MOLECULAR ECOLOGY
Molecular Ecology (2017) **26**, 413–419 doi: 10.1111/mec.13941

Recipient of the 2016 *Molecular Ecology* Prize: Louis Bernatchez – advancing the conservation of aquatic resources with his contributions on the ecological genomics of adaptation and speciation

Louis Bernatchez, professor and holder of Canadian Research Chair in Genomics and Conservation of Aquatic Resources at Université Laval, Québec City, Québec, Canada, is the Molecular Ecology Prize winner of 2016. As long-standing collaborators, friends and, in the case of one of us (SMR), student of Louis Bernatchez, we can only applaud this as an exceptionally good choice. For three decades, Louis has represented a Herculean scientific force influencing and shaping the field of molecular ecology and there are definitely no signs that this should not continue. He was a pioneer in the early days of phylogeography, a pioneer in applying functional genomics to the study of nonmodel organisms and is currently a pioneer in population genomics and its integration into a holistic framework, encompassing physiological, life history and population historical components of adaptation. His study organisms cover a wide taxonomic span from marine invertebrates, birds and mammals to fishes, but with the latter being the most important in his research. Louis runs a big research group and is immensely productive, with more than 375 published papers at the time of writing and a continuing trend of strong growth. This staggering productivity is matched by an impressive flow of talented graduate students, postdocs and research professionals who have worked in his laboratory. Louis clearly inspires his students to continue in the field, with the majority of his graduates pursuing successful careers in related science fields. In fact, well over 100 highly qualified personnel have moved on from the Bernatchez Lab, with over 20% now working as professors/instructors worldwide in eight different countries. The field of molecular ecology is in good hands considering this extensive and impressive training.

It is simply impossible to do justice to all the excellent contributions that have come out of Louis' laboratory, so in addition to a more formal biographical sketch, we decided to focus on three main themes: his early contributions to our understanding of the phylogeography of freshwater fishes, his long-standing research programme in understanding the mechanisms of adaptive divergence in dwarf and normal-sized lake whitefish (*Coregonus clupeaformis*) and his research into genetic structure and adaptive responses in panmictic Atlantic eels (*Anguilla rostrata* and *A. anguilla*). This has been a hard choice and for instance leaves out highly substantial contributions towards understanding adaptive divergence and genetic structure of such important species as Atlantic salmon (*Salmo salar*) and brook char (*Salvelinus fontinalis*) (Castric & Bernatchez 2003; Fraser *et al.* 2004; Fraser & Bernatchez 2005a,b; Garant *et al.* 2005; Roberge *et al.* 2007; Dionne *et al.* 2008, 2009; Gauthier-Ouellet *et al.* 2009; Bougas *et al.* 2013; Bourret *et al.* 2013, 2014; Moore *et al.* 2014; Ferchaud *et al.* 2016) and several important contributions to conservation biology (Fraser & Bernatchez 2001, 2005a; Fraser *et al.* 2004; Lippé *et al.* 2006; Roberge *et al.* 2006, 2008; Milot *et al.* 2007; Marie *et al.* 2010, 2012; April *et al.* 2011; Lamaze *et al.* 2012, 2013; Valiquette *et al.* 2014; Bernatchez 2016). Overall, Louis' passion and dedication to the genetic conservation of aquatic resources has significantly advanced these fields, such that the notions of genetic health and evolutionary adaptive potential are synonymous with his achievements in all of these areas.

Curriculum

Louis Bernatchez obtained his PhD in 1990 at Université Laval, Québec City, Quebec, Canada, in 1990 with Prof. Julian Dodson as supervisor. Whereas most of his Ph.D. work concerned the phylogeography of salmonid fishes, it is interesting to note that his very first paper focused on the bioenergetics of fishes (Bernatchez & Dodson 1985), a theme he has later revisited in his pursuit of understanding adaptive divergence of sympatric lake whitefish species pairs (Dalziel *et al.* 2015). From 1990 to 1991, he was a postdoc at Université Montpellier II, France, in the laboratory of Prof. Francois Bonhomme and from 1991 to 1992 a postdoc at the University of Guelph, Canada, collaborating with Profs. Moira Ferguson and Roy Danzmann. From 1992 to 1995, he was first a research associate and subsequently assistant professor at the Université du Québec (INRS). Finally, in 1995 he returned to Université Laval to continue his curriculum and became full professor in 2004 and since 2006 holder of a Canadian Research Chair in Genomics and Conservation of Aquatic Resources. In between he has been a visiting scientist at the University of Brisbane, Queensland, Australia (2000–2001), and the University of Konstanz, Germany (2002). He has received numerous awards; in addition to his Canadian Research Chair, some highlights include the E.W.R. Steacie Award from NSERC (2002), elected member of the Royal Society of Canada (2011), elected Fellow of the American Association for the Advancement of Science (2011), the Prix du Québec, Marie-Victorin (2012) and invited membership of FacultyRow's Super Professors (2013). This year he has also been elected into the Hall of Excellence, Genetics Section, American Fisheries Society

Louis has done extensive services to the scientific community, and many readers will have been in contact with him in his editorial capacities. Among others, he has previously been Associate Editor of Evolution and Journal of Evolutionary Biology. He currently serves as Reviews Editor of Molecular Ecology and Editor-in-Chief of Evolutionary Applications and is a key force behind the success of both journals. It is characteristic for Louis' editorial work that he maintains a deep respect for the submissions he handles, understanding that behind many manuscripts lie a motivated student who may be experiencing the peer review process for the first time. His capacity to foresee the future of the field has resulted in *Molecular Ecology* reviews having extremely high citations for the journal.

Phylogeography of salmonid fishes

Louis Bernatchez' early research career coincided with the rise of phylogeography as a research field (Avise *et al.* 1987). It was an obvious question to ask whether the remarkable phenotypic and ecological diversity observed in salmonid fishes and freshwater fishes in general could reflect circumstances of phylogeographical history. Some of the first papers focused on lake whitefish, where phylogeography seems to play an important – but not sole – role in the occurrence of sympatric morphs (Bernatchez & Dodson 1990), and where intriguing patterns of postglacial recolonization were revealed, encompassing four distinct lineages from different refugia and a contact zone between a local lineage and a Eurasian lineage in Beringia (Bernatchez & Dodson 1991, 1994).

In 1992, as a result of his postdoc at Université Montpellier II, he published a paper that remains a milestone in phylogeographical research (Bernatchez *et al.* 1992). It was one of the first papers that employed sequencing, as opposed to restriction fragment length polymorphism analysis of mitochondrial DNA, and it demonstrated the presence of five distinct phylogeographical lineages within the brown trout (*Salmo trutta*) that made perfect sense in the light of glaciation history and geography. Along with follow-up papers (Giuffra *et al.* 1994; Bernatchez & Osinov 1995; Bernatchez 2001), it became a virtual paradigm for more than a decade of phylogeographical studies of freshwater biota in Europe and elsewhere.

His subsequent phylogeographical studies have focused on other both salmonid and nonsalmonid species, such as brook trout and rainbow smelt (*Osmerus mordax*) (Bernatchez & Danzmann 1993; Bernatchez 1997), including fascinating cases of hybridization between species leading to fixation of exogenous mitogenomes within populations (Bernatchez *et al.* 1995; Wilson & Bernatchez 1998). Wilson and Bernatchez (1998) have written an excellent review on the phylogeography of freshwater fishes of the Northern Hemisphere that summarizes the findings from the Bernatchez and many other laboratories. Even two decades after its publication, it still serves as a refreshing and excellent introduction to the topic and it continues to be a highly cited paper.

The adaptive evolution of dwarfism and ecological speciation in the lake whitefish species complex

The study of adaptation and speciation and the engines of biological diversity have been a primary focus of Louis' research programme. Louis has addressed many fundamental evolutionary questions with his work on the lake whitefish species complex, a widespread group of fishes in the Northern Hemisphere that exhibit extraordinary variation (Lindsey & Woods 1970). Their broad distribution and successful colonization of lake and river environments following the retreat of glacial ice has contributed to the repeated evolution of a small, derived 'dwarf' ecotype that persists in sympatry with a 'normal' benthic ecotype (Bernatchez *et al.* 2010;

Renaut *et al.* 2012; Rogers *et al.* 2013; Mee *et al.* 2015). I (SMR) shared Louis' fascination for the evolution of dwarfism following my first field trip to the Allagash Basin in Maine, USA, with fellow student Bob St-Laurant and Maine Fish and Wildlife biologist, Dave Basely at the outset of my PhD. Dwarf salmonids exhibit remarkable behavioural, physiological and morphological adaptations, namely slower growth and earlier maturation in association with their limnetic environment. Louis has published >60 contributions on Lake Whitefish that have significantly advanced the field of ecological speciation by teaching us: (i) the role of history and historical contingency. Louis' phylogeographic studies on allopatric divergence and demographic history among glacial races have demonstrated that secondary contact has significantly influenced adaptation and reproductive isolation in lake whitefish (Bernatchez *et al.* 1996; Lu *et al.* 2001; Rogers *et al.* 2001). (ii) Ecological opportunity during ecological speciation. In new postglacial environments, trophic niche availability (Pigeon *et al.* 1997) and limnological features of lakes (Landry *et al.* 2007; Landry & Bernatchez 2010) promote parallel population divergence in whitefish, with trophic specialization correlating strongly with genetic divergence in sympatric lake whitefish ecotypes (Lu & Bernatchez 1999; Renaut *et al.* 2011; Gagnaire *et al.* 2013). (iii) Adaptation is extremely multifaceted in lake whitefish (Rogers & Bernatchez 2007; Whiteley *et al.* 2009; Dalziel *et al.* 2015; Laporte *et al.* 2015, 2016a), with the genetic architecture of ecological speciation associated with several genes of variable effect size that underlie adaptation (Rogers & Bernatchez 2007; Gagnaire *et al.* 2013; Laporte *et al.* 2015) and contribute to both intrinsic (Lu & Bernatchez 1998; Rogers & Bernatchez 2006; Renaut *et al.* 2009; Dion-Côté *et al.* 2014, 2015) and extrinsic (Chouinard & Bernatchez 1998; Rogers & Bernatchez 2007) postzygotic reproductive isolation. (iv) The evolutionary significance of regulatory genes, as revealed by extensive sequencing and gene expression analyses (St-Cyr *et al.* 2008; Nolte *et al.* 2009; Jeukens *et al.* 2010; Filteau *et al.* 2013; Hebert *et al.* 2013), provides a genomic basis for the observed trade-offs in life history traits distinguishing dwarf and normal whitefish species pairs, wherein enhanced survival via increased activity in feeding and predator avoidance is associated with higher energetic costs that translate into slower growth rate and reduced fecundity in dwarf relative to normal whitefish (v) Evolution is rapid. These studies have reinforced that rapid evolutionary processes contribute to the generation of this important biodiversity in Canada, with up to 20 species pairs from five distinct glacial races that deserve protection under federal guidelines. Louis' work extends the importance of maintaining genetic diversity to preserve the evolutionary potential of species (Mee *et al.* 2015) and that human disturbance of such evolutionary processes can lead to extinction (Smith & Bernatchez 2008; Mee *et al.* 2015) or unintended evolutionary consequences such as fisheries-induced evolution (Chebib *et al.* 2016). (vi) Collectively, these results reinforce the importance of nonmodel organisms studied in their ecological context towards understanding adaptation and its role in the speciation process. Perhaps of equal importance, Louis' enthusiasm has clearly achieved his personal goal of stimulating the interest of evolutionary ecologists for molecular genetics, but also that of molecular biologists for ecology (Bernatchez & Wilson 1998; Bernatchez *et al.* 1999). His extensive research on lake whitefish speciation has promoted the fusion of what were once remote fields of research and represents one of his most important achievements in molecular ecology as a discipline. Louis continues to push the envelope here. This is exemplified by recent contributions of cytogenic and other complementary approaches to study evolution in lake whitefish (Dion-Côté *et al.* 2016) and ongoing efforts to sequence the lake whitefish genome, as well as a return to a more holistic view of the mechanistic roles that these associated genes have on phenotypic variation during the speciation process.

Elusive eels

Atlantic eels remain some of the most enigmatic animals. From an evolutionary perspective, they represent extreme life histories, encompassing spawning migrations over thousands of kilometres to the remote Sargasso Sea, labile sex determination and panmictic population structure.

Louis has provided numerous important contributions towards understanding the biology of eels and has in general developed Atlantic eels into models for understanding how geographically varying adaptive responses can occur in cases where panmixia precludes local adaptation. The work conducted by him and his collaborators includes testing the panmixia hypothesis in both species (Wirth & Bernatchez 2001; Als *et al.* 2011; Côté *et al.* 2013), demonstrating that transient patterns of geographically varying selection occur despite panmixia (Gagnaire *et al.* 2012b; Pujolar *et al.* 2014) and demonstrating a complex but nevertheless genetic basis of different ecotypes and adaptive responses to human stressors (Pavey *et al.* 2015; Laporte *et al.* 2016b). Some results are really mind-boggling, such as differences in reaction norms and growth patterns between eels from different localities (Côté *et al.* 2014, 2015); this is not to be expected in panmictic species but could perhaps indicate a role of epigenetics, not exclusive to the consequences of spatially varying selection. Other important contributions include studying the dynamics behind the strange phenomenon of hybrid eels that occur almost exclusively in Iceland (Albert *et al.* 2006; Gagnaire *et al.* 2009) and showing that cytonuclear incompatibility may be an important factor underlying postzygotic reproductive isolation between European and American eel (Gagnaire *et al.* 2012a).

Atlantic eels are probably as far from being classical model organisms as one can imagine. Adult eels have never been caught nor observed in the Sargasso Sea, and identification of the spawning area is based exclusively on catches of eel larvae. It is also still not possible to rear the species in captivity through a full life cycle. Nevertheless, Louis and coworkers have recently sequenced and assembled a draft genome of the American eel (Pavey *et al.* 2016). This tells something about the increasingly blurred boundaries between model and nonmodel organisms, but also about Louis' high levels of ambition.

Louis Bernatchez as a supervisor and colleague

We are sure that everybody who has interacted with Louis can subscribe him as being a friendly, generous and easy-going person with a very well developed sense of humour. Louis is a dedicated, energetic supervisor who fosters an inspirational laboratory dynamic. He has always maintained a large, active group. Yet, somehow he has the time to be equally supportive of every single student. I (SMR) can still recall the manner in which Louis would introduce us to visiting speakers or his colleagues during a conference. He is clearly very proud of his students, their accomplishments and achievements. He also challenges us to challenge ourselves, encouraging his students to be collaborative and seek solutions to problems together. Whether it was a one on one meeting with Louis or during a laboratory meeting, Louis was always on point when it came to the data or topic at hand. I learned a great deal about evolution from Louis, but I learned even more about the importance of communication and collaboration. The laboratory dynamic has always been incredibly social. My very first trip to Quebec involved a laboratory party that the police eventually asked us to take down a notch. Louis would almost certainly attribute this dynamic environment and success to the incredible research professionals that have been part of his group. Lucie Papillon has worked with Louis for almost 20 years and has been an unbelievable resource for the group. Bob St-Laurant, Guillaume Côté, Eric Normandeau, Serge Higgins and the dedicated staff of the aquatic facility at Université Laval (Laboratoire de Recherche en Sciences Aquatiques, LARSA), among many others, have been an integral part of the success of Louis and his students.

As a collaborator Louis has always been dedicated, enthusiastic and generous with good ideas and suggestions. One of us (MMH) has particularly fond memories of research expeditions to remote places. In 2007, Louis joined the Danish Galathea 3 marine expedition on a trip to the Sargasso Sea, with the intention to sample larvae and adult European and American eels on their spawning grounds. Whereas the latter purpose was unsuccessful (and remains so to this day), substantial numbers of larvae were collected that formed the backbone of subsequent studies. The expedition involved, among other things, a bone-breaking transfer by zodiac in 4 metre waves from a trawler to the main expedition vessel, identifying eel larvae in plankton samples at midnight on a rolling ship while at the same time attempting to control one's stomach, but also numerous thoughtful scientific discussions and countless moments of fun and excitement when hauling in sampling nets from deep in the ocean in the middle of the night. In 2014, Louis and another good colleague, Dylan Fraser, participated in an expedition to Greenland in order to sample Arctic char and three-spined sticklebacks. Due to the inaccessibility of many of the sampling locations, it is often the easiest option to sample Arctic char by angling. However, this involves the inherent problem that anglers tend to go for the biggest fish. It was a concern if all sizes and cohorts would be sufficiently represented, but knowing Louis' reputation as an angler, he was enrolled to solve the problem. He did not let us down and as a result the representation of small fish in the samples was substantially increased.

In total, there are numerous reasons for celebrating Louis Bernatchez as recipient of the Molecular Ecology Prize. The best, however, relates to the fact that he is at the stage of mid-career. We can therefore expect even more exciting scientific contributions in the years to come.

Michael M. Hansen* and Sean M. Rogers†
*Department of Bioscience, Aarhus University, Ny Munkegade 116., DK-8000 Aarhus C, Denmark and
†Department of Biological Sciences, University of Calgary, 2500 University Dr., NW, Calgary, AB T2N 1N4 Canada

References

Albert V, Jonsson B, Bernatchez L (2006) Natural hybrids in Atlantic eels (*Anguilla anguilla*, *A. rostrata*): evidence for successful reproduction and fluctuating abundance in space and time. *Molecular Ecology*, **15**, 1903–1916.

Als TD, Hansen MM, Maes GE *et al.* (2011) All roads lead to home: panmixia of European eel in the Sargasso Sea. *Molecular Ecology*, **20**, 1333–1346.

April J, Mayden RL, Hanner RH, Bernatchez L (2011) Genetic calibration of species diversity among North America's freshwater fishes. *Proceedings of the National Academy of Sciences of the United States of America*, **108**, 10602–10607.

Avise JC, Arnold J, Ball RM *et al.* (1987) Intraspecific phylogeography – the mitochondrial DNA bridge between population genetics and systematics. *Annual Review of Ecology and Systematics*, **18**, 489–522.

Bernatchez L (1997) Mitochondrial DNA analysis confirms the existence of two glacial races of rainbow smelt *Osmerus mordax* and their reproductive isolation in the St Lawrence River estuary (Québec, Canada). *Molecular Ecology*, **6**, 73–83.

Bernatchez L (2001) The evolutionary history of brown trout (*Salmo trutta* L.) inferred from phylogeographic, nested clade, and mismatch analyses of mitochondrial DNA variation. *Evolution*, **55**, 351–379.

Bernatchez L (2016) On the maintenance of genetic variation and adaptation to environmental change: considerations from population genomics in fishes. *Journal of Fish Biology*, **89**, 2519–2556.

Bernatchez L, Danzmann RG (1993) Congruence in control region sequence and restriction site variation in mitochondrial DNA of brook charr (*Salvelinus fontinalis* Mitchill). *Molecular Biology and Evolution*, **10**, 1002–1014.

Bernatchez L, Dodson JJ (1985) Influence of temperature and current speed on the swimming capacity of lake whitefish (*Coregonus clupeaformis*) and cisco (*C. artedii*). *Canadian Journal of Fisheries and Aquatic Sciences*, **42**, 1522–1529.

Bernatchez L, Dodson JJ (1990) Allopatric origin of sympatric populations of lake whitefish (*Coregonus clupeaformis*) as revealed by mitochondrial DNA restriction analysis. *Evolution*, **44**, 1263–1271.

Bernatchez L, Dodson JJ (1991) Phylogeographic structure in mitochondrial DNA of the lake whitefish (*Coregonus clupeaformis*) and its relation to Pleistocene glaciations. *Evolution*, **45**, 1016–1035.

Bernatchez L, Dodson JJ (1994) Phylogenetic relationships among Palearctic and Nearctic whitefish (*Coregonus sp.*) populations as revealed by mitochondrial DNA variation. *Canadian Journal of Fisheries and Aquatic Sciences*, **51**, 240–251.

Bernatchez L, Osinov A (1995) Genetic diversity of trout (Genus *Salmo*) from its most Eastern native range based on mitochondrial DNA and nuclear gene variation. *Molecular Ecology*, **4**, 285–297.

Bernatchez L, Wilson CC (1998) Comparative phylogeography of nearctic and palearctic fishes. *Molecular Ecology*, **7**, 431–452.

Bernatchez L, Guyomard R, Bonhomme F (1992) DNA sequence variation of the mitochondrial control region among geographically and morphologically remote European brown trout *Salmo trutta* populations. *Molecular Ecology*, **1**, 161–173.

Bernatchez L, Glémet H, Wilson CC, Danzmann RG (1995) Introgression and fixation of Arctic char (*Salvelinus alpinus*) mitochondrial genome in an allopatric population of brook trout (*Salvelinus fontinalis*). *Canadian Journal of Fisheries and Aquatic Sciences*, **52**, 179–185.

Bernatchez L, Vuorinen JA, Bodaly RA, Dodson JJ (1996) Genetic evidence for reproductive isolation and multiple origins of sympatric trophic ecotypes of whitefish (*Coregonus*). *Evolution*, **50**, 624–635.

Bernatchez L, Chouinard A, Lu GQ (1999) Integrating molecular genetics and ecology in studies of adaptive radiation: whitefish, *Coregonus* sp., as a case study. *Biological Journal of the Linnean Society*, **68**, 173–194.

Bernatchez L, Renaut S, Whiteley AR *et al.* (2010) On the origin of species: insights from the ecological genomics of lake whitefish. *Philosophical Transactions of the Royal Society B-Biological Sciences*, **365**, 1783–1800.

Bougas B, Audet C, Bernatchez L (2013) The influence of parental effects on transcriptomic landscape during early development in brook charr (*Salvelinus fontinalis*, Mitchill). *Heredity*, **110**, 484–491.

Bourret V, Kent MP, Primmer CR *et al.* (2013) SNP-array reveals genome-wide patterns of geographical and potential adaptive divergence across the natural range of Atlantic salmon (*Salmo salar*). *Molecular Ecology*, **22**, 532–551.

Bourret V, Dionne M, Bernatchez L (2014) Detecting genotypic changes associated with selective mortality at sea in Atlantic salmon: polygenic multilocus analysis surpasses genome scan. *Molecular Ecology*, **23**, 4444–4457.

Castric V, Bernatchez L (2003) The rise and fall of isolation by distance in the anadromous brook charr (*Salvelinus fontinalis* Mitchill). *Genetics*, **163**, 983–996.

Chebib J, Renaut S, Bernatchez L, Rogers SM (2016) Genetic structure and within-generation genome scan analysis of fisheries-induced evolution in a Lake Whitefish (*Coregonus clupeaformis*) population. *Conservation Genetics*, **17**, 473–483.

Chouinard A, Bernatchez L (1998) A study of trophic niche partitioning between larval populations of reproductively isolated whitefish (*Coregonus* sp.) ecotypes. *Journal of Fish Biology*, **53**, 1231–1242.

Côté CL, Gagnaire PA, Bourret V *et al.* (2013) Population genetics of the American eel (*Anguilla rostrata*): FST = 0 and North Atlantic Oscillation effects on demographic fluctuations of a panmictic species. *Molecular Ecology*, **22**, 1763–1776.

Côté CL, Castonguay M, Kalujnaia MS, Cramb G, Bernatchez L (2014) In absence of local adaptation, plasticity and spatially varying selection rule: a view from genomic reaction norms in a panmictic species (*Anguilla rostrata*). *Bmc Genomics*, **15**, 403.

Côté CL, Pavey SA, Stacey JA *et al.* (2015) Growth, female size, and sex ratio variability in American eel of different origins in both controlled conditions and the wild: implications for stocking programs. *Transactions of the American Fisheries Society*, **144**, 246–257.

Dalziel AC, Martin N, Laporte M, Guderley H, Bernatchez L (2015) Adaptation and acclimation of aerobic exercise physiology in Lake Whitefish ecotypes (*Coregonus clupeaformis*). *Evolution*, **69**, 2167–2186.

Dion-Côté AM, Renaut S, Normandeau E, Bernatchez L (2014) RNA-seq reveals transcriptomic shock involving transposable elements reactivation in hybrids of young Lake Whitefish species. *Molecular Biology and Evolution*, **31**, 1188–1199.

Dion-Côté AM, Symonova R, Rab P, Bernatchez L (2015) Reproductive isolation in a nascent species pair is associated with aneuploidy in hybrid offspring. *Proceedings of the Royal Society B-Biological Sciences*, **282**, 20142862.

Dion-Côté AM, Symonova R, Lamaze FC *et al.* (2016) Standing chromosomal variation in Lake Whitefish species pairs: the role of historical contingency and relevance for speciation. *Molecular Ecology*, **25**. In press.

Dionne M, Caron F, Dodson JJ, Bernatchez L (2008) Landscape genetics and hierarchical genetic structure in Atlantic salmon: the interaction of gene flow and local adaptation. *Molecular Ecology*, **17**, 2382–2396.

Dionne M, Miller KM, Dodson JJ, Bernatchez L (2009) MHC standing genetic variation and pathogen resistance in wild Atlantic salmon. *Philosophical Transactions of the Royal Society B-Biological Sciences*, **364**, 1555–1565.

Ferchaud AL, Perrier C, April J *et al.* (2016) Making sense of the relationships between Ne, Nb and Nc towards defining conservation thresholds in Atlantic salmon (*Salmo salar*). *Heredity (Edinb)*, **117**, 268–278.

Filteau M, Pavey SA, St-Cyr J, Bernatchez L (2013) Gene coexpression networks reveal key drivers of phenotypic divergence in Lake Whitefish. *Molecular Biology and Evolution*, **30**, 1384–1396.

Fraser DJ, Bernatchez L (2001) Adaptive evolutionary conservation: towards a unified concept for defining conservation units. *Molecular Ecology*, **10**, 2741–2752.

Fraser DJ, Bernatchez L (2005a) Adaptive migratory divergence among sympatric brook charr populations. *Evolution*, **59**, 611–624.

Fraser DJ, Bernatchez L (2005b) Allopatric origins of sympatric brook charr populations: colonization history and admixture. *Molecular Ecology*, **14**, 1497–1509.

Fraser DJ, Lippé C, Bernatchez L (2004) Consequences of unequal population size, asymmetric gene flow and sex-biased dispersal on population structure in brook charr (*Salvelinus fontinalis*). *Molecular Ecology*, **13**, 67–80.

Gagnaire PA, Albert V, Jonsson B, Bernatchez L (2009) Natural selection influences AFLP intraspecific genetic variability and introgression patterns in Atlantic eels. *Molecular Ecology*, **18**, 1678–1691.

Gagnaire PA, Normandeau E, Bernatchez L (2012a) Comparative genomics reveals adaptive protein evolution and a possible cytonuclear incompatibility between European and American eels. *Molecular Biology and Evolution*, **29**, 2909–2919.

Gagnaire PA, Normandeau E, Côté C, Hansen MM, Bernatchez L (2012b) The genetic consequences of spatially varying selection in the panmictic American eel (*Anguilla rostrata*). *Genetics*, **190**, 725–733.

Gagnaire PA, Pavey SA, Normandeau E, Bernatchez L (2013) The genetic architecture of reproductive isolation during speciation-with-gene-flow in lake whitefish species pairs asessed by RAD sequencing. *Evolution*, **67**, 2483–2497.

Garant D, Dodson JD, Bernatchez L (2005) Offspring genetic diversity increases fitness of female Atlantic salmon (*Salmo salar*). *Behavioral Ecology and Sociobiology*, **57**, 240–244.

Gauthier-Ouellet M, Dionne M, Caron F, King TL, Bernatchez L (2009) Spatiotemporal dynamics of the Atlantic salmon (*Salmo salar*) Greenland fishery inferred from mixed-stock analysis. *Canadian Journal of Fisheries and Aquatic Sciences*, **66**, 2040–2051.

Giuffra E, Bernatchez L, Guyomard R (1994) Mitochondrial control region and protein-coding genes sequence variation among phenotypic forms of brown trout *Salmo trutta* from Northern Italy. *Molecular Ecology*, **3**, 161–171.

Hebert FO, Renaut S, Bernatchez L (2013) Targeted sequence capture and resequencing implies a predominant role of regulatory regions in the divergence of a sympatric lake whitefish species pair (*Coregonus clupeaformis*). *Molecular Ecology*, **22**, 4896–4914.

Jeukens J, Renaut S, St-Cyr J, Nolte AW, Bernatchez L (2010) The transcriptomics of sympatric dwarf and normal lake whitefish (*Coregonus clupeaformis* spp., Salmonidae) divergence as revealed by next-generation sequencing. *Molecular Ecology*, **19**, 5389–5403.

Lamaze FC, Sauvage C, Marie A, Garant D, Bernatchez L (2012) Dynamics of introgressive hybridization assessed by SNP population genomics of coding genes in stocked brook charr (*Salvelinus fontinalis*). *Molecular Ecology*, **21**, 2877–2895.

Lamaze FC, Garant D, Bernatchez L (2013) Stocking impacts the expression of candidate genes and physiological condition in introgressed brook charr (*Salvelinus fontinalis*) populations. *Evolutionary Applications*, **6**, 393–407.

Landry L, Bernatchez L (2010) Role of epibenthic resource opportunities in the parallel evolution of lake whitefish species pairs (*Coregonus* sp.). *Journal of Evolutionary Biology*, **23**, 2602–2613.

Landry L, Vincent WF, Bernatchez L (2007) Parallel evolution of lake whitefish dwarf ecotypes in association with limnological features of their adaptive landscape. *Journal of Evolutionary Biology*, **20**, 971–984.

Laporte M, Rogers SM, Dion-Côté AM *et al.* (2015) RAD-QTL mapping reveals both genome-level parallelism and different genetic architecture underlying the evolution of body shape in Lake Whitefish (*Coregonus clupeaformis*) species pairs. *G3-Genes Genomes Genetics*, **5**, 1481–1491.

Laporte M, Dalziel AC, Martin N, Bernatchez L (2016a) Adaptation and acclimation of traits associated with swimming capacity in Lake Whitefish (*Coregonus clupeaformis*) ecotypes. *Bmc Evolutionary Biology*, **16**, 160.

Laporte M, Pavey SA, Rougeux C *et al.* (2016b) RAD sequencing reveals within-generation polygenic selection in response to anthropogenic organic and metal contamination in North Atlantic Eels. *Molecular Ecology*, **25**, 219–237.

Lindsey CC, Woods CS (1970) *Biology of Coregonid Fishes*. University of Manitoba Press, Winnipeg, Canada.

Lippé C, Dumont P, Bernatchez L (2006) High genetic diversity and no inbreeding in the endangered copper redhorse, *Moxostoma hubbsi* (Catostomidae, Pisces): the positive sides of a long generation time. *Molecular Ecology*, **15**, 1769–1780.

Lu GQ, Bernatchez L (1998) Experimental evidence for reduced hybrid viability between dwarf and normal ecotypes of lake whitefish (*Coregonus clupeaformis* Mitchill). *Proceedings of the Royal Society of London Series B-Biological Sciences*, **265**, 1025–1030.

Lu GQ, Bernatchez L (1999) Correlated trophic specialization and genetic divergence in sympatric lake whitefish ecotypes (*Coregonus clupeaformis*): support for the ecological speciation hypothesis. *Evolution*, **53**, 1491–1505.

Lu G, Basley DJ, Bernatchez L (2001) Contrasting patterns of mitochondrial DNA and microsatellite introgressive hybridization between lineages of lake whitefish (*Coregonus clupeaformis*): relevance for speciation. *Molecular Ecology*, **10**, 965–985.

Marie AD, Bernatchez L, Garant D (2010) Loss of genetic integrity correlates with stocking intensity in brook charr (*Salvelinus fontinalis*). *Molecular Ecology*, **19**, 2025–2037.

Marie AD, Bernatchez L, Garant D (2012) Environmental factors correlate with hybridization in stocked brook charr

(*Salvelinus fontinalis*). *Canadian Journal of Fisheries and Aquatic Sciences*, **69**, 884–893.

Mee JA, Bernatchez L, Reist JD, Rogers SM, Taylor EB (2015) Identifying designatable units for intraspecific conservation prioritization: a hierarchical approach applied to the lake whitefish species complex (*Coregonus* spp.). *Evolutionary Applications*, **8**, 423–441.

Milot E, Weimerskirch H, Duchesne P, Bernatchez L (2007) Surviving with low genetic diversity: the case of albatrosses. *Proceedings of the Royal Society B-Biological Sciences*, **274**, 779–787.

Moore JS, Bourret V, Dionne M *et al*. (2014) Conservation genomics of anadromous Atlantic salmon across its North American range: outlier loci identify the same patterns of population structure as neutral loci. *Molecular Ecology*, **23**, 5680–5697.

Nolte AW, Renaut S, Bernatchez L (2009) Divergence in gene regulation at young life history stages of whitefish (*Coregonus* sp.) and the emergence of genomic isolation. *BMC Evolutionary Biology*, **9**, 59.

Pavey SA, Gaudin J, Normandeau E *et al*. (2015) RAD sequencing highlights polygenic discrimination of habitat ecotypes in the panmictic American eel. *Current Biology*, **25**, 1666–1671.

Pavey SA, Laporte M, Normandeau E *et al.* (2016) Draft genome of the American eel (*Anguilla rostrata*). *Molecular Ecology Resources*, **16**. In press.

Pigeon D, Chouinard A, Bernatchez L (1997) Multiple modes of speciation involved in the parallel evolution of sympatric morphotypes of lake whitefish (*Coregonus clupeaformis*, Salmonidae). *Evolution*, **51**, 196–205.

Pujolar JM, Jacobsen MW, Als TD *et al.* (2014) Genome-wide single-generation signatures of local selection in the panmictic European eel. *Molecular Ecology*, **23**, 2514–2528.

Renaut S, Nolte AW, Bernatchez L (2009) Gene expression divergence and hybrid misexpression between Lake Whitefish species pairs (*Coregonus* spp. Salmonidae). *Molecular Biology and Evolution*, **26**, 925–936.

Renaut S, Nolte AW, Rogers SM, Derome N, Bernatchez L (2011) SNP signatures of selection on standing genetic variation and their association with adaptive phenotypes along gradients of ecological speciation in lake whitefish species pairs (*Coregonus* spp.). *Molecular Ecology*, **20**, 545–559.

Renaut S, Maillet N, Normandeau E *et al.* (2012) Genome-wide patterns of divergence during speciation: the lake whitefish case study. *Philosophical Transactions of the Royal Society B-Biological Sciences*, **367**, 354–363.

Roberge C, Einum S, Guderley H, Bernatchez L (2006) Rapid parallel evolutionary changes of gene transcription profiles in farmed Atlantic salmon. *Molecular Ecology*, **15**, 9–20.

Roberge C, Guderley H, Bernatchez L (2007) Genomewide identification of genes under directional selection: Gene transcription Q_{ST} scan in diverging Atlantic salmon subpopulations. *Genetics*, **177**, 1011–1022.

Roberge C, Normandeau E, Einum S, Guderley H, Bernatchez L (2008) Genetic consequences of interbreeding between farmed and wild Atlantic salmon: insights from the transcriptome. *Molecular Ecology*, **17**, 314–324.

Rogers SM, Bernatchez L (2006) The genetic basis of intrinsic and extrinsic post-zygotic reproductive isolation jointly promoting speciation in the lake whitefish species complex (*Coregonus clupeaformis*). *Journal of Evolutionary Biology*, **19**, 1979–1994.

Rogers SM, Bernatchez L (2007) The genetic architecture of ecological speciation and the association with signatures of selection in natural lake whitefish (*Coregonus sp.* Salmonidae) species pairs. *Molecular Biology and Evolution*, **24**, 1423–1438.

Rogers SM, Campbell D, Baird SJE, Danzmann RG, Bernatchez L (2001) Combining the analyses of introgressive hybridisation and linkage mapping to investigate the genetic architecture of population divergence in the lake whitefish (*Coregonus clupeaformis*, Mitchill). *Genetica*, **111**, 25–41.

Rogers SM, Mee JA, Bowles E (2013) The consequences of genomic architecture on ecological speciation in postglacial fishes. *Current Zoology*, **59**, 53–71.

Smith TB, Bernatchez L (2008) Evolutionary change in human-altered environments. *Molecular Ecology*, **17**, 1–8.

St-Cyr J, Derome N, Bernatchez L (2008) The transcriptomics of life-history trade-offs in whitefish species pairs (*Coregonus* sp.). *Molecular Ecology*, **17**, 1850–1870.

Valiquette E, Perrier C, Thibault I, Bernatchez L (2014) Loss of genetic integrity in wild lake trout populations following stocking: insights from an exhaustive study of 72 lakes from Québec, Canada. *Evolutionary Applications*, **7**, 625–644.

Whiteley AR, Persaud KN, Derome N, Montgomerie R, Bernatchez L (2009) Reduced sperm performance in backcross hybrids between species pairs of whitefish (*Coregonus clupeaformis*). *Canadian Journal of Zoology*, **87**, 566–572.

Wilson CC, Bernatchez L (1998) The ghost of hybrids past: fixation of arctic charr (*Salvelinus alpinus*) mitochondrial DNA in an introgressed population of lake trout (*S. namaycush*). *Molecular Ecology*, **7**, 127–132.

Wirth T, Bernatchez L (2001) Genetic evidence against panmixia in the European eel. *Nature*, **409**, 1037–1040.

doi: 10.1111/mec.13941