


### Population structure and genetic stock identification of brown trout (*S. trutta*) from Mid Shannon system (Lough Ree and Lough Sheelin)

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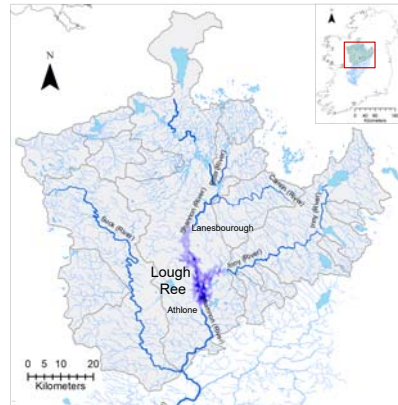


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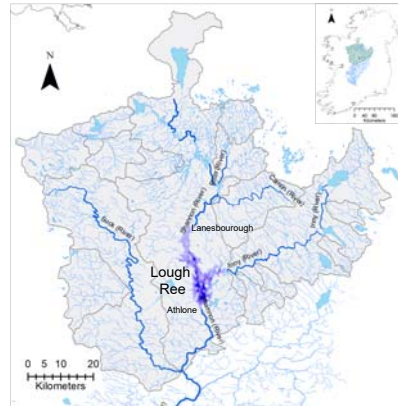
### Area of study: Lough Ree

- With an area 103.5 km<sup>2</sup>, it is the 2nd largest lake on the Shannon after Lough Derg
- lake stretches ~30km from Lanesborough in Co Longford to Athlone in Co Westmeath
- 3 major associated rivers:
  - 2 major inflowing rivers:
    - River Shannon (North)
    - River Inny (63km)
  - River Suck (133km)




### Area of study: Lough Ree

- Regarded as one of the premier angling venues in the country
- Mixed fishery with good stocks of trout, pike and coarse fish present
- Improved water quality and habitat rehabilitation has led to increasing wild trout stocks
- Lough Ree Fish Hatchery operates from Coosan, Athlone




### Key Aims & Questions

- Describe patterns of brown trout population genetic structure within the system (i.e. genetically distinct populations)
- Quantify contributions of brown trout populations inhabiting the various sub-catchments to the Lough Ree adult mixed brown trout stock (Genetic Stock Identification → GSI)
- To investigate how are the trout from the various sub-catchments distributed within the lake (contrast two data sets)
  - Fish caught by anglers in the lake over a full angling season
  - Fish caught in the fish stock survey over a 3 week period in Feb/March, 2014
- Is there any evidence for Roscrea hatchery fish on the "wild" populations in Lough Derravaragh, Lough Ree or any of the other riverine baseline samples?
- How different are the Lough Owel fish samples genetically to the other stocks in the mid Shannon area?



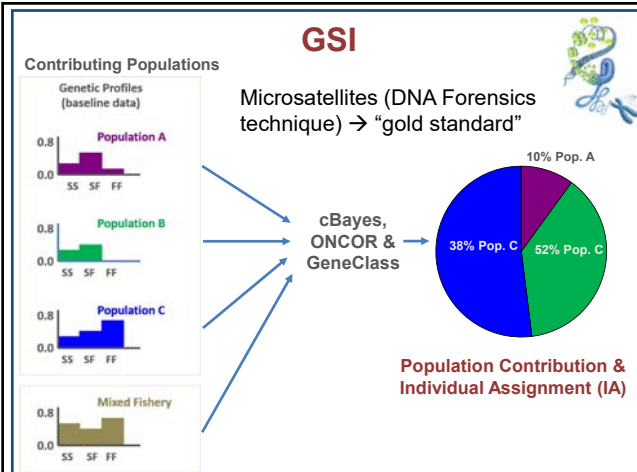
### Population Structuring and GSI

- Genetic Stock Identification: widely applied methodology for the management of mixed-stock fisheries (e.g. Pacific salmon, Atlantic salmon)
- GSI estimates the composition of the mixed fishery stock by comparing genetic profiles generated from a set of markers to a baseline of similar genetic profiles collected from spawning ground samples
- Requirements: (1) knowledge of which populations are contributing to the mixed fishery; (2) existence of genetic differences among those groups; (3) ability to identify these genetic differences



### GSI

Microsatellites (DNA Forensics technique) → "gold standard"



Contributing Populations

Genetic Profiles (baseline data)

Population A

Population B

Population C

Mixed Fishery


cBayes, ONCOR & GeneClass

10% Pop. A

38% Pop. C

52% Pop. C

Population Contribution & Individual Assignment (IA)

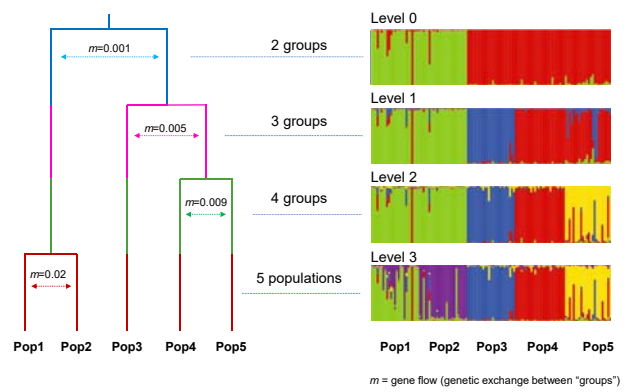


### Finding Population Structuring

- All samples screened for a panel of 20 microsatellite marker loci (genetic tags)
- “STRUCTURE” mathematical approach used for assessing population genetic structuring
- Hierarchical approach → detect broader patterns of population structuring (i.e. regional groups) in the first instance;
- Repeat process within each regional group until no further substructuring is possible from the data (i.e. individual population level)
- Useful for identifying genetically similar populations and reporting groups



### Hierarchical Structure Analysis

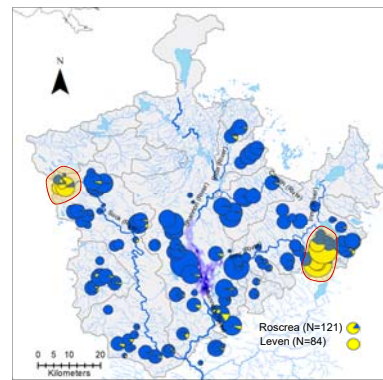


### Lough Ree: river (baseline) & lake sampling

- N = 2,834 - Electrofishing & angling sampled over a four year period (2011 – 2015)
- N = 1,497 juveniles (0+ and 1+)
- N = 1,317 adults (lake and rivers)
- 151 sites: 66 streams & tributary rivers
- 1 - 47 specimens per site (avg. ~14/site)
- Scales retained for DNA analysis
- GPS for most samples



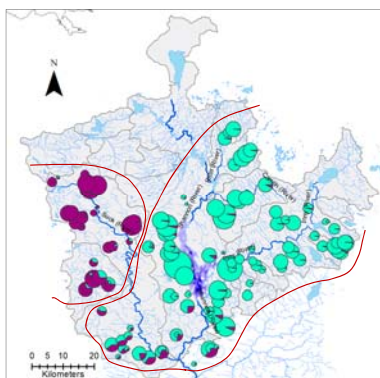
### STRUCTURE: presence of Roscrea hatchery fish



- Investigate the presence of Roscrea hatchery-reared fish on the catchment
- Used fish from Roscrea and Leven as references in STRUCTURE analysis
- Excluding samples from Lough Owel and Upper Lough O'Flynn, no substantial evidence of hatchery fish in the system



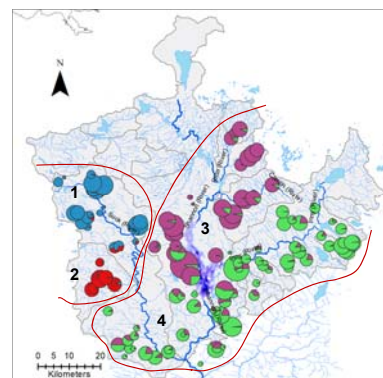
### STRUCTURE: Level 0



- Remove Loughs Owel and O'Flynn – Repeat STRUCTURE analysis
- 2 Main groups
- River Suck (Upper & Middle)
- Lower Suck and rest of Lough Ree system

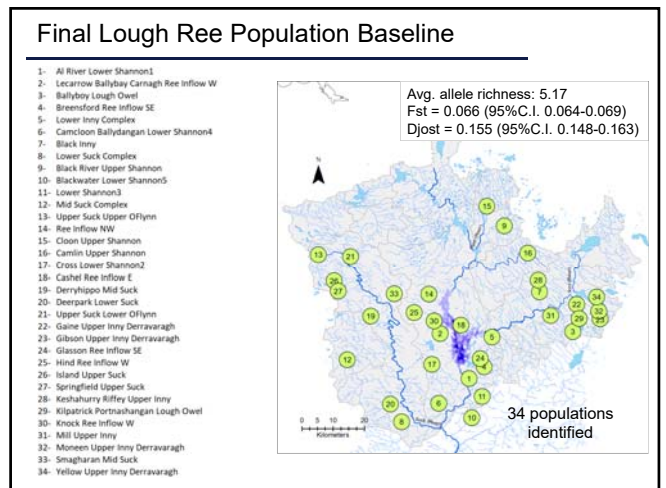
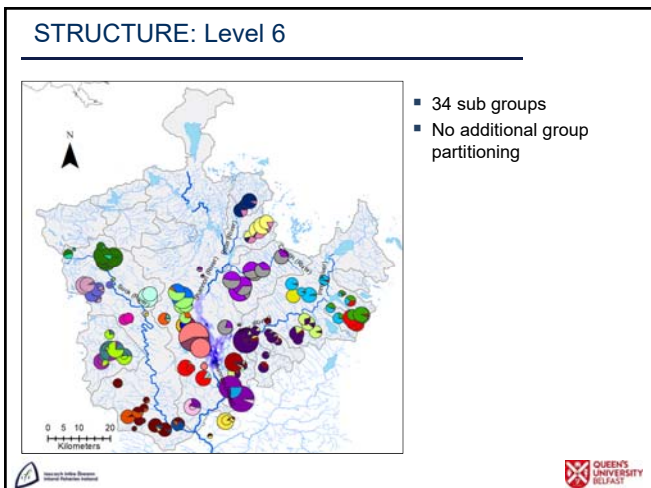
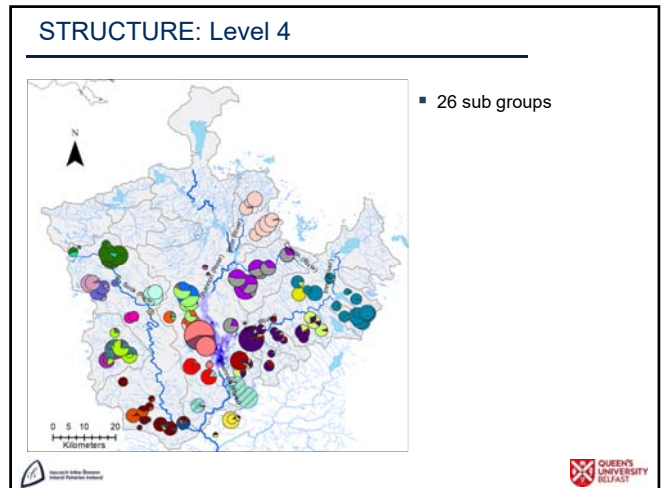
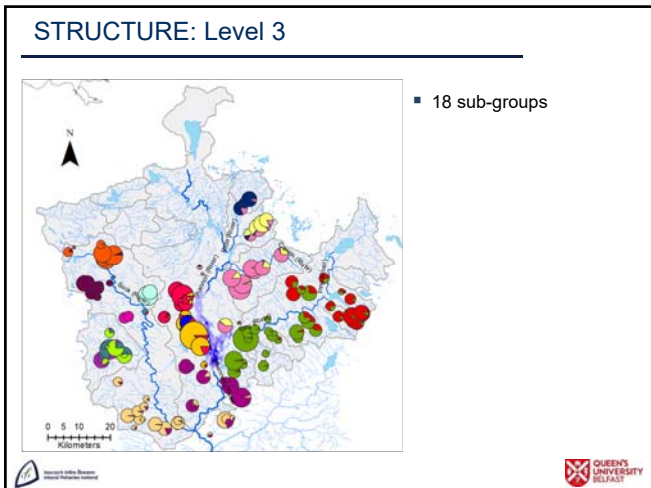
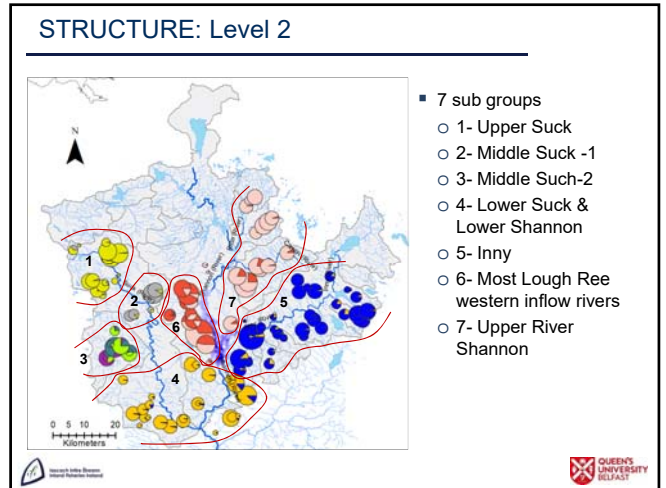
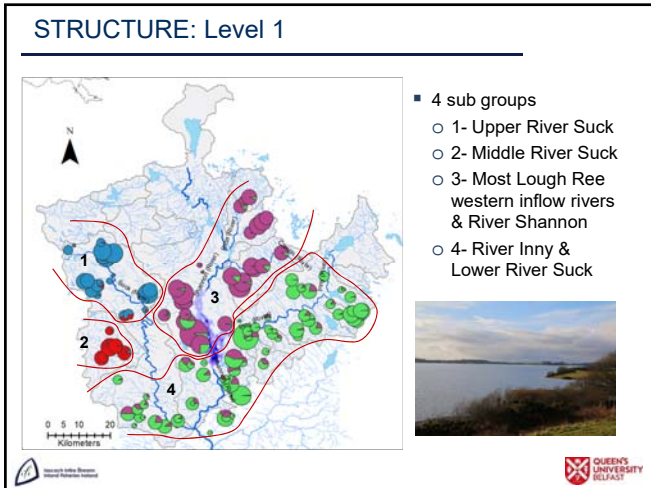


### STRUCTURE: Level 1

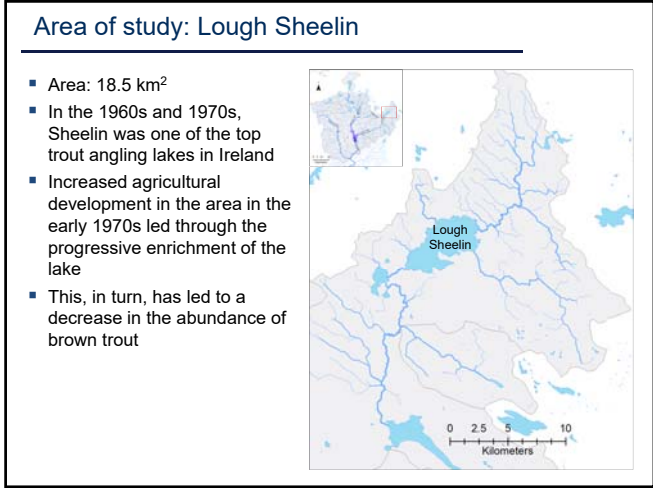
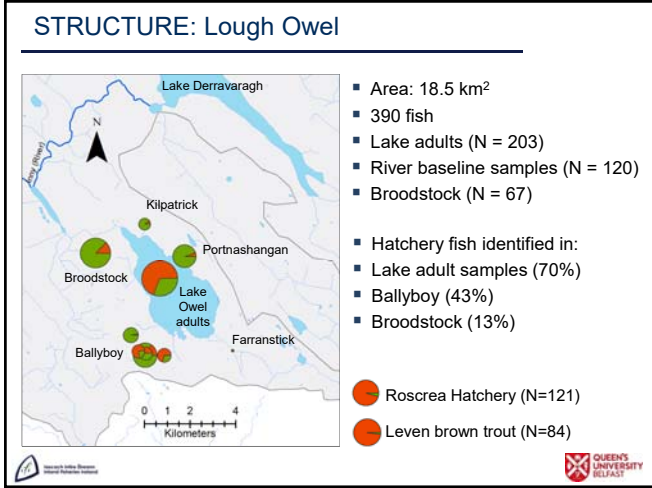
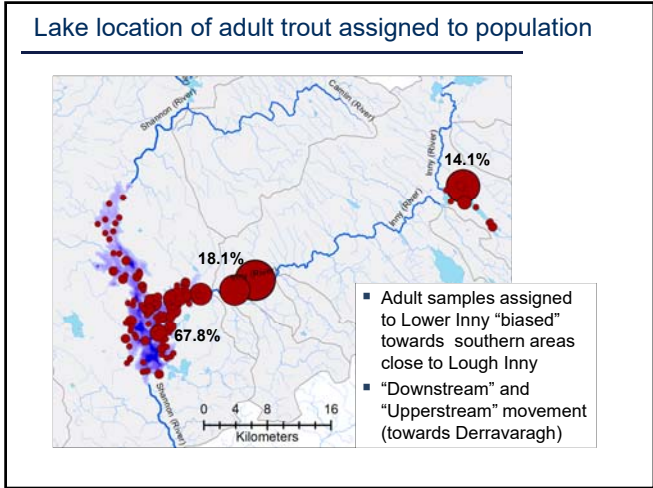
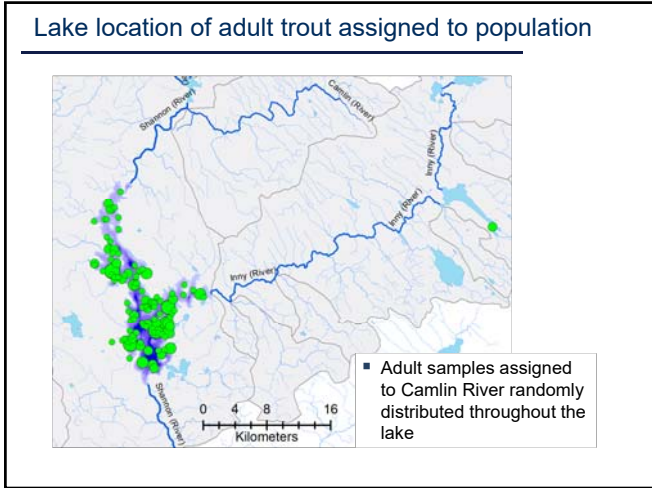
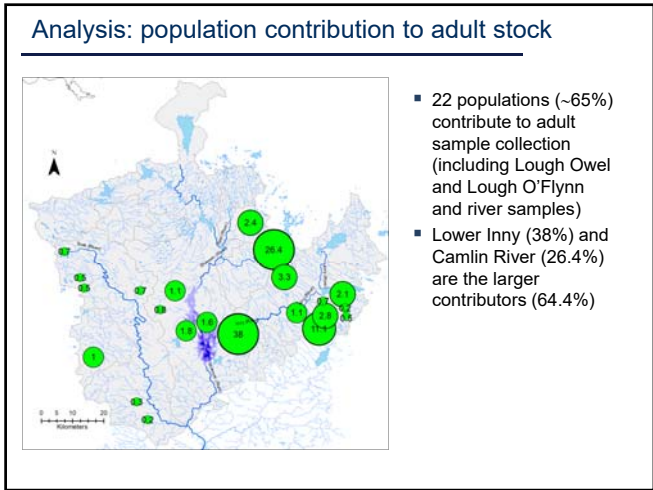
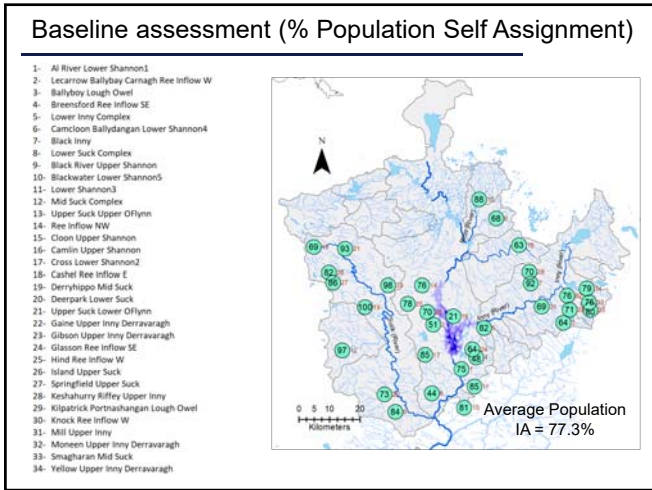


- 4 sub groups
  - 1- Upper River Suck
  - 2- Middle River Suck
  - 3- Most Lough Ree western inflow rivers & River Shannon
  - 4- River Inny & Lower River Suck



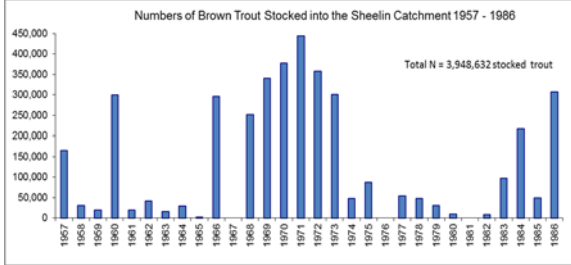






Area of study: Lough Sheelin

- From 1957 to 1986, the lake was systematically stocked with over 3,945 Million brown trout of farm origin as follows: fry = 1,41 Million; Fingerlings = 0.952 Million; Summerlings = 1,124 Million; Yearlings = 0.568 Million; 2 yr olds = 0.164 Million



Key Aims & Questions (Lough Sheelin)

- Recent surveys (IFI) indicate reduced levels for enrichment
- Assess current status of the Lough Sheelin brown trout populations taking in consideration known stocking history
- Determine possible impact(s) of the considerable stocking history in the lake on wild populations



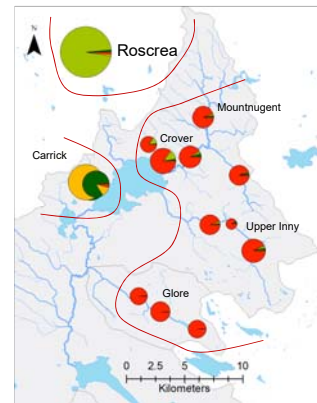
Area of study: Lough Sheelin

- 761 fish
- River genetic baseline: samples ( :
  - Carrick Site 1 (N=37)
  - Carrick Site 2 (N=62)
  - Maughera (N=37)
  - Crover (N=50)
  - Mountrugent (N=78)
  - Glore (N=50)
  - Upper Inny (N=55);
- Lake adults (N = 203)
- Roscrea hatchery (N = 159)



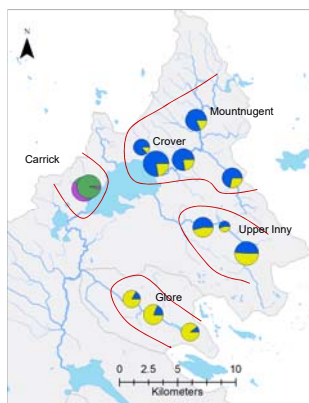
STRUCTURE: Level 0

- 3 groups
  - Roscrea
  - Carrick River
  - Mountrugent, Crover, Upper Inny, Glore
- Very little contemporary direct impact of Roscrea derived fish on wild stocks



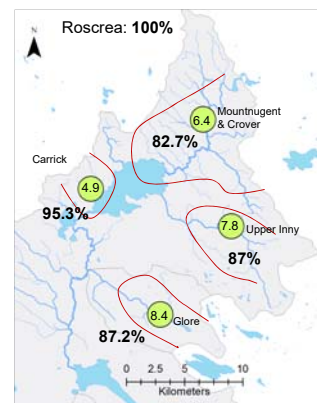
STRUCTURE: Level 1 (removing Roscrea)

- 3 groups
  - Mountrugent & Crover
  - Upper Inny
  - Glore
- No further partitioning



Results: Average allelic richness = 6.8

- Carrick → lower level of allelic richness
- $F_{st} = 0.074$  (95% C.I. 0.067-0.081)
- $D_{jost} = 0.120$  (95% C.I. 0.107-0.134)
- High levels of population self assignment



### Analysis: population contribution to adult stock

- Mountnugent & Crover → larger contributors
- 18% of adult fish in the lake likely to be of hatchery origin

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### Summary & Concluding Remarks – Lough Ree

- Substantial population substructuring within each catchment (i.e. reduced gene flow among areas.  $F_{st} = 0.066$ )
- With the exception of Lough Owel and Lough O'Flynn, no contemporary evidence of hatchery derived fish among adults
- The major contributors to the Lough Ree brown trout stock are the populations from the Lower Inny (38%) and Camlin River (26.4%).
- While the River Suck is a comparatively poor contributor to the lake stock, fish from the lower Suck can access Lough Ree (i.e. no impassable barrier)
- The Lower Inny population complex produces both downstream migrants to Lough Ree and upstream migrants to Lough Derravaragh
- Some differences were observed in the geographical distribution of fish caught by anglers in the lake (over a full angling season) and those caught during a fish stock survey over a 3 week period in Feb/March, 2014
- Evidence for Roscrea derived hatchery fish were noted in Lough Owel and Upper Lough O'Flynn. These seem to be contained into these areas/lakes

### Summary & Concluding Remarks – Lough Sheelin

- Results suggest the existence of considerable genetic sub-structuring among populations inhabiting the main catchment rivers of Lough Sheelin (reduced gene flow)
- "Gradient" patterns of genetic structuring observed among samples from Mountnugent, Upper Inny and Glore indicates isolation by distance and restricted gene flow
- Despite stocking history, there is no evidence suggesting major impact in terms of direct contribution of farm derived fish to wild stocks

### Acknowledgements

- To all the many people that made this possible..... many thanks!