Supplementary Material

Ten years of landscape genomics: challenges and opportunities

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# 1 Supplementary Table

**Table S1 | Review of 37 articles in landscape genomics from 2007 to 2016.**

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| No. | Year | Title | Molecular Marker | Sampling strategy | Sequencing Technology  | Statistical methods | Research Category |
| 1 | 2007 | A spatial analysis method (SAM) to detect candidate loci for selection: towards a landscape genomics approach to adaptation. | SSRs and AFLPs | Random sampling at population level | Not involve | SAM, DFIST, FDIST2 | (2) |
| 2 | 2008 | Genome-wide association to fine-scale ecological heterogeneity within a continuous population of Biscutella laevigata (Brassicaceae) | AFLPs | Random sampling at population level | Not involve | CCA, partial Mantel tests | (1) |
| 3 | 2009 | Landscape genomics and biased FST approaches reveal single nucleotide polymorphisms under selection in goat breeds of North-East Mediterranean | SNPs | Random sampling at population level | PCR-RFLP, SSCP, SnaPshot, or Taqman | SAM, FDIST2 | (2) |
| 4 | 2010 | Back to nature: ecological genomics of loblolly pine (Pinus taeda, Pinaceae) | SNPs | Random sampling at population level | Illumina infinium platform | Bayesian geographical analysis | (2) |
| 5 | 2010 | Tracking genes of ecological relevance using a genome scan in two independent regional population samples of Arabis alpina | AFLPs | Random sampling at population level | Not involve | GEE | (2) |
| 6 | 2012 | Environmental adaptation contributes to gene polymorphism across the Arabidopsis thaliana genome | SNPs | Random sampling at individual level | Illumina sequencing platform | PCA, CCA, partial Mantel tests | (2) |
| 7 | 2012 | Local adaptation in the flowering-time gene network of balsam poplar, Populus balsamifera L. | SNPs | Random sampling at population level | Sequenom MassARRAY platform | BayeScan, BAYENV, FDIST2 | (2) |
| 8 | 2013 | Integrating landscape genomics and spatially explicit approaches to detect loci under selection in clinal populations | AFLPs | Stratified sampling at individual level | Not involve | GLMs, GLMMs, GAMMs, DFDIST, BayeScan | (2) |
| 9 | 2013 | Landscape genomics in Atlantic salmon (Salmo salar): searching for gene-environment interactions driving local adaptation. | SNPs | Random sampling at population level | CIGENE SNP array platform | RDA | (1) |
| 10 | 2013 | The role of selection in driving landscape genomic structure of the waterflea Daphnia magna | SSRs and SNPs | Random sampling at population level | Sequenom MassARRAY platform | RDA, partial Mantel tests | (2) |
| 11 | 2014 | Adaptations to Climate-Mediated Selective Pressures in Sheep | SNPs | Random sampling at population level | ISGC SNP50K BeadChip platform | FDIST2, SAM, LFMM | (2) |
| 12 | 2014 | Landscape genomics of Populus trichocarpa: the role of hybridization, limited gene flow, and natural selection in shaping patterns of population structure | SNPs | Random sampling at population level | Infinium II assay platform | FDIST2, BayeScan, Bayenv | (2) |
| 13 | 2014 | Landscape genomics and a common garden trial reveal adaptive differentiation to temperature across Europe in the tree species Alnus glutinosa | SNPs | Random sampling at population level | Genotyping by sequencing Illumina HiSeq 2000 platform | BayeScan, LFMM  | (2) |
| 14 | 2014 | Assessing The spatial dependence of adaptive loci in 43 European and Western Asian goat breeds using AFLP markers | AFLPs | Random sampling at population level | Not involve | SAM, DFDIST, BayeScan | (2) |
| 15 | 2015 | Landscape genomics of Sphaeralcea ambigua in the Mojave Desert: a multivariate, spatially-explicit approach to guide ecological restoration | AFLPs | Random sampling at population level | Not involve | BayeScan, GLMs | (2) |
| 16 | 2015 | Environmental adaptation in Chinook salmon (Oncorhynchus tshawytscha) throughout their North American range | SNPs | Random sampling at population level | Restriction-site associated DNA sequencing Illumina platform | FDIST2, RDA,  | (2) |
| 17 | 2015 | Landscape genomics reveal signatures of local adaptation in barley (Hordeum vulgare L.) | SNPs | Random sampling at individual level | Genotyping by sequencing Illumina HiSeq 2000 platform | Bayenv, LFMM, RDA | (2) |
| 18 | 2015 | Genome-wide analyses suggest parallel selection for universal traits may eclipse local environmental selection in a highly mobile carnivore | SNPs | Random sampling at population level | Illumina CanineHD BeadChip microarray platform | BayeScan, SAM | (2) |
| 19 | 2015 | Isolation by environment in White-breasted Nuthatches (Sitta carolinensis) of the Madrean Archipelago sky islands: a landscape genomics approach | SNPs | Random sampling at population level | Restriction site associated DNA sequencing Illumina HiSeq 2500 platform | partial Mantel tests, BayeScan, Bayenv, LFMM | (2) |
| 20 | 2015 | Adaptation to low salinity promotes genomic divergence in Atlantic cod (Gadus morhua L.) | SNPs | Random sampling at population level | Illumina SNP chip platform | BayeScan, FDIST2, Bayenv | (2) |
| 21 | 2015 | Sun skink landscape genomics: assessing the roles of micro-evolutionary processes in shaping genetic and phenotypic diversity across a heterogeneous and fragmented landscape | SNPs | Random sampling at population level | Restriction site associated DNA sequencing Illumina HiSeq 2500 platform | partial Mantel tests | (1) |
| 22 | 2015 | Combining niche modelling and landscape genetics to study local adaptation: A novel approach illustrated using alpine plants | AFLPs | Random sampling at population level | Not involve | GEE | (2) |
| 23 | 2015 | Ecological genomics meets community-level modelling of biodiversity: mapping the genomic landscape of current and future environmental adaptation | SNPs | Random sampling at population level | Sequenom MassARRAY platform | GDM, the hierarchical model in ARLEQUIN, BayeScan, Bayenv | (2) |
| 24 | 2016 | Landscape genomics reveals altered genome wide diversity within revegetated stands of Eucalyptus microcarpa (Grey Box) | SNPs | Random sampling at population level | Diversity Arrays Technology Illumina seqencing platform | PCA, IBD | (2) |
| 25 | 2016 | Signatures of local adaptation in candidate genes of oaks (Quercus spp.) with respect to present and future climatic conditions | SSRs and SNPs | Random sampling at population level | Illumina MiSeq platform | LFMM  | (2) |
| 26 | 2016 | Genome scan reveals selection acting on genes linked to stress response in wild pearl millet | SNPs | Random sampling at population level | Illumina HighSeq 2000 platform  | PCA, F ST approach, BayeScan, Bayenv | (2) |
| 27 | 2016 | Seascape genomics provides evidence for thermal adaptation and current-mediated population structure in American lobster (Homarus americanus) | SNPs | Random sampling at population level | Restriction-site associated DNA sequencing Illumina platform | the infinite island model in ARLEQUIN, BayeScan, Outflank, Pearson correlation tests, Bayenv, LFMM, RDA | (2) |
| 28 | 2016 | Riverscape genomics of a threatened fish across a hydroclimatically heterogeneous river basin | SNPs | Random sampling at population level | Restriction-site associated DNA sequencing Illumina HiSeq 2000 platform | the hierarchical model in ARLEQUIN, BayeScan, GLMMs, RDA | (2) |
| 29 | 2016 | Environmental versus geographical effects on genomic variation in wild soybean (Glycine soja) across its native range in northeast Asia | SNPs | Random sampling at individual level | Illumina infinium platform | CCA, RDA | (1) |
| 30 | 2016 | SNP discovery in candidate adaptive genes using exon capture in a free-ranging alpine ungulate | SNPs | Random sampling at population level | microfluidicqPCR-based SNP chip | FDIST2, BayeScan, SAM | (2) |
| 31 | 2016 | Patterns of neutral and adaptive genetic diversity across the natural range of sugar pine (Pinus lambertiana Dougl.) | SNPs | Random sampling at population level | Illumina GoldenGate SNP genotyping platform | Bayenv, LFMM | (2) |
| 32 | 2016 | Genome-environment association study suggests local adaptation to climate at the regional scale in Fagus sylvatica | SSRs and SNPs | Stratified sampling at population level | KASP genotyping technology | LFMM  | (2) |
| 33 | 2016 | Climate-related adaptive genetic variation and population structure in natural stands of Norway spruce in the South-Eastern Alps | SNPs | Random sampling at population level | Illumina GoldenGate SNP genotyping platform | BayeScan, Bayenv | (2) |
| 34 | 2016 | Signatures of natural selection on Pinus cembra and P. mugo along elevational gradients in the Alps | SNPs | Random sampling at population level | Illumina GoldenGate SNP genotyping  | BayeScan, Bayenv, LFMM | (2) |
| 35 | 2016 | Climate variables explain neutral and adaptive variation within salmonid metapopulations: the importance of replication in landscape genetics | SNPs | Random sampling at population level | ABI Taqmanassays platform | GESTE, DISTLM | (2) |
| 36 | 2016 | Evidence of divergent selection for drought and cold tolerance at landscape and local scales in Abies alba Mill. in the French Mediterranean Alps | SNPs | Random sampling at population level | KASP genotyping technology | HFDIST, BayeScan, FLK, LFMM | (2) |
| 37 | 2016 | Contributions of historical and contemporary geographic and environmental factors to phylogeographic structure in a Tertiary relict species, *Emmenopterys henryi* (Rubiaceae) | AFLPs | Random sampling at population level | Not involve | IBD, IBE, MMRR, SEM | (1) |
| Research Category: (1) quantifying influence of spatial environmental variables on genomic divergence; (2) uncovering the environmental factors that shape adaptive genetic variation and the genetic basis of adaptive change. |

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