# Red grouse in Ireland and Scotland: Adaptive genetic divergence and implications for conservation

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*Lagopus lagopus scoticus*

## Situation of the red grouse

Facing **risk of extinction** in Ireland, but relative abundant in Scotland and England. To restock the fragmented and small populations in Ireland, an **introduction** of Scottish red grouse is considered.

## Question

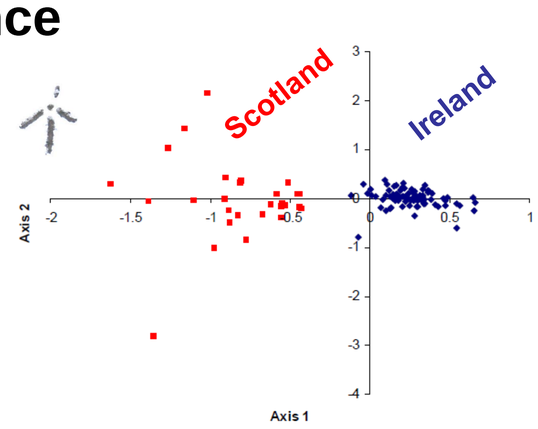
Do red grouse populations in Ireland and Scotland show significant **divergence in adaptive genetic variation**?

If so, they should be recognized as separate evolutionary lineages for conservation purposes.

## Neutral genetic divergence

Significant divergence between Irish and Scottish birds was found in a study on 19 microsatellite markers, with a significant Fst of 0.068 (McMahon et al. 2012).

BUT, is this due to **drift** or **selection**?



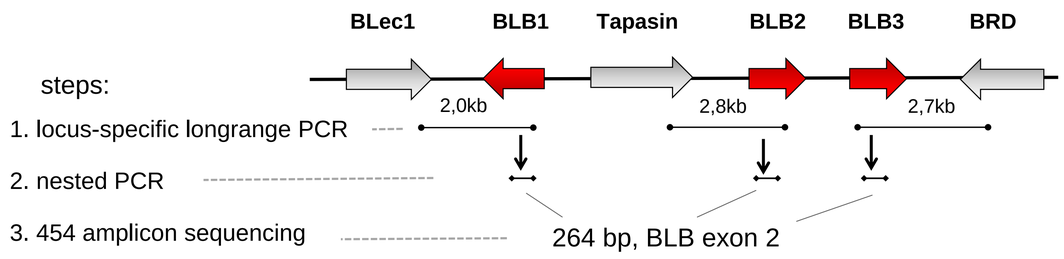

AFC 2D plot of 89 Irish and 27 Scottish red grouse genotyped for 19 microsatellite markers

## Samples

73 Irish and 223 Scottish red grouse.

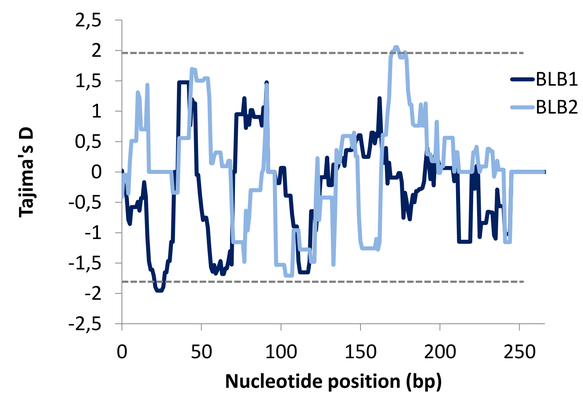
## Genetic Marker

Single locus amplification system for two immune genes of the MHC class II: **BLB1** and **BLB2.** Genotyped using 454 amplicon sequencing.




## Results

1. Both MHC genes are **expressed** and **under selection**:




Tajima's D sliding window:
Certain positions are under balancing selection, others under purifying selection.

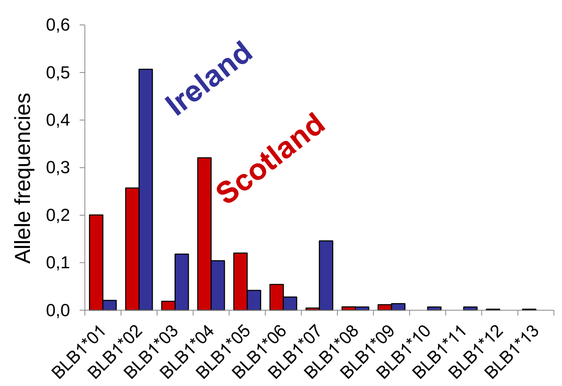
| | Locus | $d_N/d_S$ | Z | p |
|---|---|---|---|---|
| All | BLB1 | 0.96 | -0,185 | 0,85 |
| | BLB2 | **1.66** | 1.78 | **0.04*** |
| PBR | BLB1 | 1.35 | 1.13 | 0.13 |
| | BLB2 | **1.94** | 1.92 | **0.03*** |

$d_N/d_S$ ratio: Balancing selection on BLB2.

2. **Significant divergence** in adaptive genetic variation:

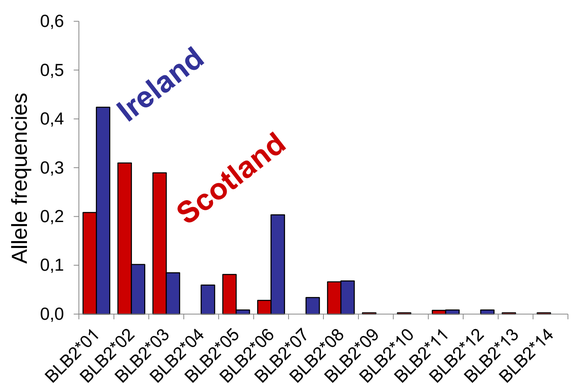
**BLB1**

Fst Ireland-Scotland 0.119, $p < 0.0001$




**BLB2**

Fst Ireland-Scotland 0.101, $p < 0.0001$




| | Locus | N | # Alleles | $H_{obs}$ | $H_{exp}$ |
|---|---|---|---|---|---|
| Ireland | BLB1 | 72 | 11 | **0.685*** | 0.674 |
| | BLB2 | 59 | 10 | **0.754*** | 0.735 |
| Scotland | BLB1 | 212 | 11 | 0.770 | 0.766 |
| | BLB2 | 197 | 11 | 0.745 | 0.766 |

Observed and expected heterozygosities ($H_{obs}$ and $H_{exp}$) are similar in Ireland and Scotland. Significant excess of heterozygotes in Ireland according to Hardy-Weinberg.

3. Divergence is significantly **higher** in the MHC markers than in neutral variation:

$Fst_{MHC}$ 0.11 (95% CI = 0.101-0.119) **>>** $Fst_{Microsat}$ 0.068 (95% CI = 0.043 – 0.098)

## Conclusion

Divergence in adaptive genetic variation between Irish and Scottish red grouse is not due to drift but to selection.

We advise against the introduction of Scottish red grouse to supplement Irish populations.

## Additional result

Evidence for Copy Number Variation: 11% of the Irish individuals revealed a third BLB gene.

**Thanks to Barry McMahon and Marianne James for providing samples and to Niall Corbet for the picture of the red grouse**

**Reference**: McMahon BJ, Johansson MP, Piertney SB, Buckley K, Höglund J (2012) Genetic variation among endangered Irish red grouse (*Lagopus lagopus hibernicus*) populations: implications for conservation and management. *Cons Gen* **13**, 639-647

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