comprised of >26,400 genetically tagged families
- Assuming 10,000-15,000 eggs = ~265 – 397M tagged individuals
- One of the most comprehensive multi-generation family genetic database for any marine species



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## Summary of NELCO scheme

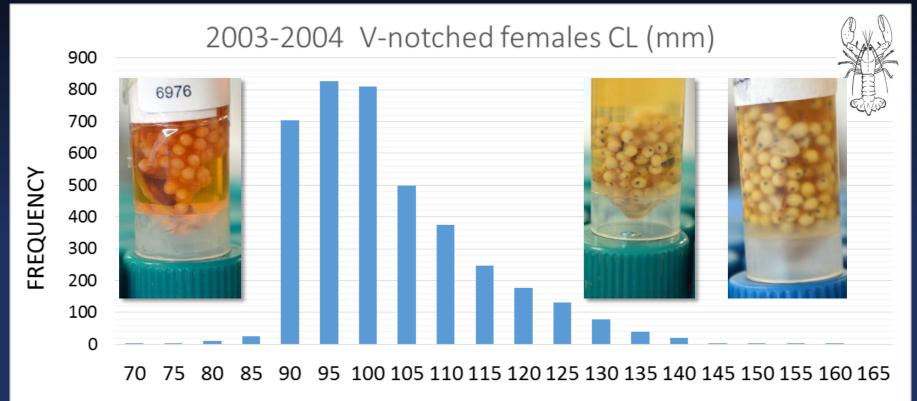


	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	Total
Jan				88	7	14	11	41		100	394		655
Feb			21	9		6	304	27	98	136	23		624
Mar		43	87	206		117	252	151	229	38			1,123
Apr		202	181	168			194	40	64	350			1,199
Мау	150	179	605	409		130	926		76		10		2,485
Jun	408	317	125	195	10	149	322	323	293	235	85		2,462
Jul	178	238	280	111	269	40	298	164	600	112	176		2,466
Aug	198	322	58	29	410	147	319	308	357	762	374		3,284
Sep	275	4 <mark>34</mark>	372	47	291	962	412	205	167	582	58	346	4,151
Oct	287	129	319	26	414	282	264	30	287	611	302	183	3,134
Nov	127	139	449		412	178	471	208	141	330	534	405	3,394
Dec	49	309	179	21	8	99		305	185	329	12		1,496
Total	1,672	2,312	2,676	1,309	1,821	2,124	3,773	1,802	2,497	3,585	1,968	934	26,473

- Samples screened for a panel consisting of 13 microsatellite marker loci
- *Power analysis = 99% probability of assignment to correct family*

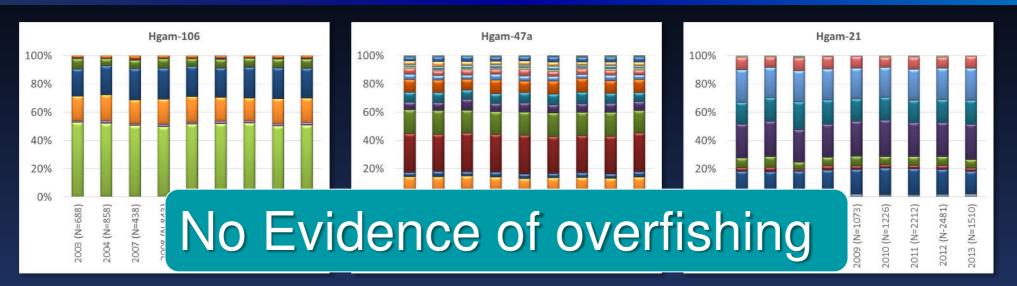
#### Parental pool - features

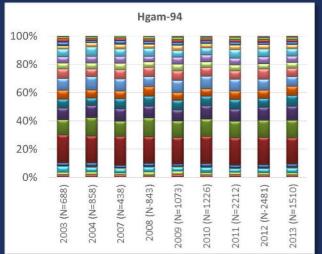


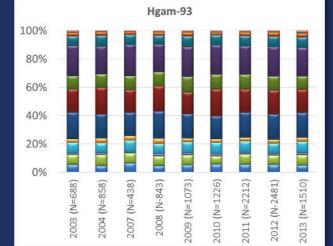


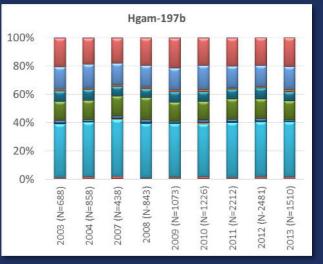
CARAPACE LENGTH

## Temporal stability in allele frequencies









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## Summary Results: impact assessment



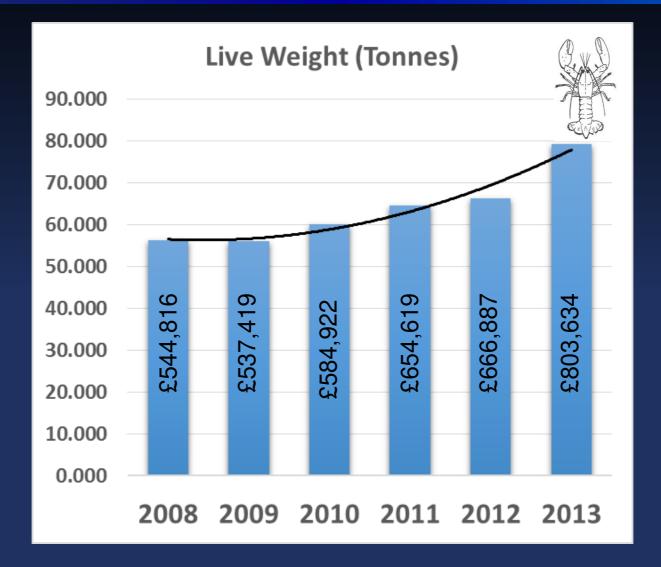
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V-notched lobsters (summer – spring)

Allowing for 4 - 8 2007/ 2008/ 2009/ 2010/ 2011/ 2012/ 2013/ years recruitment 2009 2010 2008 2011 2012 2013 2014 Avg. 2,200 ind./year 2003/04 Genetic baseline Families families from 2003/2004 n=1,596 No. lobsters assigned to 2003/04 families + 49 760 536 568 793 94 1148 % in relation to lobster (27%) (38%) (24%) (21%) (23%) (6%) (3%)caught by NELCO and sent to QUB

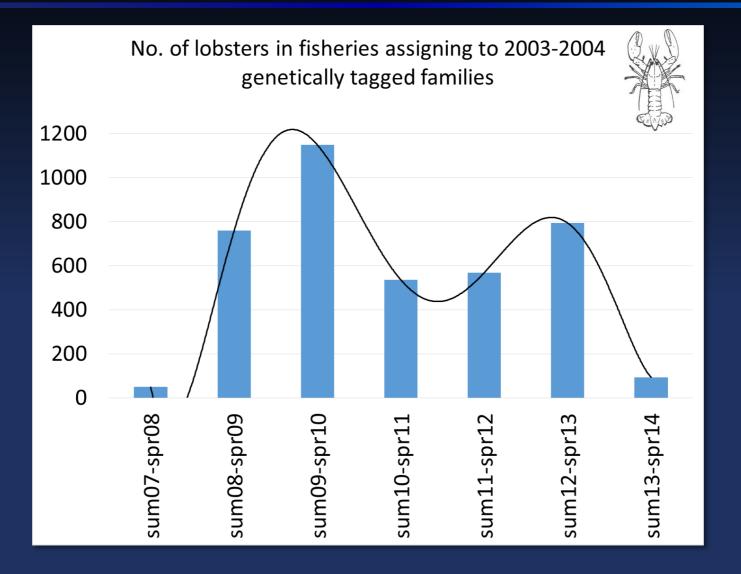
## Increasing landings





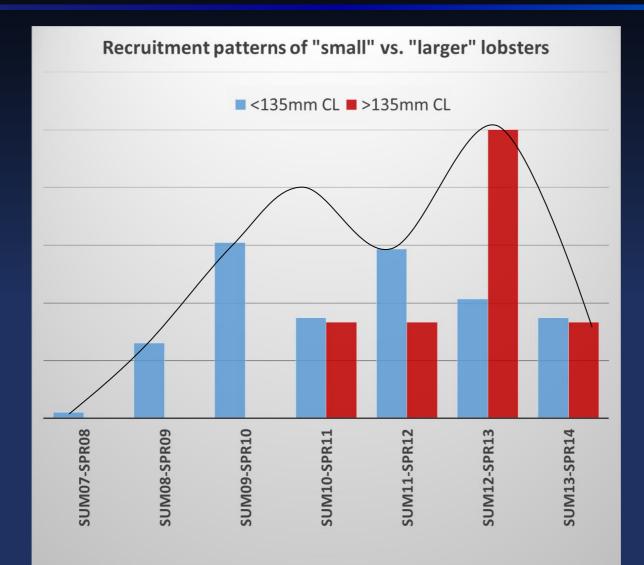
## Summary Results: preliminary





## Summary Results: preliminary

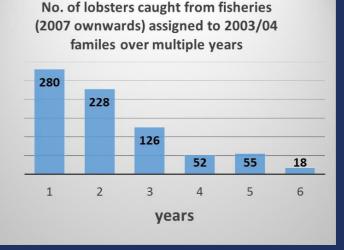






## Summary Results: preliminary

- Queen's University Belfast
- Maturation peak: 7 9+ years from hatching for "small" and "larger" lobsters respectively
- 60% (N=957) of 2003/2004 lobsters families contributed between 1 and 20 (avg. 2) lobsters to fishery from 2007 onwards – *i.e. recruited locally*
- Recruitment for 63% of families was spread over 2 to 6 years



#### Local recruitment pattern





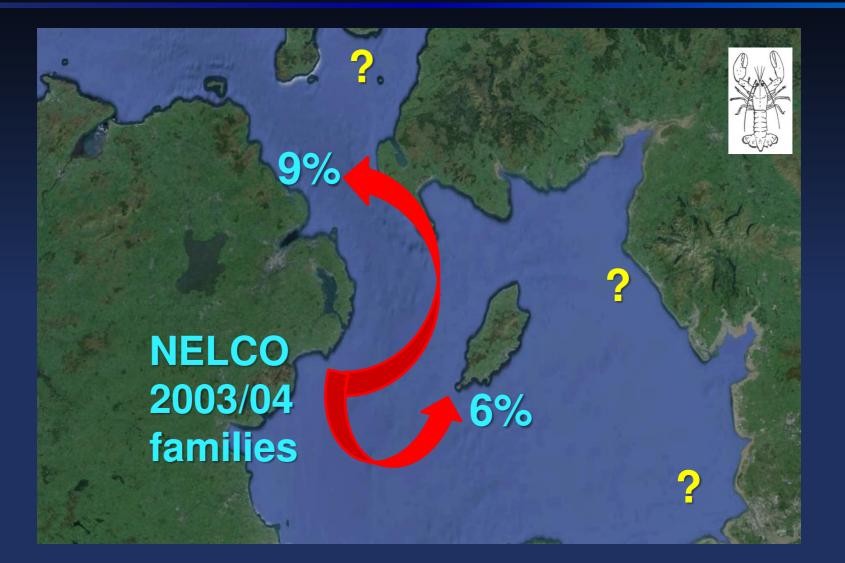
## Dispersal pattern – "north-south"

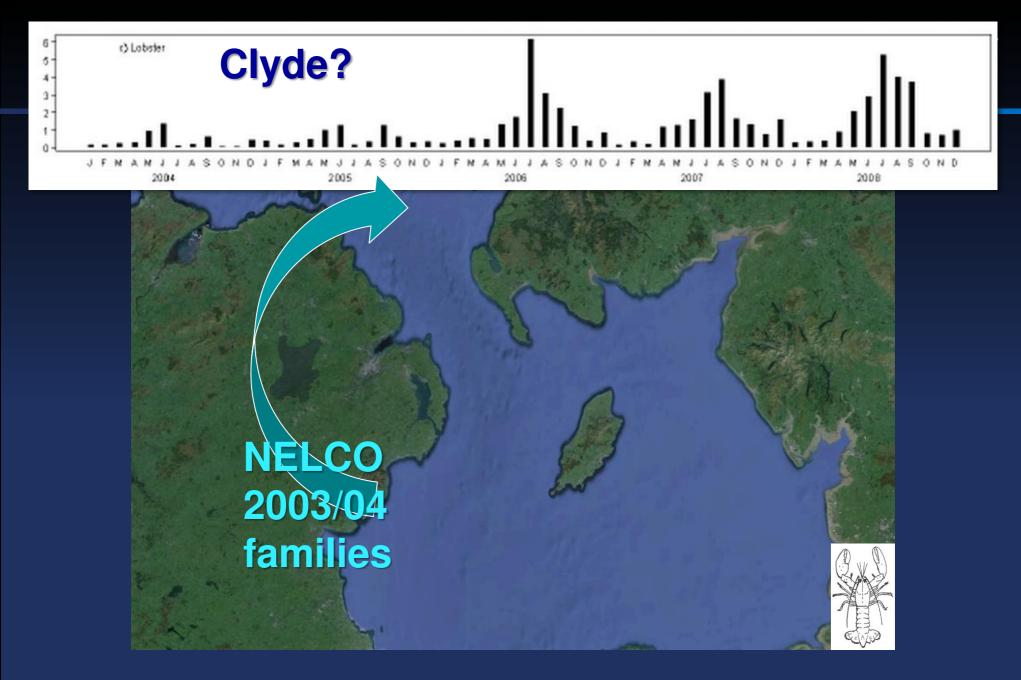




## Dispersal pattern (NCLFA & IoM)









- First measurable evidence for positive impact of Vnotching
- The Maine lobstermen haven been doing it right! (records landings in 2015) → V-notching does work!
- In comparison to other approaches (e.g. supplemental stocking) – cheaper, more effective and without risks i.e. "natural"



 Hatchery systems: bypass *natural selection* (i.e. decreasing mortality at early stages) = introduction of "less fit" genetic material into the wild



- Despite potential for dispersal, there seems to be strong evidence for local recruitment
- Strong selection to stay close to suitable rocky habitats
- Lobster larvae likely capable of "vertical" movement in water column?
- Work is still ongoing (e.g. reliable estimates of population size – *extended pedigrees*)



## Acknowledgements

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- Colin Nelson (NELCO's Director initiated discussions with QUB) & all NELCO members
- QUB Fish Genetics Research Group: Andy Ferguson, John Taggart, Rosaleen Hynes, Caroline Bradley, Maria Hughes, Sean Fitzpatrick, Clio Surgenor, Amanda Kovalczyk
- AFBI: Carrie McMinn, Matt Service & Walter Crozier
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