

Post-Doctoral Fellowship: Proposal Outline

Topic	Feralisation (or reverse domestication) in Atlantic salmon
Research Theme(s)	<ol style="list-style-type: none"> 1) Bioresources 2) Climate Change
Background and Rationale	<p>Humans are a major agent shaping the genomes and traits of domesticated, wild and feral animals and plants¹. In captive, populations, the biology of organisms is radically altered by environmental effects on phenotypes, potentially underpinned by epigenetic modifications that can be transmitted to offspring, and by genetic drift, inbreeding and selection. The domestication process thus entails “unnatural selection on unnatural phenotypes”. If captive individuals are released or escape into the wild, they can interbreed with free-living individuals or establish self-sustaining feral populations in vacant habitats. Maladaptive alleles might then be purged by “natural selection on unnatural phenotypes”, but very little is known about the eco-evolutionary mechanisms involved in this feralisation (“reverse domestication”) process, complicated by changes to the recipient wild environments themselves as a consequence of global warming.</p> <p>Feral organisms, however, do not fit easily into ‘wild’ or ‘domesticated’ categories, but rather straddle and blur the lines between them². Feralisation can be defined as the process by which domesticated organisms or artificially selected gene variants become established in (potentially highly human modified) wild environments in the absence of purposeful anthropogenic propagation. Simply put, feralisation involves ‘rewilding’ of individuals and genomes.</p> <p>The study of feralisation is relevant to invasion biology, conservation, hybridisation, ‘rewilding’ and speciation³. Feral individuals can derive from one or more domesticated sources, forming ‘endoferal’ populations in vacant ecological niches, or ‘exoferal’ populations following admixture with wild populations². These situations offer fascinating windows into ‘natural selection on artificial phenotypes and a unique opportunity to examine genetic and ecological mechanisms mediating reverse domestication and (mal)adaptation to complex and changing natural environments. Yet feralisation research remains in its infancy. Despite the ubiquity of feral populations (e.g. dingoes in Australia, chickens and feral pigs in Hawaii, Soay sheep in Scotland, weedy rice in Southeast Asia, feral pigeons the world over), little is known about the when, why and how of feralisation. In particular, there is a dearth of knowledge on the genomic mechanisms underpinning feralisation, the selective targets and agents involved.</p> <p>This ‘Fellowship’ would tackle these big questions in an excellent model system, Atlantic salmon (<i>Salmo salar</i>) – a culturally, economically and ecologically important species experiencing widespread population decline in the wild and reared in captivity for food or stocking/ranching programmes. A powerful experimental design, in which offspring from wild- or captive-ancestry genetic backgrounds are reared under common-garden conditions in replicate natural streams, as well as in an artificial captive environment,</p>

	<p>would be used to test and evaluate potential molecular and phenotypic mechanisms involved in feralisation. This would allow dissection of genetic versus environmental effects on traits and performance, as well as associated epigenetic and transcriptomic mechanisms. Modern genomic approaches will be used to test for DNA-level signatures of within-generation natural selection and across-generation genetic changes in feral populations using new and archived samples. In addition to their value for conservation and management, findings acquired from the ‘Fellowship’ would generate novel insights into ecological and evolutionary processes driving intraspecific diversity in the Anthropocene. The ‘Fellowship’ would impact a wide scientific community, raise public interest in science, and inform biodiversity policy.</p> <p>This ‘Fellowship’ would enable a continuation of and build on history of world leading research on the interactions between captive bred and wild salmon pioneered at the Marine Institute’s Newport Research Station enabled by EU FP5, FP6 and FP7 awards, the Beaufort Marine Research Award, the Marine Research Programme 2014-2020 Principal investigator Awards in Fish Population Genetics, and the Science Foundation Ireland and BBSRC (UK) Investigator Awards^{4,5,6,7}.</p>
<p>Scope of Research (Scientific/ Technical Challenge)</p>	<p>The overarching aim of this fellowship would be to extend understanding of feralisation/rewilding using salmon as a model, based on two core, integrated, objectives:</p> <ol style="list-style-type: none"> (1) To gain molecular insights (genomics, epigenomics, transcriptomics) into the feralisation process, and (2) To gain phenotypic insights into the feralisation process. <p>The fellowship should address key research objectives as follows:</p> <p>In respect of core objective 1 molecular insights.</p> <ol style="list-style-type: none"> 1.1 Explore genomic signatures of ontogenetic selection in experimental first-generation farm releases; 1.2 Exploit archival samples from historical common garden experiments to test for parallel signatures of feralisation selection; 1.3 Explore genomic changes over time in a natural feralisation experiment; 1.4 Study the role of epigenetic variation/inheritance and associated transcriptomic differences in feralisation; <p>In respect of core objective 2 phenotypic insights.</p> <ol style="list-style-type: none"> 2.1 Investigate the role of the microbiome in feralisation and links to brain chemistry; 2.2 Examine the role of energetic phenotypes in feralisation.
<p>Expected Impact(s)</p>	<p>The fellow will engage with relevant national and international networks, and explore opportunities for collaboration and securing further research funding under Horizon Europe.</p>

	<p>This fellowship will help to build national expertise in this research area.</p> <p>The Fellow will produce policy briefs for stakeholders, and publish their research findings as widely as possible through peer-reviewed papers, conference presentations, articles, etc.</p>
Outcomes	<p>A ‘Fellow’ equipped and effective working in the fields of evolutionary biology, population genetics, fisheries and climate change.</p> <p>Continuation and enhancement of the Marine Institute’s international standing and reputation in research into farm x wild interactions and climate change.</p>
Specific Collaboration	<p>The successful undertaking of the Fellowship would require co-operation, study facilitation and working relationship with aquaculture industry particularly MOWI Ireland.</p>
Location of Fellow	<p>Marine institute, Newport, Co. Mayo</p>
Duration and Funding Available	<p>4 years</p> <p>€100,000 per annum (i.e. total €400,000 maximum for duration of four years)</p>
References	<ol style="list-style-type: none"> 1. Palumbi, S. R. Humans as the world’s greatest evolutionary force. <i>Science</i> 293, 1786–1790 (2001). 2. Gering, E. <i>et al.</i> Getting back to nature: feralization in animals and plants. <i>Trends in ecology & evolution</i> 34, 1137–1151 (2019). 3. Henriksen, R., Gering, E. & Wright, D. Feralisation—the understudied counterpoint to domestication. <i>Origin and evolution of biodiversity</i> 183–195 (2018). 4. McGinnity, P. <i>et al.</i> Fitness reduction and potential extinction of wild populations of Atlantic salmon, <i>Salmo salar</i>, as a result of interactions with escaped farm salmon. <i>Proceedings of the Royal Society of London. Series B: Biological Sciences</i> 270, 2443–2450 (2003). 5. Glover, K. A. <i>et al.</i> Half a century of genetic interaction between farmed and wild Atlantic salmon: status of knowledge and unanswered questions. <i>Fish and Fisheries</i> 18, 890–927 (2017). 6. Reed, T. E. <i>et al.</i> Quantifying heritable variation in fitness-related traits of wild, farmed and hybrid Atlantic salmon families in a wild river environment. <i>Heredity</i> (2015).