

Full list of literature

List of papers with summaries consulted by the Plant Genetic Resources domain

Atwell S, Huang YS, Vilhjalmsson BJ, Willems G, Horton M, Li Y, Meng DZ, Platt A, Tarone AM, Hu TT, Jiang R, Mulyati NW, Zhang X, Amer MA, Baxter I, Brachi B, Chory J, Dean C, Debieu M, Meaux Jd, Ecker JR, Faure N, Kniskern JM, Jones JDG, Michael T, Nemri A (2010) Genome-wide association study of 107 phenotypes in *Arabidopsis thaliana* inbred lines. *Nature* 465:627-631

The article is useful as an example of the potential value of GWA studies in plant research and improvement.

Becker C, Hagmann J, Muller J, Koenig D, Stegle O, Borgwardt K, Weigel D (2011) Spontaneous epigenetic variation in the *Arabidopsis thaliana* methylome. *Nature* 480:245-249

This study sheds light on the interesting phenomenon of epigenetic variation, and shows that epigenetic mutations are very different from genetic mutations in reversibility.

Bergelson J, Roux F (2010) Towards identifying genes underlying ecologically relevant traits in *Arabidopsis thaliana*. *Nature Reviews Genetics* 11:867-879

This article is a useful extension of Atwell et al. (2010), focusing on mapping methods and the ecological context of phenotype–genotype association studies.

Boyd LA, Ridout C, O'Sullivan DM, Leach JE, Leung H (2013) Plant-pathogen interactions: disease resistance in modern agriculture. *Trends in Genetics* 29:233-240

This article reviews recent advances in the genetics of plant–pathogen interactions, methods of identification and the assessment of genetic variability for disease resistance, with the ultimate goal of developing sustainable disease resistance in crops.

Brenchley R, Spannagl M, Pfeifer M, Barker GLA, D'Amore R, Allen AM, McKenzie N, Kramer M, Kerhornou A, Bolser D, Kay S, Waite D, Trick M, Bancroft I, Gu Y, Huo NX, Luo MC, Sehgal S, Gill B, Kianian S, Anderson O, Kersey P, Dvorak J, McCombie WR, Hall A, Mayer KFX (2012) Analysis of the bread wheat genome using whole-genome shotgun sequencing. *Nature* 491:705-710

This article is noteworthy, because the sequencing of the bread wheat genome is a major achievement, in view of the importance of the crop in the EU and elsewhere (providing 20% of the calories consumed by humans).

Carvalho MAAPd, Bebeli PJ, Bettencourt E, Costa G, Dias S, Santos TMM de, Slaski JJ (2013) Cereal landraces genetic resources in worldwide GeneBanks. A review. *Agronomy for Sustainable Development* 33:177-203

This article gives a good, though not very concise, overview of the importance of ex-situ collections and documentation systems in general, and their role in the conservation of cereal landraces in particular. It also gives useful recommendations on the way forward for genebanks, i.e. expansion of the user group base.

Dhondt S, Wuyts N, Inze D (2013) Cell to whole-plant phenotyping: the best is yet to come. Trends in Plant Science 18:428-439

This article gives a good and thorough overview of phenotyping and its potential in breeding.

Feuillet C, Langridge P, Waugh R (2008) Cereal breeding takes a walk on the wild side. Trends in Genetics 24:24-32

This article clearly underlines the importance of CWR for cereal breeding, and identifies advances that are needed to enhance the use of CWR in cereal breeding.

Fischer RA (2011) Wheat physiology: a review of recent developments. Crop & Pasture Science 62:95-114

This article makes clear that, so far, the contribution of genomics to wheat improvement has mostly remained limited to relatively simple traits, linked to a small number of genes.

Flachowsky H, Hanke MV (2014) The "German National Fruit Genebank", a first review five years after launching. Acta Horticulturae: 227-230

This article shows how national coordination of public as well as private conservation efforts, in this case by means of fruit crop networks, can be useful to prevent loss of genetic diversity and avoid duplication of efforts. The article is very concise and general, however, and quantitative details are lacking.

Flood PJ, Harbinson J, Aarts MGM (2011) Natural genetic variation in plant photosynthesis. Trends in Plant Science 16:327-335

This study provides a good example of how the ability to connect phenotypes and genotypes will make more rapid selection and breeding for desirable traits possible.

Furbank RT, Tester M (2011) Phenomics--technologies to relieve the phenotyping bottleneck. Trends in Plant Science 16:635-644

This is a very useful article, reviewing new highthroughput and high-resolution phenotyping tools and discussing their application to plant biology, functional genomics and crop breeding.

Gebhardt C (2013) Bridging the gap between genome analysis and precision breeding in potato. Trends in genetics: 29:248-256

This article shows, with potato as an example crop, that much progress has been made in the identification of molecular markers, but that practical application of markers associated with complex agronomic traits has been limited. It also indicates that whole-genome association mapping holds promise to remedy this.

Glaszmann JC, Kilian B, Upadhyaya HD, Varshney RK (2010) Accessing genetic diversity for crop improvement. *Current opinion in plant biology* 13:167-173

This highly relevant article explores how developments in genomics can be used to improve access to germplasm collections.

Gross BL, Olsen KM (2010) Genetic perspectives on crop domestication. *Trends in Plant Science* 15:529-537

This review article summarizes methodologies ranging from quantitative trait locus mapping to resequencing used in genetic analyses of crop evolution. It concludes with the expectation that over the next ten years, the application of genome resequencing, genome scans, and selective sweep mapping will greatly expand the understanding of domestication pool of non-model plants.

Hodgins-Davis A, Townsend JP (2009) Evolving gene expression: from G to E to G x E. *Trends in Ecology & Evolution* 24:649-658

This useful article addresses the important issue of taking into account G x E interactions when relating genotypes to phenotypes.

Holderegger R, Buehler D, Gugerli F, Manel S (2010) Landscape genetics of plants. *Trends in Plant Science* 15:675-683

This article is useful in sketching the field of 'landscape genetics' and its potential value in studying the adaptation of plants to climate change.

Huang X, Lu T, Han B (2013) Resequencing rice genomes: an emerging new era of rice genomics. (Special Issue: Genetic pastures.). *Trends in Genetics* 29:225-232

This article reviews the recent advances in rice genomics, and because rice is a model system for crop genomics studies, these advances are highly relevant for other crops as well.

Jarvis A UH, Gowda CLL, Aggarwal PK, Fujisaka S, Anderson B (2008) Climate Change and its effect on conservation and use of plant genetic resources for food and agriculture and associated biodiversity for food security. Thematic background study. FAO, Rome, Italy. p 26.

This report summarizes the likely implications of climate change for the conservation and use of plant genetic resources for food and agriculture and associated biodiversity.

Jump AS, Marchant R, Penuelas J (2009) Environmental change and the option value of genetic diversity. *Trends in Plant Science* 14:51-58

This article argues that the conservation of wild relatives of cultivated plants can be justified on the basis of their 'option value'. Unfortunately, the study does not address the practical consequences of the assumption that all genetic variation in natural populations is inherently valuable.

Kaczmarczyk A, Rokka VM, Keller ERJ (2011) Potato shoot tip cryopreservation. A review. *Potato Research* 54:45-79

This review article gives an extensive overview of cryopreservation in potato (including existing collections and various techniques), which may not only be relevant for good conservation, but also for virus elimination.

Khoury C, Laliberte B, Guarino L (2010) Trends in ex situ conservation of plant genetic resources: a review of global crop and regional conservation strategies. *Genetic Resources and Crop Evolution* 57:625-639

This article gives an extensive overview of the constraints that currently have limiting effects on ex situ conservation efforts, and calls for more funding and support for ex situ germplasm conservation.

Kloosterman B, Abelenda JA, Gomez MdMC, Oortwijn M, Boer JMd, Kowitzanich K, Horvath BM, Eck HJv, Smaczniak C, Prat S, Visser RGF, Bachem CWB (2013), Naturally occurring allele diversity allows potato cultivation in northern latitudes. *Nature* 495:246-250

This article gives insight in the mechanism of daylength sensitivity in potato, which may be useful in potato breeding for different latitudes.

Klümper W, Qaim M (2014) A meta-analysis of the impacts of genetically modified crops. *PloS one* 9:e111629

This article presents a meta-analysis of studies on the agronomic and economic effects of GM crops, and concludes that these crops have led to substantial increases in yields and profits and reduction of pesticide use.

Kramer AT, Havens K (2009) Plant conservation genetics in a changing world. (Plant science research in botanic gardens - solutions to global challenges.). *Trends in Plant Science* 14:599-607

This article discusses the application of plant conservation genetics to guide conservation and restoration efforts, especially in view of climate change.

Kushalappa AC, Gunnaiah R (2013) Metabolo-proteomics to discover plant biotic stress resistance genes. *Trends in Plant Science* 18:522-531

This article gives a conceptual background to plant-pathogen relationships and proposes ten steps to streamline the application of metabolo-proteomics to improve plant resistance to biotic stress.

Langridge P, Fleury D (2011) Making the most of 'omics' for crop breeding. *Trends in Biotechnology* 29:33-40

This study gives a good general overview of 'omics' technologies and their potential, including practical examples. It indicates that it is possible now to generate extensive omics datasets for many crop species. On the other hand, it also states that the high costs of metabolomics still limit direct application in crop improvement.

Lenser T, Theissen G (2013) Molecular mechanisms involved in convergent crop domestication. Trends in Plant Science 18:704-713

This article gives more insight in the molecular background of plant domestication, and indicates how this can be used for more targeted efforts to domesticate new species.

Li DZ, Pritchard HW (2009) The science and economics of ex situ plant conservation. Trends in Plant Science 14:614-621

This article advocates the application of cryopreservation for the long-term conservation of recalcitrant seeds as well as orthodox seeds, because of technical (longevity) and economical reasons.

Liu S, Liu Y, Yang X, Tong C, Edwards D, Parkin IAP, Zhao M, Ma J, Yu J, Huang S, Wang XY, Wang J, Lu K, Fang Z, Bancroft I, Yang T, Hu Q, Wang X, Yue Z, Li H, Yang L, Wu J, Zhou Q, Wang W, King GJ, Pires JC (2014) The *Brassica oleracea* genome reveals the asymmetrical evolution of polyploid genomes. Nature Communications 5

*This article describes the genomic sequence of *B. oleracea*, its features in comparison with its relatives, and the genome evolution mechanisms revealed. It also indicates how this information can be used for genetic improvement of this species.*

McCouch S, Baute GJ, Bradeen J, Bramel P, Bretting PK, Buckler E, Burke JM, Charest D, Cloutier S, Cole G, Dempewolf H, Dingkuhn M, Feuillet C, Gepts P, Grattapaglia D, Guarino L, Jackson S, Knapp S, Langridge P, Lawton-Rauh A, Lijua Q, Lusty C, Michael T, Myles S, Naito K, Nelson RL, Pontarollo R, Richards CM, Rieseberg L, Ross-Ibarra J, Rounsley S, Hamilton RS, Schurr U, Stein N, Tomooka N, van der Knaap E, van Tassel D, Toll J, Valls J, Varshney RK, Ward J, Waugh R, Wenzl P, Zamir D (2013) Agriculture: Feeding the future. Nature 499:23-24

This important article sets out the steps to be taken to achieve better utilization of gene bank materials to contribute to increased food security.

McMahon SM, Harrison SP, Armbruster WS, Bartlein PJ, Beale CM, Edwards ME, Kattge J, Midgley G, Morin X, Prentice IC (2011) Improving assessment and modelling of climate change impacts on global terrestrial biodiversity. Trends in Ecology & Evolution 26:249-259

This article deals with the current limitations of models describing how species and ecosystems respond to climate change, and proposes research areas in which improvements are possible and a range of measures to be taken.

Morrell PL, Buckler ES, Ross-Ibarra J (2012) Crop genomics: advances and applications. Nature Reviews Genetics 13:85-96

This article gives a good general overview of the rapid developments in the field of the genome sequencing and their implications for crop improvement.

Newton AC, Akar T, Baresel JP, Bebeli PJ, Bettencourt E, Bladenopoulos KV, Czembor JH, Fasoula DA, Katsiotis A, Koutis K, Koutsika-Sotiriou M, Kovacs G, Larsson H, Carvalho MAAPd, Rubiales D, Russell J, Santos TMMd, Patto MCV (2010) Cereal landraces for sustainable agriculture. A review. *Agronomy for Sustainable Development* 30:237-269

This review article gives a thorough and extensive overview of the role landraces, and material conserved in ex-situ or in-situ conditions, can play in crop improvement, and how this role can be enhanced.

Odong TL, Jansen J, Eeuwijk FAv, Hintum TJLv (2013) Quality of core collections for effective utilisation of genetic resources review, discussion and interpretation. *Theoretical and Applied Genetics* 126:289-305

This article explains the rationale of core collections, points at limitations in their implementation, and gives recommendations on the criteria to be used for the evaluation of the quality of core collections.

Pautasso M, Aistara G, Barnaud A, Caillon S, Clouvel P, Coomes OT, Deletre M, Demeulenaere E, Santis P de, Doring T, Eloy L, Emperaire L, Garine E, Goldringer I, Jarvis D, Joly HI, Leclerc C, Louafi S, Martin P, Massol F, McGuire S, McKey D, Padoch C, Soler C, Thomas M, Tramontini S (2013) Seed exchange networks for agrobiodiversity conservation. A review. *Agronomy for Sustainable Development* 33:151-175

This review article presents an overview of concepts, methods, and challenges to better understand seed exchange networks, with the aim of improving the chances that traditional crop varieties (landraces) will be preserved and used, and agrobiodiversity is conserved.

Pecinka A, Abdelsamad A, Vu GTH (2013) Hidden genetic nature of epigenetic natural variation in plants. *Trends in Plant Science* 18:625-632

This article discusses the mechanisms underlying epigenetic variation and indicates that, in the species studied so far, most epigenetic changes do not affect gene functioning.

Qi J, Liu X, Shen D, Miao H, Xie B, Li X, Zeng P, Wang S, Shang Y, Gu X, Du Y, Li Y, Lin T, Yuan J, Yang X, Chen J, Chen H, Xiong X, Huang K, Fei ZJ, Mao LY, Tian L, Stadler T, Renner SS, Kamoun S, Lucas WJ (2013) A genomic variation map provides insights into the genetic basis of cucumber domestication and diversity. *Nature Genetics* 45:1510-1515

This article presents a map of genome variation for cucumber, discusses how this has provided new insights in domestication, and indicates that the knowledge obtained is useful in further breeding. As such, it is a good example of the application of next-generation sequencing technologies.

Roy SJ, Tucker EJ, Tester M (2011) Genetic analysis of abiotic stress tolerance in crops. *Current opinion in plant biology* 14:232-239

This diversity is a possible source for abiotic stress tolerance traits, which can be exploited using genetic approaches.

Ruiz KB, Biondi S, Oses R, Acuna-Rodriguez IS, Antognoni F, Martinez-Mosqueira EA, Coulibaly A, Canahua-Murillo A, Pinto M, Zurita-Silva A, Bazile D, Jacobsen SE, Molina-Montenegro MA (2014) Quinoa biodiversity and sustainability for food security under climate change. A review. *Agronomy for Sustainable Development* 34:349-359

This article gives information on various characteristics (origin, genetic diversity, tolerance to drought and salinity) of quinoa, crop traditionally grown in South America but now rapidly spreading to other countries. As such it provides an example of the increasing interest in non-traditional crops to broaden the base of European agriculture.

Schmitz RJ, Ecker JR (2012) Epigenetic and epigenomic variation in *Arabidopsis thaliana*. *Trends in Plant Science* 17:149-154

*This article provides a good introduction into epigenetics and the important role of *Arabidopsis thaliana* in epigenetic research. It shows that genetic and epigenetic effects are closely interrelated, and that new techniques such as high-throughput DNA sequencing can help to unravel the intricate relationship between genotype, epigenotype and phenotype, allowing this knowledge to be applied to a wide range of species.*

Schneeberger K, Weigel D (2011) Fast-forward genetics enabled by new sequencing technologies. *Trends in Plant Science* 16:282-288

This article sketches the vast impact of new sequencing technologies on plant breeding, and is especially enthusiastic about the possibilities they create for using genes from non-crop plants for the improvement of crops. They, however, do not address the social resistance to genetic modification.

Sinclair TR (2011) Challenges in breeding for yield increase for drought. *Trends in Plant Science* 16:289-293

This article shows the problems of translating the rapidly increasing knowledge at the molecular level in improved plants in the field, and discusses ways to help overcome these problems, with drought-resistance as an example.

Springer NM (2013) Epigenetics and crop improvement. *Trends in Genetics* 29:241-247

This article reviews the potential and limitations of epigenetic variation in crop improvement.

Stapley J, Reger J, Feulner PGD, Smadja C, Galindo J, Ekblom R, Bennison C, Ball AD, Beckerman AP, Slate J (2010) Adaptation genomics: the next generation. *Trends in Ecology & Evolution* 25:705-712

This article discusses the impact of next generation sequencing on the study of the genetics of adaptation, and argues that it will greatly enhance progress.

Todesco M, Sureshkumar B, Hu TT, Traw MB, Horton M, Epple P, Kuhns C, Sridevi S, Schwartz C, Lanz C, Laitinen RAE, Huang Y, Chory J, Lipka V, Borevitz JO, Dangl JL, Bergelson J, Nordborg M, Weigel D (2010) Natural allelic variation underlying a major fitness trade-off in *Arabidopsis thaliana*. *Nature* 465:632-636

This article gives a nice example of how an allele that favours pathogen resistance may also leads to decreased growth. This study illustrates that in breeding for resistance, one should not solely look at resistance effects of alleles, but also at other effects on plant performance.

Varshney RK, Bansal KC, Aggarwal PK, Datta SK, Craufurd PQ (2011) Agricultural biotechnology for crop improvement in a variable climate: hope or hype? *Trends in Plant Science* 16:363-371

This article sketches the potential of molecular breeding and genetic engineering, but also indicates that adoption of biotech crops will depend on public perceptions and public acceptance.

Varshney RK, Glaszmann JC, Leung H, Ribaut JM (2010) More genomic resources for less-studied crops. *Trends in Biotechnology* 28:452-460

This article gives a good overview of the availability of genomic resources of a range of crops, and how these were used for making core reference sets. It also sets out how the combination of genotyping, core reference sets and phenotyping can be used to enhance breeding.

Varshney RK, Nayak SN, May GD, Jackson SA (2009) Next-generation sequencing technologies and their implications for crop genetics and breeding. *Trends in Biotechnology* 27:522-530

This article discusses the concept, advantages, applications and potential implications of NGS technologies for crop genetics and breeding.

Walck J, Dixon K (2009) Time to future-proof plants in storage. *Nature* 462:721

This article deals with the collection and conservation of wild species by seed banks, with the ambitious aim to “capture sufficient genetic diversity to rebuild the world’s ecosystems” after climate change.

Zaharieva M, Ayana NG, Al-Hakimi A, Misra SC, Monneveux P (2010) Cultivated emmer wheat (*Triticum dicoccon* Schrank), an old crop with promising future: a review. *Genetic Resources and Crop Evolution* 57:937-962

This article presents a review of the taxonomy, diversity and history of cultivation of emmer wheat. Successful examples of emmer wheat utilization for the development of durum or bread wheat cultivars are examined, and the perspectives in using emmer wheat as health food and for the development of new breeding germplasm are discussed. As such it provides an example of revived interest in old crops and crop varieties to broaden the base of European agriculture, and of the

importance of minor species as reservoirs of genes for improving major species, in this case bread and durum wheat.

List of papers with summaries consulted by the Forest Genetic Resources domain

Abril N, Gion JM, Kerner R, Muller-Starck G, Navarro Cerrillo RM, Plomion C, Renaut J, Valledor L, Jorin-Novo JV (2011) Proteomics research on forest trees, the most recalcitrant and orphan plant species. (Special Issue: Plant proteomics 2011.). *Phytochemistry* 72:1219-1242

Proteomics research overview in trees.

Alberto FJ, Aitken SN, Alia R, Gonzalez-Martinez SC, Hanninen H, Kremer A, Lefevre F, Lenormand T, Yeaman S, Whetten R, Savolainen O (2013) Potential for evolutionary responses to climate change - evidence from tree populations. *Glob Change Biol* 19:1645-1661

Review on predicting evolutionary responses to climate change of tree populations. The greatest adaptive response is expected when populations are large, have high genetic variability, selection is strong, and there is ecological opportunity for establishment of better adapted genotypes.

Allendorf FW, Hohenlohe PA, Luikart G (2010) Genomics and the future of conservation genetics. *Nat Rev Genet* 11:697-709

Authors discuss problems in conservation biology in which genomics will be most valuable in providing new insights and recognise limitations in applying genomic tools to conservation issues. Review focus on conservation genetics in general, not specifically on trees.

Aravanopoulos FA (2011) Genetic monitoring in natural perennial plant populations. *Botany* 89:75-81

Genetic monitoring should concentrate on gene conservation units of such species, to be advanced in a dynamic gene conservation scheme. Three indicators are proposed for genetic monitoring based on a gene-ecological approach: natural selection, genetic drift, and a gene flow-mating system.

Bacles CFE, Jump AS (2011) Taking a tree's perspective on forest fragmentation genetics. *Trends Plant Sci* 16:13-18

Despite longstanding research, how anthropogenic disturbance affects the genetics of tree populations remains poorly understood. Empirical evidence frequently does not fit with theoretical expectations, a disparity that has recently been dubbed the 'paradox of forest fragmentation genetics'.

Birol I, Raymond A, Jackman SD, Pleasance S, Coope R, Taylor GA, Saint Yuen MM, Keeling CI, Brand D, Vandervalk BP, Kirk H, Pandoh P, Moore RA, Zhao YJ, Mungall AJ, Jaquish B, Yanchuk A, Ritland C, Boyle B, Bousquet J, Ritland K, MacKay J, Bohlmann J, Jones SJM (2013) Assembling the 20 Gb white

spruce (*Picea glauca*) genome from whole-genome shotgun sequencing data. *Bioinformatics* 29:1492-1497

The Picea glauca genome sequenced and assembled.

De Kort H, Vandepitte K, Bruun HH, Closset-Kopp D, Honnay O, Mergeay J (2014) Landscape genomics and a common garden trial reveal adaptive differentiation to temperature across Europe in the tree species *Alnus glutinosa*. *Molecular Ecology* 23:4709-4721

A total of 24 European populations of black alder were studied in a common garden and through landscape genomic approaches, providing empirical evidence of local adaptation to temperature.

Eckert AJ, Bower AD, Gonzalez-Martinez SC, Wegrzyn JL, Coop G, Neale DB (2010) Back to nature: ecological genomics of loblolly pine (*Pinus taeda*, Pinaceae). (Special Issue: Landscape genetics.). *Molecular Ecology* 19:3789-3805

Review on the central-marginal hypothesis based on 134 studies, not trees specifically. The review concludes that there has been little effort to determine whether geographical trends in putatively neutral variation at marker loci are reflected by quantitative genetic-trait variation likely to influence the adaptive potential of populations. As long as it is not clear what the relative contribution of contemporary demographic factors to the geographical variation in population genetic parameters is, it is not possible to apply the results to management of peripheral populations.

FAO (2014), The State of the World's Forest Genetic Resources, <SoW-FGR_2014.pdf>

The first report on The State of the World's Forest Genetic Resources.

Funk WC, McKay JK, Hohenlohe PA, Allendorf FW (2012) Harnessing genomics for delineating conservation units. *Trends Ecol Evol* 27:489-496

The use of genomics for delineating conservation units. Authors' opinion is that both neutral and adaptive markers provide information that should be combined to make optimal management decisions.

Gailing O, Vornam B, Leinemann L, Finkeldey R (2009) Genetic and genomic approaches to assess adaptive genetic variation in plants: forest trees as a model. *Physiol Plant* 137:509-519

Review on genetic and genomic approaches to assess adaptive genetic variation in forest trees, especially oaks. The authors conclude that genome-wide association mapping studies are not feasible in tree species because of the enormous amount of SNP markers required in outcrossing trees where

recombination over many generations had broken up the LD. The success of such an approach depends largely on the reasonable selection and sequencing of candidate genes.

Geburek T, Konrad H (2008) Why the conservation of forest genetic resources has not worked. Conservation Biology 22:267-274

Impediments to the implementation of FGR conservation in Europe.

Gonzalez-Martinez SC, Krutovsky KV, Neale DB (2006) Forest-tree population genomics and adaptive evolution. New Phytol 170:227-238

The authors review how developments in forest genomics can provide us with tools to identify the genes controlling adaptive traits (functional genomics) and methods to carry out new-generation population genetic studies. Especially population genomics, through deciphering allelic effects on phenotypes and identifying patterns of adaptive variation at the landscape level can be a useful tool in the future to design conservation strategies for forest trees.

Grattapaglia D, Plomion C, Kirst M, Sederoff RR (2009) Genomics of growth traits in forest trees. Curr Opin Plant Biol 12:148-156

This review discusses recent advances towards a genomic understanding of tree growth, and the potential applications to forest productivity and sustainability. Five complementary genomic approaches to identify genomic regions, genes or polymorphisms involved in the control of growth traits in trees are discussed.

Grattapaglia D, Resende MDV (2011) Genomic selection in forest tree breeding. Tree Genet Genomes 7:241-255

Chapter on current status and perspectives of GS in tree breeding including review of some experimental studies of GS in Eucalyptus and Loblolly pine.

Hamanishi ET, Campbell MM (2011) Genome-wide responses to drought in forest trees. Forestry 84:273-283

Review on genome-wide dissection of forest tree response to drought, including transcriptome analyses, QTL mapping, association studies, proteomics.

Hampe A, Petit RJ (2005) Conserving biodiversity under climate change: the rear edge matters. Ecol Lett 8:461-467

In contrast to the expanding edge, the low-latitude limit (rear edge) of species ranges remains

understudied, and the critical importance of rear edge populations as long-term stores of species' genetic diversity and foci of speciation has been little acknowledged. The authors argue that rear edge populations are important for the survival and evolution of biota.

Hamrick JL (2004) Response of forest trees to global environmental changes. For Ecol Manage 197:323-335

The author concludes that the combination of individual longevity, high intra-population genetic diversity and the potential for high rates of pollen flow should make tree species especially resistant to extinction and the loss of genetic diversity during changing environmental conditions.

Harfouche A, Meilan R, Altman A (2011) Tree genetic engineering and applications to sustainable forestry and biomass production. Trends in Biotechnology 29:9-17

Review on recent progress in the development of GM trees including recent scientific discoveries and key targets for genetic engineering

Harfouche A, Meilan R, Kirst M, Morgante M, Boerjan W, Sabatti M, Mugnozza GS (2012) Accelerating the domestication of forest trees in a changing world. Trends Plant Sci 17:64-72

The authors give their opinion on novel and improved tree breeding strategies including genomic selection and transgenic approaches and how these can be used to speed up progress in tree improvement.

Holderegger R, Buehler D, Gugerli F, Manel S (2010) Landscape genetics of plants. Trends Plant Sci 15:675-683

Landscape genetics of plants lags behind that of animals, both in number of studies and consideration of landscape elements. The classical landscape distance/resistance approach to study gene flow is challenging in plants, whereas boundary detection and the assessment of contemporary gene flow are more feasible. By contrast, the new field of landscape genetics of adaptive genetic variation, establishing the relationship between adaptive genomic regions and environmental factors in natural populations, is prominent in plant studies.

Isaac-Renton MG, Roberts DR, Hamann A, Spiecker H (2014) Douglas-fir plantations in Europe: a retrospective test of assisted migration to address climate change. Glob Change Biol 20:2607-2617

Douglas-fir plantations in Europe: a retrospective test of assisted migration to address climate change.

Isik F (2014) Genomic selection in forest tree breeding: the concept and an outlook to the future. *New For* 45:379-401

Overview of genomic selections in trees is presented including discussion on challenges and opportunities of implementation of GS. A few empirical proof of concept studies suggest that GS could be successful.

Khan MA, Korban SS (2012) Association mapping in forest trees and fruit crops. *J Exp Bot* 63:4045-4060

Review on importance, current status and potential of association mapping and LD studies in forest trees and their role in genetic improvement. Several studies mentioned in this review demonstrate the utility of LD mapping in detecting associations.

Koskela, J., Buck, A. and Teissier du Cros, E., editors. 2007. *Climate change and forest genetic diversity: Implications for sustainable forest management in Europe*. Bioversity International, Rome, Italy. 111 pp.

Report of Bioversity International and IUFRO meeting on Climate change and forest genetic diversity: Implications for sustainable forest management in Europe.

Koskela J, Lefevre F, Schueler S, Kraigher H, Olrik DC, Hubert J, Longauer R, Bozzano M, Yrjana L, Alizoti P, Rotach P, Vietto L, Bordacs S, Myking T, Eysteinnsson T, Souvannavong O, Fady B, Cuyper Bd, Heinze B, Wuhlisch Gv, Ducouso A, Ditlevsen B (2013) Translating conservation genetics into management: Pan-European minimum requirements for dynamic conservation units of forest tree genetic diversity. *Biol Conserv* 157:39-49

Review on theoretical and practical aspects of genetic management of forest trees including presentation of pan-European minimum requirements for genetic conservation units of forest trees.

Koskela and Lefevre (2013) In: Kraus D., Krumm F. (eds) 2013. *Integrative approaches as an opportunity for the conservation of forest biodiversity*. European Forest Institute. 284 pp.

Conservation of forest genetic diversity and the integration of genetic aspects into biodiversity conservation and forest management.

Kremer, 2007. How well can existing forests withstand climate change? In: Koskela, J., Buck, A. and Teissier du Cros, E., editors. 2007. *Climate change and forest genetic diversity: Implications for sustainable forest management in Europe*. Bioversity International, Rome, Italy. 111 pp.

Report of Evoltree meeting, giving an overview of the advances of genomics of forest and ecosystem health in the Fagaceae: development of tools and application of genomic resources.

Kremer A, Abbott AG, Carlson JE, Manos PS, Plomion C, Sisco P, Staton ME, Ueno S, Vendramin GG (2012) Genomics of Fagaceae. *Tree Genet Genomes* 8:583-610

An overview of recent achievements and development of genomic resources in the Fagaceae.

Kremer A, Ronce O, Robledo-Arnuncio JJ, Guillaume F, Bohrer G, Nathan R, Bridle JR, Gomulkiewicz R, Klein EK, Ritland K, Kuparinen A, Gerber S, Schueler S (2012) Long-distance gene flow and adaptation of forest trees to rapid climate change. *Ecol Lett* 15:378-392

Review of data on the extent of long-distance gene flow to examine the hypothesis that long-distance gene flow could compensate for the long generation time of trees facilitating adaptation of trees to rapid climate change.

Kremer A, Potts BM, Delzon S (2014) Genetic divergence in forest trees: understanding the consequences of climate change. (Special Issue: Climate change and species range shifts.). *Funct Ecol* 28:22-36

Predicted climate change is heading in many respects into untested environmental conditions for trees and to the reshuffling of species distributions. Exploration of the consequences that these changes are likely to have on population differentiation of adaptive traits.

Krutovsky K.V., J. Burczyk , I. Chybicki, R. Finkeldey ,T. Pyhäjärvi , and J.J. Robledo-Arnuncio (2012) Chapter four, Gene Flow, Spatial Structure, Local Adaptation, and Assisted Migration in Trees. In: R.J. Schnell & P.M. Priyadarshan (eds). *Genomics of Tree Crops*. Springer. 369 pp.

Book chapter in Genomics of tree crops on gene flow, spatial structure, local adaptation, and assisted migration in trees.

Lefevre F, Koskela J, Hubert J, Kraigher H, Longauer R, Olrik DC, Schuler S, Bozzano M, Alizoti P, Bakys R, Baldwin C, Ballian D, Black-Samuelsson S, Bednarova D, Bordacs S, Collin E, Cuyper Bd, Vries SMGd, Eysteinnsson T, Frydl J, Haverkamp M, Ivankovic M, Konrad H, Koziol C, Maaten T, Paino EN (2013) Dynamic conservation of forest genetic resources in 33 European countries. *Conservation Biology* 27:373-384

Assessment of the dynamic conservation network of Forest genetic resources (conservation units) across Europe including a genetic gap analysis.

Lindner M, Maroschek M, Netherer S, Kremer A, Barbati A, Garcia-Gonzalo J, Seidl R, Delzon S, Corona P, Kolstrom M, Lexer MJ, Marchetti M (2010) Climate change impacts, adaptive capacity, and vulnerability of European forest ecosystems. *For Ecol Manage* 259:698-709

This study compiles and summarizes the existing knowledge about observed and projected impacts of climate change on forests in Europe.

Loo J (2011) <Loo et al_2011_backgroundpaper 56.pdf>

Background FAO paper. Review of the impacts of climate change on forest genetic resources and the potential role of these resources in mitigating and adapting to change

Loss SR, Terwilliger LA, Peterson AC (2011) Assisted colonization: integrating conservation strategies in the face of climate change. *Biol Conserv* 144:92-100

Review on the discussion and criticism associated with assisted colonization. The authors propose an integrated conservation strategy that includes management for habitat connectivity, conservation genetics, and when necessary, assisted colonization of species that are still unable to shift their ranges.

Mackay J, Dean JFD, Plomion C, Peterson DG, Canovas FM, Pavy N, Ingvarsson PK, Savolainen O, Guevara MA, Fluch S, Vinceti B, Abarca D, Diaz-Sala C, Cervera MT (2012) Towards decoding the conifer giga-genome. *Plant Molecular Biology* 80:555-569

Review outlines the current accomplishments in conifer genomics, specifically transcriptomics, mapping, QTL and association studies.

Manel S, Holderegger R (2013) Ten years of landscape genetics. *Trends in Ecology & Evolution* 28:614-621

Review on the past 10 years of landscape genetics, including recent methodological and conceptual advances and discussion on potential applications in terms of adaptation to global change and the conservation of natural resources.

Máttyás C, Vendramin GG, Fady B (2009) Forests at the limit: evolutionary — genetic consequences of environmental changes at the receding (xeric) edge of distribution. Report from a research workshop. *Ann For Sci* 66:800-800

Forests at the limit: evolutionary — genetic consequences of environmental changes at the receding (xeric) edge of distribution. Report from a research workshop.

McLachlan JS, Hellmann JJ, Schwartz MW (2007) A framework for debate of assisted migration in an era of climate change. *Conservation biology: the journal of the Society for Conservation Biology* 21:297-302

Authors suggest a spectrum of policy options, and outline a framework for moving toward a consensus on assisted migration.

Myburg AA, Grattapaglia D, Tuskan GA, Hellsten U, Hayes RD, Grimwood J, Jenkins J, Lindquist E, Tice H, Bauer D, Goodstein DM, Dubchak I, Poliakov A, Mizrachi E, Kullam ARK, Hussey SG, Pinard D, Van der Merwe K, Singh P, Van Jaarsveld I, Silva OB, Togawa RC, Pappas MR, Faria DA, Sansaloni CP, Petroli CD, Yang XH, Ranjan P, Tschaplinski TJ, Ye CY, Li T, Sterck L, Vanneste K, Murat F, Soler M, Clemente HS, Saidi N, Cassan-Wang H, Dunand C, Hefer CA, Bornberg-Bauer E, Kersting AR, Vining K, Amarasinghe V, Ranik M, Naithani S, Elser J, Boyd AE, Liston A, Spatafora JW, Dharmwardhana P, Raja R, Sullivan C, Romanel E, Alves-Ferreira M, Lheim CK, Foley W, Carocha V, Paiva J, Kudrna D, Brommonschenkel SH, Pasquali G, Byrne M, Rigault P, Tibbits J, Spokevicius A, Jones RC, Steane DA, Vaillancourt RE, Potts BM, Joubert F, Barry K, Pappas GJ, Strauss SH, Jaiswal P, Grima-Pettenati J, Salse J, Peer YV, Rokhsar DS, Schmutz J (2014) The genome of *Eucalyptus grandis*. *Nature* 510:356

The genome of Eucalyptus grandis sequenced.

Neale DB (2007) Genomics to tree breeding and forest health. (Special Issue: Genomes and evolution.). *Current Opinion in Genetics & Development* 17:539-544

Overview on genomic-based breeding technologies. Applications begin by first dissecting complex traits in trees to their individual gene components and for that the association genetics approach is quite powerful in trees.

Neale DB, Kremer A (2011) Forest tree genomics: growing resources and applications. *Nat Rev Genet* 12:111-122

This review summarizes the highlights of forest genomics research done in the past two decades and gives priorities for future research in the next decade. They describe how basis research is translated to applications in tree breeding and management of natural populations.

Neale DB, Langley CH, Salzberg SL, Wegrzyn JL (2013) Open access to tree genomes: the path to a better forest. *Genome Biol* 14:8

A brief summary of the rapid progress made in developing genomic resources in a small number of forest tree species. The authors give their view on what is needed in case of investments in database resources and understanding ecological functions such as an open-access culture and a well-developed comparative genomics infrastructure.

Nystedt B, Street NR, Wetterbom A, Zuccolo A, Lin Y, Scofield DG, Vezzi F, Delhomme N, Giacomello S, Alexeyenko A, Vicedomini R, Sahlin K, Sherwood E, Elfstrand M, Gramzow L, Holmberg K, Hallman J, Keech O, Klasson L, Koriabine M, Kucukoglu M, Kaller M, Luthman J, Lysholm F, Niittyla T, Olson A (2013) The Norway spruce genome sequence and conifer genome evolution. *Nature* 497:579-584

Authors present the draft assembly of the 20-gigabase genome of Norway spruce (Picea abies), the first available for any gymnosperm.

Paques, (2013), Forest Tree Breeding in Europe – Current State of the Art and Perceptions. *State of the art of forest tree breeding in Europe.*

Parisod C, Holderegger R (2012) Adaptive landscape genetics: pitfalls and benefits. *Molecular Ecology* 21:3644-3646

Review on landscape genetics: pitfalls and benefits. Considerable amounts of genetic and/or environmental data can now be collected. Showing the links between landscapes and adaptive genetic variation will ultimately move the field beyond association studies.

Park A, Talbot C (2012) Assisted migration: uncertainty, risk and opportunity. *For Chron* 88:412-419

Discussion paper on aspects of assisted migration, including scientific uncertainties around future warming, recent ecophysiological results that have implications for the adaptation and acclimation of trees to climate change, opportunities for innovative forest management, the influence of economic trends on the future of the Canadian forest industry, and limitations on public knowledge of climate change, all of which are factors that will influence the feasibility of AM schemes in the future.

Pautasso M (2009) Geographical genetics and the conservation of forest trees. *Perspectives in Plant Ecology, Evolution and Systematics* 11:157-189

Overview of range-wide molecular studies of genetic variation in tree species.

Pedlar JH, McKenney DW, Aubin I, Beardmore T, Beaulieu J, Iverson L, O'Neill GA, Winder RS, Ste-Marie C (2012) Placing forestry in the assisted migration debate. *Bioscience* 62:835-842

Example of practice of assisted migration on a larger scale, by existing North American forestry operations with a focus on moving populations of widely distributed, nonthreatened tree species within their current range limits.

Petit RJ, Aguinalalde I, Beaulieu J, Bittkau C, Brewer S, Cheddadi R, Ennos R, Fineschi S, Grivet D, Lascoux M, Mohanty A, Muller-Starck G, Demesure-Musch B, Palme A, Martin JP, Rendell S,

Vendramin GG (2003) Glacial refugia: hotspots but not melting pots of genetic diversity. *Science* 300:1563-1565

A study of the chloroplast DNA variation in 22 widespread European trees and shrubs sampled in the same forests.

Petit RJ, Duminil J, Fineschi S, Hampe A, Salvini D, Vendramin GG (2005) Comparative organization of chloroplast, mitochondrial and nuclear diversity in plant populations. *Molecular Ecology* 14:689-701

A survey of population studies of organelle DNA in plants including data from 183 species. The authors suggest that gene flow through pollen is quantitatively much more important than through seeds.

Petit RJ, Hampe A (2006) Some evolutionary consequences of being a tree. *Annual Review of Ecology, Evolution, and Systematics* 37:187-214

Authors discuss trees' major ecological characteristics and examine why trees generally harbor such high levels of genetic diversity and can adapt rapidly to local conditions.

Porth I, Klapste J, Skyba O, Hannemann J, McKown AD, Guy RD, DiFazio SP, Muchero W, Ranjan P, Tuskan GA, Friedmann MC, Ehling J, Cronk QCB, El-Kassaby YA, Douglas CJ, Mansfield SD (2013) Genome-wide association mapping for wood characteristics in *Populus* identifies an array of candidate single nucleotide polymorphisms. *New Phytol* 200:710-726

Example of genome-wide association mapping for wood characteristics in Populus: identification of an array of candidate single nucleotide polymorphisms.

Pritchard HW, Moat JF, Ferraz JBS, Marks TR, Camargo JLC, Nadarajan J, Ferraz IDK (2014) Innovative approaches to the preservation of forest trees. *For Ecol Manage*

Review of some of the recent successes relating mainly to tree seed biology that have resulted in the development and application of innovative actions in vitro storage technology of tree seeds.

Ritland C (2011) <Ritland-et-al-2011_Ch5_Genetic Mapping in Conifers.pdf>

Book chapter that summarizes the history and current status of genetic mapping in conifers.

Ruotsalainen S (2014) Increased forest production through forest tree breeding. *Scand J Forest Res* 29:333-344

Review on methods in tree breeding programmes aimed at increased wood production and describes how breeding can fulfil the raw material needs of bio economy.

Savolainen O, Pyhajarvi T (2007) Genomic diversity in forest trees. (Special issue: Genome studies and molecular genetics.). *Curr Opin Plant Biol* 10:162-167

Summary on the estimation of nucleotide diversity in forest trees.

Savolainen O, Pyhajarvi T, Knurr T (2007) Gene flow and local adaptation in trees. *Annual Review of Ecology, Evolution, and Systematics* 38:595-619

Review on gene flow and local adaptation, describing that gene flow in forest trees is extensive, and has given rise in many cases to uniform neutral allele frequencies. The extent of gene flow through pollen is difficult to estimate because of the long tail of the distribution. In the face of this gene flow, most trees studied show signals of adaptive differentiation in reciprocal transplant experiments or common garden experiments. The strength of selection on the different adaptive traits remains to be quantified.

Schueler S, Kapeller S, Konrad H, Geburek T, Mengl M, Bozzano M, Koskela J, Lefevre F, Hubert J, Kraigher H, Longauer R, Olrik DC (2013) Adaptive genetic diversity of trees for forest conservation in a future climate: a case study on Norway spruce in Austria. *Biodivers Conserv* 22:1151-1166

Gap analysis of the Austrian genetic conservation units in the EUGIS Portal suggests adequate coverage of the genetic hotspots in southern parts of Austria, but not in eastern and northern Austria. Therefore conservation measures and sustainable utilization of the valuable genetic resources in these regions need to be expanded to cover their high adaptive genetic variation and local adaptation to a warmer climate. The study shows that current conservation efforts need to be evaluated for their effectiveness to protect genetic resources that are important for the survival of trees in a future climate.

Schueler S, Falk W, Koskela J, Lefevre F, Bozzano M, Hubert J, Kraigher H, Longauer R, Olrik DC (2014) Vulnerability of dynamic genetic conservation units of forest trees in Europe to climate change. *Glob Change Biol* 20:1498-1511

Study on the projected impact of climate change on the large scale network of genetic conservation units of forest trees in Europe with focus on six major species. The study suggests that there is a strong need to intensify monitoring efforts and to develop additional conservation measures for populations in the most vulnerable units, to establish dynamic conservation populations outside the current species distribution ranges with European assisted migration schemes and to increase the size of the conservation units.

Sork VL, Aitken SN, Dyer RJ, Eckert AJ, Legendre P, Neale DB (2013) Putting the landscape into the genomics of trees: approaches for understanding local adaptation and population responses to changing climate. *Tree Genet Genomes* 9:901-911

Review on traditional approaches in forest genetics for studying local adaptation and identifying loci underlying locally adapted phenotypes and existing and emerging methods available for landscape genomic analyses.

Steane DA, Potts BM, McLean E, Prober SM, Stock WD, Vaillancourt RE, Byrne M (2014) Genome-wide scans detect adaptation to aridity in a widespread forest tree species. *Molecular Ecology* 23:2500-2513

Example of the use of genomic scans and outlier marker detection to detect signals of adaptation to aridity in wild populations of Eucalyptus.

Strauss SH, Schmitt M, Sedjo R (2009) Forest scientist views of regulatory obstacles to research and development of transgenic forest biotechnology. *J For* 107:350-357

Discussion paper on Forest biotech in relation to the Cartagena Protocol.

Suzuki H (2014) <Suzuki et al_2014.pdf>

Review on recent advances in forest tree biotechnology.

Tuskan GA, DiFazio S, Jansson S, Bohlmann J, Grigoriev I, Hellsten U, Putnam N, Ralph S, Rombauts S, Salamov A, Schein J, Sterck L, Aerts A, Bhalerao RR, Bhalerao RP, Blaudez D, Boerjan W, Brun A, Brunner A, Busov V, Campbell M, Carlson J, Chalot M, Chapman J, Chen GL, Cooper D, Coutinho PM, Couturier J, Covert S, Cronk Q, Cunningham R, Davis J, Degroeve S, Dejardin A, Depamphilis C, Detter J, Dirks B, Dubchak I, Duplessis S, Ehlting J, Ellis B, Gendler K, Goodstein D, Gribskov M, Grimwood J, Groover A, Gunter L, Hamberger B, Heinze B, Helariutta Y, Henrissat B, Holligan D, Holt R, Huang W, Islam-Faridi N, Jones S, Jones-Rhoades M, Jorgensen R, Joshi C, Kangasjarvi J, Karlsson J, Kelleher C, Kirkpatrick R, Kirst M, Kohler A, Kalluri U, Larimer F, Leebens-Mack J, Leple JC, Locascio P, Lou Y, Lucas S, Martin F, Montanini B, Napoli C, Nelson DR, Nelson C, Nieminen K, Nilsson O, Pereda V, Peter G, Philippe R, Pilate G, Poliakov A, Razumovskaya J, Richardson P, Rinaldi C, Ritland K, Rouze P, Ryaboy D, Schmutz J, Schrader J, Segerman B, Shin H, Siddiqui A, Sterky F, Terry A, Tsai CJ, Uberbacher E, Unneberg P, Vahala J, Wall K, Wessler S, Yang G, Yin T, Douglas C, Marra M, Sandberg G, Van de Peer Y, Rokhsar D (2006) The genome of black cottonwood, *Populus trichocarpa* (Torr. & Gray). *Science* 313:1596-1604

The first forest tree genome to have its complete DNA sequence determined.

Uchiyama K, Iwata H, Moriguchi Y, Ujino-Ihara T, Ueno S, Taguchi Y, Tsubomura M, Mishima K, Iki T, Watanabe A, Futamura N, Shinohara K, Tsumura Y (2013) Demonstration of genome-wide association studies for identifying markers for wood property and male strobili traits in *Cryptomeria japonica*. PLoS One 8:e79866

*A demonstration of genome-wide association studies for identifying markers for wood property and male strobili traits in *Cryptomeria japonica*.*

Williams MI, Dumroese RK (2013) Preparing for climate change: forestry and assisted migration. J For 111:287-297

Review on current thinking on assisted migration of forest tree species. Lack of operating procedures, uncertainties about future climate conditions, risks associated with moving plants outside their current ranges, and existing policies have hampered formal actions in forest management and conservation.

Zimin A, Stevens KA, Crepeau MW, Holtz-Morris A, Koriabine M, Marcais G, Puiu D, Roberts M, Wegrzyn JL, Jong PJD, Neale DB, Salzberg SL, Yorke JA, Langley CH (2014) Sequencing and assembly of the 22-Gb loblolly pine genome. Genetics 196:875-890

Sequencing and assembly of the 22-Gb loblolly pine genome.

List of papers with summaries consulted by the Animal Genetic Resources Domain

Farm animal genetic diversity in view of sustainable development

Baumung, R., & Hoffmann, I. (2012). Animal genetic diversity and sustainable diets. *SUSTAINABLE DIETS AND BIODIVERSITY*, 2000.

This paper explains the value of farm animal genetic diversity in view of sustainable development of the livestock sector and sustainable human diets. Authors suggest the need for better characterization of breeds in different environments.

Godfray, H. C. J., Beddington, J. R., Crute, I. R., Haddad, L., Lawrence, D., Muir, J. F., . . . Toulmin, C. (2010). Food security: the challenge of feeding 9 billion people. *Science*, 327(5967), 812-818.

Domestication inevitably means that only a subset of the genes available in the wild-species progenitor gene pool is represented among crop varieties and livestock breeds. Unexploited genetic material from land races, rare breeds, and wild relatives will be important in allowing breeders to respond to new challenges. International collections and gene banks provide valuable repositories for such genetic variation, but it is nevertheless necessary to ensure that locally adapted crop and livestock germplasm is not lost in the process of their displacement by modern, improved varieties and breeds.

Hoffmann, I. (2010). Climate change and the characterization, breeding and conservation of animal genetic resources. *Animal Genetics*, 41 Suppl 1(s1), 32-46. doi: 10.1111/j.1365-2052.2010.02043.

Because of the potential impact of climate change on the use of animal genetic diversity there is a need for mitigation and adaptation strategies. A range of measures are proposed, including better characterization, genetic improvement and conservation measures.

Koohafkan, P., & Cruz, M. J. D. (2011). Conservation and adaptive management of globally important agricultural heritage systems (GIAHS). *Journal of Resources and Ecology*, 2(1), 22-28.

International partnership GIAHS (Globally Important Agricultural Heritage Systems) shows how agricultural biodiversity, associated biodiversity knowledge systems, landscapes, food and livelihood security and cultures are interconnected.

Seré, C., van der Zijpp, A., Persley, G., & Rege, E. (2008a). Dynamics of livestock production systems, drivers of change and prospects for animal genetic resources. *Animal Genetic Resources Information*, 42, 3-24.

Analysis of the key drivers of change in the global livestock sector, and highlighting the need for complementary actions to improve the management of animal genetic resources and to maintain future options in an uncertain world.

Strategies for conservation and sustainable use

FAO. (2012). Cryoconservation of animal genetic resources. *FAO Animal Production and Health Guidelines. No. 12. Rome.*

FAO guidelines for cryoconservation of animal genetic resources provide an overview of the fundamental issues involved in developing and operating gene banks as elements in comprehensive national strategies for the management of animal genetic resources.

FAO. (2013). In vivo conservation of animal genetic resources. *FAO Animal Production and Health Guidelines. No. 14. Rome.*

The Guidelines present the basic concepts involved in the development and implementation of in vivo conservation plans for animal genetic resources for food and agriculture.

Gandini, G., and Oldenbroek, K. (2007). Strategies for moving from conservation to utilization. *Utilisation and conservation of farm animal genetic resources, 29-54.*

General framework to choose the most appropriate (in situ and/or ex situ) conservation strategy.

Lauvie, A., Audiot, A., Couix, N., Casabianca, F., Brives, H., & Verrier, E. (2011). Diversity of rare breed management programs: Between conservation and development. *Livestock Science, 140(1), 161-170.*

Breed development initiatives can help maintain the population size, but also revealed situations where some aspects of development actions induced tensions with conservation. This was concluded on the basis of analysis of 132 rare breeds in France.

Marshall, K. (2014). Optimizing the use of breed types in developing country livestock production systems: a neglected research area. *Journal of Animal Breeding and Genetics, 131(5), 329-340.* doi: 10.1111/jbg.12080

Author emphasizes the diversity and dynamics of developing country livestock production systems and development pathways. More strategic research is to assist policy makers and livestock keepers to make informed decisions on the potential use of new breed types.

Martin-Collado, D., Diaz, C., Maki-Tanila, A., Colinet, F., Duclos, D., Hiemstra, S. J., . . . Consortium, E. (2013). The use of SWOT analysis to explore and prioritize conservation and development strategies for local cattle breeds. *Animal*, 7(6), 885-894. doi: Doi 10.1017/S175173111200242x

A quantified SWOT (Strengths, Weaknesses, Opportunities and Threats) analysis method was developed as a decision-making tool for identification and ranking of conservation and development strategies of local breeds. The method was applied to a set of 13 cattle breeds in six European countries.. The most important strengths and weaknesses were related to production systems and farmers. The most important opportunities were found in marketing new products, whereas the most relevant threats were found in selling the current products.

Breed risk assessment

Alderson, L. (2009). Breeds at risk: Definition and measurement of the factors which determine endangerment. *Livestock Science*, 123(1), 23-27.

A model breed monitoring system is proposed which encompasses – besides population size - other important factors of geographical concentration and genetic erosion.

FAO. (2013). In vivo conservation of animal genetic resources. *FAO Animal Production and Health Guidelines. No. 14. Rome.*

The Guidelines present the basic concepts involved in the development and implementation of in vivo conservation plans for animal genetic resources for food and agriculture.

Hiemstra, S. J., de Haas, Y., Mäki-Tanila, A., & Gandini, G. (2010). Local cattle breeds in Europe. *Development of policies and strategies for self-sustaining breeds. Wageningen Academic Publ., Wageningen, The Netherlands.*

The EURECA project analyzed genetic and non-genetic factors that can affect the endangerment of local (cattle) breeds in Europe. Different sources of data were used to assess the (self) sustainability of breeds including the use of information from stakeholder perceptions. Decision making tools for the development of breed strategies and policies were examined in this project.

Valuation of AnGR

Drucker, A. G. (2010). Where's the beef? The economics of AnGR conservation and its influence on policy design and implementation. *Animal Genetic Resources/Ressources génétiques animales/Recursos genéticos animales*, 47, 85-90.

Adam Drucker reviewed methodologies, analytical tools and decision-support tools in the field of economics of agrobiodiversity conservation and sustainable use. He stressed the importance of valuation and the potential future role of economics in the design of cost-effective conservation programmes.

Narloch, U., Drucker, A. G., & Pascual, U. (2011). Payments for agrobiodiversity conservation services for sustained on-farm utilization of plant and animal genetic resources. *Ecological Economics*, 70(11), 1837-1845. doi: DOI 10.1016/j.ecolecon.2011.05.018

This paper discusses theoretical and applied insights related to Payments for Ecosystem Services (PACS) and its application to tackle market failures, associated with the public good characteristics of agrobiodiversity conservation services.

Zander, K. K., Signorello, G., De Salvo, M., Gandini, G., & Drucker, A. G. (2013). Assessing the total economic value of threatened livestock breeds in Italy: Implications for conservation policy. *Ecological Economics*, 93, 219-229. doi: DOI 10.1016/j.ecolecon.2013.06.002

The paper explains the methodology used and the results of a 'willingness to pay' (WTP) – choice experiment study to investigate the total economic value (TEV) of local breeds.

Ecosystem services

CGRFA, F. (2014). The nature of ecosystem services provided by livestock species and breeds. *CGRFA/WG-AnGR-8/14/5*.

The document summarizes the nature of ecosystem services provided by livestock species and breeds, based on a European and global survey and literature review. More details are presented in Background Study Paper 66 (CGRFA, to be published 2014).

Hoffmann, I., Gandini, G., From, T., Hiemstra, S.J. (2014). Reconciling nature protection with breed conservation – the environmental values of local livestock breeds in Europe.

The paper presents the outcomes of a European wide survey, collecting cases of breeds linked to agro-ecosystem of particular conservation value. Authors discuss motivations and tools to maintain or enhance the beneficial impacts of local livestock grazing on European biodiversity.

Jackson, L. E., Pascual, U., & Hodgkin, T. (2007). Utilizing and conserving agrobiodiversity in agricultural landscapes. *Agriculture, ecosystems & environment*, 121(3), 196-210.

This paper has emphasized the need for more research on agrobiodiversity and its ecosystem services. Society will need to invest more heavily in agrobiodiversity research, as well as conservation for the sake of option and quasi-option value, not only of genetic resources but of the much broader set of organisms and habitats that occupy the range of ecosystems in agricultural landscapes.

Prioritization for conservation

Boettcher P. J., T.-B. M., Toro M. A., Simianer H., Eding H., Gandini G., Joost S., Garcia D., Colli L., Ajmone-Marsan P. And The Globaldiv Consortium. (2010). Objectives, criteria and methods for using molecular genetic data in priority setting for conservation of animal genetic resources. *Animal Genetics*, 41, Suppl 1, 64-77.

The paper reviewed the state of the art in approaches for prioritization of breeds for conservation. A variety of technically sound methods and software has been developed, but the authors conclude that there is still limited application in practise.

Hall, S., Lenstra, J., & Deeming, D. (2012). Prioritization based on neutral genetic diversity may fail to conserve important characteristics in cattle breeds. *Journal of Animal Breeding and Genetics*, 129(3), 218-225.

Using public information on beef cattle breeds it was shown that maximizing conserved neutral genetic variation with current techniques may conserve breed-level genetic variation in some traits but not in others. This supports the view that genetic distance measurements based on neutral genetic variation are not sufficient as a determinant of conservation priority among breeds.

Joost, S., Colli, L., Baret, P., Garcia, J., Boettcher, P., Tixier-Boichard, M., & Ajmone-Marsan, P. (2010). Integrating geo-referenced multiscale and multidisciplinary data for the management of biodiversity in livestock genetic resources. *Animal Genetics*, 41(s1), 47-63.

Data integration based on the use of geographic coordinates and Geographic Information Systems (GIS). Integration of genetic and demographic characteristics, environmental conditions, and role of the breed in the local or regional economy for decision making about conservation priorities.

High density SNP arrays and whole genome sequencing

Daetwyler, H. D., Capitan, A., Pausch, H., Stothard, P., van Binsbergen, R., Brondum, R. F., . . . Hayes, B. J. (2014). Whole-genome sequencing of 234 bulls facilitates mapping of monogenic and complex traits in cattle. *Nat Genet*, 46(8), 858-865. doi: 10.1038/ng.3034 <http://www.nature.com/ng/journal/v46/n8/abs/ng.3034.html#supplementary-information>

Whole genomes of 234 cattle were sequenced, including data for 129 individuals from the global Holstein-Friesian population, 43 individuals from the Fleckvieh breed and 15 individuals from the

Jersey breed. The use of this database was demonstrated in identifying a recessive mutation underlying embryonic death and a dominant mutation underlying lethal chondrodysplasia. Genome-wide association studies were also performed for milk production and curly coat, using imputed sequence variants, and identified variants associated with these traits in cattle.

FAO. (2011). Molecular genetic characterization of animal genetic resources. . *FAO Animal Production and Health Guidelines. No. 9. Rome.*

FAO Guidelines Molecular Tools

Groenen, M. A. M., Archibald, A. L., Uenishi, H., Tuggle, C. K., Takeuchi, Y., Rothschild, M. F., . . . Schook, L. B. (2012). Analyses of pig genomes provide insight into porcine demography and evolution. *Nature*, 491(7424), 393-398. doi: <http://www.nature.com/nature/journal/v491/n7424/abs/nature11622.html#supplementary-information>

Assembly and analysis of the genome sequence of a female domestic Duroc pig (Sus scrofa), and a comparison with the genomes of wild and domestic pigs from Europe and Asia.

Characterization and breed evolution

Ajmone-Marsan, P., Garcia, J. F., & Lenstra, J. A. (2010). On the origin of cattle: how aurochs became cattle and colonized the world. *Evolutionary Anthropology: Issues, News, and Reviews*, 19(4), 148-157.

Recent genetic data suggest that maternal lineages of taurine cattle originated in the Fertile Crescent with a possible contribution of South-European wild cattle populations, while zebu cattle originate from the Indus Valley. Subsequently, cattle accompanied human migrations, which led to the dispersal of domestic cattle of taurine, indicine, or mixed origin over Asia, Africa, Europe, and the New World. This has resulted in their adaptation to different environments and considerable variation in appearance and performance.

Bosse, M., Megens, H. J., Frantz, L. A. F., Madsen, O., Larson, G., Paudel, Y., . . . Groenen, M. A. M. (2014). Genomic analysis reveals selection for Asian genes in European pigs following human-mediated introgression. *Nature Communications*, 5. doi: Artn 4392 Doi 10.1038/Ncomms5392

The presence of introgressed Asian haplotypes in European domestic pigs and selection signatures on some loci in these regions was demonstrated, using whole genome sequence data. The introgression signatures are widespread and the Asian haplotypes are rarely fixed. The Asian introgressed haplotypes are associated with regions harbouring genes involved in meat quality, development and fertility.

Groeneveld, L. F., Lenstra, J. A., Eding, H., Toro, M. A., Scherf, B., Pilling, D., . . . Weigend, S. (2010). Genetic diversity in farm animals - a review. (Special Issue: A global view of livestock biodiversity and conservation.). *Animal Genetics*, 41(s1), 6-31. doi: <http://dx.doi.org/10.1111/j.1365-2052.2010.02038.x>

Domestication of livestock species and a long history of migrations, selection and adaptation have created an enormous variety of breeds. Conservation of these genetic resources relies on demographic characterization, recording of production environments and effective data management. In addition, molecular genetic studies allow a comparison of genetic diversity within and across breeds and a reconstruction of the history of breeds and ancestral populations. This has been summarized for cattle, yak, water buffalo, sheep, goats, camelids, pigs, horses, and chickens.

Miao, Y. W., Peng, M. S., Wu, G. S., Ouyang, Y. N., Yang, Z. Y., Yu, N., . . . Zhang, Y. P. (2013). Chicken domestication: an updated perspective based on mitochondrial genomes. *Heredity*, 110(3), 277-282. doi: Doi 10.1038/Hdy.2012.83

To survey its genetic diversity and trace the history of domestication, we investigated a total of 4938 mitochondrial DNA (mtDNA) fragments from 2044 domestic chickens and 51 red junglefowl (Gallus gallus). Phylogeny lineages from the red junglefowl were mingled with those of the domestic chickens. Several local domestication events in South Asia, Southwest China and Southeast Asia were identified.

Mirkena, T., Duguma, G., Haile, A., Tibbo, M., Okeyo, A., Wurzinger, M., & Sölkner, J. (2010). Genetics of adaptation in domestic farm animals: A review. *Livestock Science*, 132(1), 1-12.

This review summarizes available information on genetics of adaptation in major livestock species focusing on small ruminants. Such information would help in identifying the most appropriate and adapted genotypes capable of coping with the environmental challenges posed by the production systems or, wherever possible, in adapting the environments to the requirements of the animals.

Genomics and breeding

Cantet, R. J. C., Christensen, O. F., Pérez-Enciso, M., & van der Werf, J. H. J. (2014). 10th WCGALP in beautiful Vancouver. *Journal of Animal Breeding and Genetics*, 131(5), 409-412. doi: 10.1111/jbgs.12119

Review of World Conference on Genetics Applied to Livestock indicating the progress in the application of whole genome sequencing, genomic selection, advances in quantitative genetics and statistics.

Hayes, B. J., Lewin, H. A., & Goddard, M. E. (2013). The future of livestock breeding: genomic selection for efficiency, reduced emissions intensity, and adaptation. *Trends in Genetics*, 29(4), 206-214.

Genomic selection, which enables prediction of the genetic merit of animals from genome-wide SNP markers, has already been adopted by dairy industries worldwide and is expected to double genetic gains for milk production and other traits. The authors review these gains and discuss how the use of whole-genome sequence data should both accelerate the rate of gain and enable rapid discovery and elimination of genetic defects from livestock populations.

Lund, M. S., Su, G., Janss, L., Guldbandsen, B., & Brøndum, R. F. (2014). Invited review: Genomic evaluation of cattle in a multi-breed context. *Livestock Science*, 166(0), 101-110. doi: <http://dx.doi.org/10.1016/j.livsci.2014.05.008>

In order to obtain accurate genomic breeding values a large number of reference animals with both phenotype and genotype data are needed. This poses a challenge for breeds with small reference populations. One option to overcome this obstacle is to use a multi-breed reference population. Results of this review show that the effect of multi-breed reference populations on the accuracy of genomic prediction is highly affected by the genetic distance between breeds.

Odegard, J., Sonesson, A. K., Yazdi, M. H., & Meuwissen, T. H. E. (2009). Introgression of a major QTL from an inferior into a superior population using genomic selection. *Genetics Selection Evolution*, 41. doi: Artn 38 Doi 10.1186/1297-9686-41-38

Selection schemes aiming at introgressing genetic material from a donor into a recipient line may be performed by backcross-breeding programs combined with selection to preserve the favourable characteristics of the donor population. Results of simulation study show substantial differences between introgression programs using classical and genomic selection. Classical selection was generally inferior with respect to both genetic gain and the ability to preserve the target QTL.

Genomics and conservation

Allendorf, F. W., Hohenlohe, P. A., & Luikart, G. (2010). Genomics and the future of conservation genetics. *Nature Reviews Genetics*, 11(10), 697-709. doi: <http://dx.doi.org/10.1038/nrg2844>

Genomic approaches have the potential to transform the management of populations for conservation in various ways, from estimates of pedigrees and inbreeding based on large numbers of

markers to identification of loci responsible for local adaptation and outbreeding depression. Emerging techniques also allow the study of epigenetics, which may have an important role in conservation genetics in the future.

de Cara, M. A. R., Fernandez, J., Toro, M. A., & Villanueva, B. (2011). Using genome-wide information to minimize the loss of diversity in conservation programmes. *Journal of Animal Breeding and Genetics*, 128(6), 456-464. doi: DOI 10.1111/j.1439-0388.2011.00971.x

The authors studied the effect of using genome-wide marker data versus genealogical data in population management for the maintenance of diversity in conservation schemes using optimal contributions. Using genome-wide marker data performed usually better than using genealogical data or estimated genealogical coancestry to maintain expected and observed heterozygosity.

Engelsma, K. A., Veerkamp, R. F., Calus, M. P. L., & Windig, J. J. (2011). Consequences for diversity when prioritizing animals for conservation with pedigree or genomic information. *Journal of Animal Breeding and Genetics*, 128(6), 473-481. doi: 10.1111/j.1439-0388.2011.00936.x

To optimize conservation strategies, genomic information can help to improve the selection of animals for conservation in those situations where pedigree information is unreliable or absent or when we want to conserve diversity at specific genome regions.

Eynard, S., Windig, J., Leroy, G., Verrier, E., Hiemstra, S., van Binsbergen, R., & Calus, M. (2014). *The Use of Whole Genome Sequence Data to Estimate Genetic Relationships Including Rare Alleles Information*. Paper presented at the 10th World Congress on Genetics Applied to Livestock Production.

Relationship matrices were computed for 118 Holstein bulls, key ancestors of the current population, from three different types of data: pedigree records, 50K SNP chips and whole genome sequences, considering three different scenarios (with, without or only using rare alleles). Rare alleles had a significant impact on relationship estimates, mostly when whole genome sequence data were used.

Hinrichs, D., Meuwissen, T. H. E., Odegard, J., Holt, M., Vangen, O., & Woolliams, J. A. (2007). Analysis of inbreeding depression in the first litter size of mice in a long-term selection experiment with respect to the age of the inbreeding. *Heredity*, 99(1), 81-88.

The paper contributed to a better understanding of inbreeding and inbreeding depression. A new method was developed, investigating differences between the effects of inbreeding in recent generations from that in the more distant past. The method was applied in a long-term selection experiment in mice. It was concluded that the departure from the classical model, which predicts no distinction between this 'old and 'new' inbreeding, must implicate natural selection and purging in influencing the magnitude of depression.

Purfield, D. C., Berry, D. P., McParland, S., & Bradley, D. G. (2012). Runs of homozygosity and population history in cattle. *Bmc Genetics*, 13. doi: 10.1186/1471-2156-13-70

Runs of homozygosity (ROH) are contiguous lengths of homozygous genotypes that are present in an individual due to parents transmitting identical haplotypes to their offspring. The extent and frequency of ROHs may inform on the ancestry of an individual and its population. ROH using high density SNP chips were correlated with the pedigree-based inbreeding coefficients. Findings suggest that ROH are frequent across all breeds but differing patterns of ROH length and burden illustrate variations in breed origins and recent management.

Sonesson, A. K., Woolliams, J. A., & Meuwissen, T. H. E. (2012). Genomic selection requires genomic control of inbreeding. *Genetics Selection Evolution*, 44, 10. doi: 10.1186/1297-9686-44-27

In the past, pedigree relationships were used to control and monitor inbreeding because genomic relationships among selection candidates were not available until recently. The aim of this study was to understand the consequences for genetic variability across the genome when genomic information is used to estimate breeding values and in managing inbreeding. Authors conclude that for controlling inbreeding, it is necessary to account for it on the same basis as what is used to estimate breeding values, i.e. pedigree-based inbreeding control with traditional pedigree-based BLUP estimated breeding values and genome-based inbreeding control with genome-based estimated breeding values.

Toro, M. A., Villanueva, B., & Fernández, J. (2014). Genomics applied to management strategies in conservation programmes. *Livestock Science*, 166(0), 48-53. doi: <http://dx.doi.org/10.1016/j.livsci.2014.04.020>

Three different aspects of the use of genomics in conservation are dealt with in this review paper. First, regarding genetic relationships between individuals, the relationship between the identity by descent (IBD) and the identity by state (IBS) concepts was clarified. Secondly, the use of genomic data for increasing the effectiveness of the management of conserved populations was reviewed. In particular, the paper reviewed the strategies aimed at maintaining within breed genetic diversity and those aimed at removing undesired introgression in order to rescue the original genetic background of a particular breed.

Gene bank collections

Blackburn, H., & Purdy, P. (2011). 38. Genebanks for conservation of livestock genetic resources. *Cryobiology*, 63(3), 316.

Overview of the activities, experiences and experiments of the National Animal Germplasm Program to conserve US livestock genetic resources. From a genebank perspective future challenges include: improving methodologies to collect, evaluate and utilize germplasm.

Danchin-Burge, C., Hiemstra, S. J., & Blackburn, H. (2011). Ex situ conservation of Holstein-Friesian cattle: Comparing the Dutch, French, and US germplasm collections. *Journal of Dairy Science*, 94(8), 4100-4108. doi: DOI 10.3168/jds.2010-3957

Genetic diversity of Holstein Friesian gene bank collections within and between countries (USA, France, Netherlands) was assessed and compared with active male HF populations in each country by using pedigree data. The cryobanks have captured substantial amounts of genetic diversity for the HF compared with the current populations.

Duchev, Z., Gandini, G., Berger, B., Hulsegge, B., Hiemstra, S., Maki-Tanila, A., . . . Marguerat-König, C. (2010). *Towards Uniform Gene Bank Documentation In Europe–The Experience From The EFABISnet Project*. Paper presented at the Proceedings of the 9th world congress on genetics applied to livestock production: August 1-6, 2010 Leipzig, Germany.

Towards Uniform Gene Bank Documentation In Europe–The Experience From The EFABISnet Project

FAO. (2012). Cryoconservation of animal genetic resources. *FAO Animal Production and Health Guidelines. No. 12. Rome.*

FAO guidelines for cryoconservation of animal genetic resources provide an overview of the fundamental issues involved in developing and operating gene banks as elements in comprehensive national strategies for the management of animal genetic resources.

Gandini, G., Pizzi, F., Stella, A., & Boettcher, P. J. (2007). The costs of breed reconstruction from cryopreserved material in mammalian livestock species. *Genetics Selection Evolution*, 39(4), 465-479. doi: Doi 10.1051/Gse:2007015

Cost comparison for the creation of gene banks for reconstruction of an extinct breed, using different strategies: embryos- only, embryos in combination with semen, and semen- only. A high variation of costs was observed across species and strategies.

Hiemstra, S. J., Martyniuk, E., Duchev, Z., & Begemann, F. (2014). *European Gene Bank Network for Animal Genetic Resources (EUGENA)*. Paper presented at the 10th World Congress on Genetics Applied to Livestock Production.

Objectives and overview of the European Gene Bank Network on Animal Genetic Resources (EUGENA), including the results of a national gene bank survey across Europe.

Paiva, S. R., McManus, C. , Blackburn, H. (2014). Conservation of Animal Genetic Resources: the Next Decade WCGALP 2014.

After 20 years, progress has been made in conserving animal genetic resources at global level. Paper also includes an overview of gene bank collections.

Silversides, F. G., Purdy, P. H., & Blackburn, H. D. (2012). Comparative costs of programmes to conserve chicken genetic variation based on maintaining living populations or storing cryopreserved material. *British Poultry Science*, 53(5), 599-607. doi: Doi 10.1080/00071668.2012.727383

Evaluation of the costs of programmes using living populations, semen cryopreservation and reconstitution, and ovary and semen cryopreservation and reconstitution over 20 years. Keeping live populations was most cost effective for periods of up to three years.

Cryobiology and reproductive technologies

Groeneveld, E., Tinh, N. H., Kues, W., & Vien, N. T. (2008). A protocol for the cryoconservation of breeds by low-cost emergency cell banks - a pilot study. *Animal*, 2(1), 1-8. doi: Doi 10.1017/S1751731107000869

A protocol was developed for collection and storage of somatic cell samples under adverse conditions with little infrastructure, for somatic-cell banks as a backup for endangered livestock breeds. The procedure included sample collection with ear taggers with an integrated tag/vial system, and recording of global positioning system (GPS) coordinates, digital images and breed information. The procedure has proved practicable and exceedingly cheap relative to the cryopreservation of semen or embryos.

Huang, K. Y., de Groot, S. A., Woelders, H., van der Horst, G. T. J., Themmen, A. P. N., Colenbrander, B., & van Vliissingen, J. M. F. (2010). Functionality of cryopreserved juvenile ovaries from mutant mice in different genetic background strains after allotransplantation. *Cryobiology*, 60(2), 129-137. doi: DOI 10.1016/j.cryobiol.2009.10.003

Paper discusses the challenge to have cheap and effective methods in addition to freezing embryos and sperm to archive the expanding mutant mouse lines. Juvenile ovaries (10-day-old) collected from genetically modified mouse lines were cryopreserved using high concentrations of cryoprotectants (dimethyl sulfoxide (Me₂SO) and ethylene glycol (EG)) and instrumented ultra-rapid freezing. The results indicate that cryopreservation of mouse ovaries is a promising method.

Long, J. A., Purdy, P. H., Zuidberg, K., Hiemstra, S.-J., Velleman, S. G., & Woelders, H. (2014). Cryopreservation of turkey semen: Effect of breeding line and freezing method on post-thaw sperm quality, fertilization, and hatching. *Cryobiology*, 68(3), 371-378.

Cryopreservation methods for poultry semen preservation are generally not very reliable, especially for turkeys, where fertility rates from frozen/thawed semen are particularly low. The objective was to evaluate cryopreservation methods for effectiveness in promoting cryosurvival and post-thaw function of sperm from five turkey lines. Overall, better fertility results were obtained with the cryoprotectant DMA, the ASG diluent and fixed sperm concentration. However, the applicability of this method for preserving semen from research populations may be line dependent.

Mara, L., Casu, S., Carta, A., & Dattena, M. (2013). Cryobanking of farm animal gametes and embryos as a means of conserving livestock genetics. *Animal Reproduction Science*, 138(1), 25-38.

Although significant progress has been made in semen, oocytes and embryo cryopreservation of several domestic species, standardized procedures have not been established yet. The aim of the review was to describe the cryobanking purposes, the collection goals, the type of genetic material to store and the reproductive biotechnologies utilized for the cryopreservation of farm animal gametes and embryos.

Pereira, R., & Marques, C. (2008). Animal oocyte and embryo cryopreservation. *Cell and tissue banking*, 9(4), 267-277.

Cryopreservation of oocytes and embryos is a crucial step for the widespread and conservation of animal genetic resources. However, oocytes and early embryos are very sensitive to chilling and cryopreservation and although new advances have been achieved in the past few years the perfect protocol has not yet been established. New strategies based on emerging studies in the field of lipid research have been used to reduce intracellular lipid content in bovine in vitro produced embryos and therefore increase their tolerance to micromanipulation and cryopreservation.

Song, Y., & Silversides, F. G. (2007a). Offspring produced from orthotopic transplantation of chicken ovaries. *Poultry Science*, 86(1), 107-111.

Techniques for freezing ova and embryos are not available for birds, and the recovery of genetic material has been a major obstacle to cryopreservation. To overcome this problem, chicken ovarian tissue was transplanted just after hatch. Findings show that cryopreservation of female germ cells in chickens with regeneration in live birds is an efficient strategy.

Song, Y., & Silversides, F. G. (2007b). Production of offspring from cryopreserved chicken testicular tissue. *Poultry Science*, 86(7), 1390-1396.

The fertility of frozen-thawed avian semen is generally much lower than that of mammalian semen and varies among species or among lines, reducing the value of semen for the preservation of genetic

resources. A simple freezing protocol was used to cryopreserve testicular tissue of day-old chicks, and after subsequent transplantation, the frozen-thawed testicular tissue developed functional seminiferous tubules that produced sufficient sperm to fertilize eggs, resulting in donor-derived offspring. This study provides an alternative to semen cryopreservation for storage of the male germline in birds.

Tijssen, M. R., Woelders, H., de Vries-van Rossen, A., van der Schoot, C. E., Voermans, C., & Lagerberg, J. M. (2008). Improved postthaw viability and in vitro functionality of peripheral blood hematopoietic progenitor cells after cryopreservation with a theoretically optimized

The freezing curve currently used for the cryopreservation of peripheral blood stem cell transplants (PBSCs) has been determined empirically. Research results indicate that the current cryopreservation method for PBSCs can be improved by either lowering the DMSO concentration to 5 percent or by using the theoretically optimized freezing curve.

Woelders, H., & Hiemstra, S. J. (2011). The potential of cryopreservation and reproductive technologies for animal genetic resources conservation strategies. *Proceedings of the 2011 Cryobiology Annual meeting, July 2011, Corvallis, OR. Cryobiology* 63, 316-317.

Review of gene banking strategies, discussing (dis)advantages of cryopreservation of semen, embryos, oocytes, primordial germ cells and somatic cells.

Woelders, H., Windig, J., & Hiemstra, S. J. (2012). How Developments in Cryobiology, Reproductive Technologies and Conservation Genomics Could Shape Gene Banking Strategies for (Farm) Animals. *Reproduction in Domestic Animals*, 47, 264-273. doi: DOI 10.1111/j.1439-0531.2012.02085.

Review of developments in cryobiology and reproductive technology for preserving germplasm in farm animals. Depending on the species, there are interesting possibilities or research developments in the use of epididymal spermatozoa, oocytes and embryos, ovarian and testicular tissue, primordial germ cells, and somatic cells for the conservation of genetic diversity in farm and other animal species.

List of papers with summaries consulted by the Microbial and Invertebrate Genetic Resources Domain

Alexandraki, V., E. Tsakalidou, et al. (2013). Status and trends of the conservation and sustainable use of micro-organisms in food processes. Rome, FAO

The use of microorganisms in food processing constitutes a major part of Food Biotechnology by which relatively bulky, perishable and frequently inedible raw materials are converted into safe, shelf-stable and palatable foods or beverages. While food fermentations contribute an important (but not necessarily vital) part to the diet in industrialised countries, they play an essential role in the nutrition of developing countries. The value and benefits of fermented foods are realised in our time perhaps more than ever before. Reasons for an increasing awareness are multi-fold, and may differ between industrialised and developing countries. Basic understanding of mechanisms by which fermentation improves food safety and stability, has resulted in the development of new concepts for food preservation by using live microbial strains for bio-preservation.

Baker, E., J. Thykaer, et al. (2008). "Fungal genome sequencing and bioenergy." Fungal Biology Reviews 22(1): 1-5.

To date, the number of ongoing filamentous fungal genome sequencing projects is almost tenfold fewer than those of bacterial and archaeal genome projects. The fungi chosen for sequencing represent narrow kingdom diversity; most are pathogens or models. In this manuscript they advocate an ambitious, forward-looking phylogenetic-based genome sequencing program, designed to capture metabolic diversity within the fungal kingdom, thereby enhancing research into alternative bioenergy sources, bioremediation, and fungal-environment interactions.

Bernardeau, M., J. P. Guguen M Fau - Vernoux, et al. (2006). "Beneficial lactobacilli in food and feed: long-term use, biodiversity and proposals for specific and realistic safety assessments." FEMS Microbiol Rev 30: 487-513.

Lactobacilli have played a crucial role in the production of fermented products for millennia. Their probiotic effects have recently been studied and used in new products. In this manuscript they have analyzed the current European guidelines for safety assessment in food/feed and conclude that they are not relevant for the Lactobacillus genus. New specific guidelines are proposed, beginning by granting a 'long-standing presumption of safety' status to Lactobacillus genus based on its long history of safe use. Then, based on the available body of knowledge and intended use, only such tests as are useful will be necessary before attributing 'qualified presumption of safety' status. FAU - Bernardeau, Marion

Blackwell, M. (2011). "The Fungi: 1, 2, 3 ... 5.1 million species?" American Journal of Botany 98: 426–438.

Fungi are major decomposers in certain ecosystems and essential associates of many organisms. They provide enzymes and drugs and serve as experimental organisms. In 1991, a landmark paper estimated that there are 1.5 million fungi on the Earth. Because only 70000 fungi had been described

at that time, the estimate has been the impetus to search for previously unknown fungi. Fungal habitats include soil, water, and organisms that may harbor large numbers of understudied fungi, estimated to outnumber plants by at least 6 to 1. More recent estimates based on high-throughput sequencing methods suggest that as many as 5.1 million fungal species exist.

Bourdichon, F., S. Casaregola, et al. (2012). "Food fermentations: microorganisms with technological beneficial use." *Int J Food Microbiol* 15(1879-3460 (Electronic)): 87-97.

Microbial food cultures have directly or indirectly come under various regulatory frameworks in the course of the last decades. Here an updated inventory of microorganisms used in food fermentations covering a wide range of food matrices (dairy, meat, fish, vegetables, legumes, cereals, beverages, and vinegar) are mentioned and the taxonomy of the microorganisms used in food fermentations are reviewed in order to bring the taxonomy in agreement with the current standing in nomenclature.

ÇaktÜ, K. and E. A. TÜRkoĞlu (2011). "Microbial Culture Collections: The Essential Resources for Life." *Gazi University Journal of Science* 24: 175-180

Microbial culture collections are crucial resource centres providing microbial materials. They act as repositories for microbial strains as part of patent deposits, confidential services to store key organisms for research, industry and society and sources of microorganisms cited in scientific papers that can be used in the confirmation of results and for further studies. Microbial culture collections are considered as libraries, but instead of books they hold microorganisms. Microorganisms provide many solutions to world problems in public health, food, environment and poverty and they are extremely important for various ecosystems.

Chapman, A. D. (2009). Numbers of living species in Australia and the World. Toowoomba, Australian Biodiversity Information Services.

Estimates of the total number of species in the world vary from 5 million to over 50 million (May 1998). In this report figures of close to 11 million species worldwide and about 570,000 for Australia are accepted. Numbers for accepted published species in the world are given here as close to 1,900,000 and 147,579 for Australia.

Clermont, D., S. Santoni, et al. (2014). "Assessment of DNA encapsulation, a new room-temperature DNA storage method." *Biopreserv Biobank* 12: 176-183.

A new procedure for room-temperature storage of DNA was evaluated whereby DNA samples from human tissue, bacteria, and plants were stored under an anoxic and anhydrous atmosphere in small glass vials fitted in stainless-steel, laser-sealed capsules (DNAsHells). This study demonstrates the many advantages of using DNAsHells for room-temperature storage, particularly in terms of long-term stability, safety, transport, and applications for molecular biology research.

Couto, S. R. and M. A. Sanromán (2006). "Application of solid-state fermentation to food industry-a review." *J. Food Eng* 76: 291-302.

Solid state fermentation (SSF) has become a very attractive alternative to submerged fermentation (SmF) for specific applications due to the recent improvements in reactor designs. This paper reviews the application of SSF to the production of several metabolites relevant for the food processing industry, centred on flavours, enzymes (α -amylase, fructosyl transferase, lipase, pectinase), organic acids (lactic acid, citric acid) and xanthan gum. In addition, different types of biorreactor for SSF processes have been described.

Cuomo, C. A., r. U. Guldene, et al. (2007). "The *Fusarium graminearum* genome reveals a link between localized polymorphism and pathogen specialization." *Science* 317: 1400-1402.

*The genome of the filamentous fungus *Fusarium graminearum*, a major pathogen of cultivated cereals was sequenced and annotated. Very few repetitive sequences were detected, and the process of repeat-induced point mutation, in which duplicated sequences are subject to extensive mutation, may partially account for the reduced repeat content and apparent low number of paralogous (ancestrally duplicated) genes. Many highly polymorphic regions contained sets of genes implicated in plant-fungus interactions and were unusually divergent, with higher rates of recombination. These regions of genome innovation may result from selection due to interactions of *F. graminearum* with its plant hosts.*

Dawyndt, P., B. Van Brabant, et al. (2007). The StrainInfo. net bioportal: WFCC goes web 2.0. Goslar.

The StrainInfo.net Bioportal currently integrates data from 55 Biological Resource Centres (BRCs) that cover all earth's continents and range from small niche-specific research collections to large general-purpose service collections into an integrated strain database. This integration process has currently lumped over 690,000 strain numbers into about 310,000 equivalence classes that represent different strains of Bacteria, Archaea, filamentous fungi, yeasts, Algae and Protozoa. Through the online interface of the StrainInfo.net Bioportal, organisms can be searched by strain number, taxonomic name as several additional parameters. Query results redirect the user on-the-fly to the online catalogues of the different culture collections that have a given strain that matches the query in their holdings.

Dedeurwaerdere, T. (2009). The role of law, institutions and governance processes in facilitating access to genomics research. Cambridge (UK), Cambridge University Press.

The purpose of this chapter is to highlight why the science commons matters, and to analyse its organization. The concern for the governance of the science commons has caught the attention of a wide range of scholars in the mid 1990s, especially in legal scholarship. The interest of these scholars is in the cooperative use of scientific data, information, materials and research tools that actually are not in the public domain, and whose licensed use is legally protected by an intellectual property (IP) regime.

Dedeurwaerdere, T. (2010). "Global microbial commons: institutional challenges for the global exchange and distribution of microorganisms in the life sciences." *Res Microbiol* 161: 414-421.

During the last decades of the twentieth century, the increasing economic importance of biotechnology and the introduction of new legislation concerning the use of and access to biological resources has subjected exchanges of genetic resources to greater controls. Their access and distribution are more strictly regulated and, therefore, exchanges are becoming more and more formalized. This paper analyzes one of the main drivers of the movement toward more formal worldwide exchange regimes, which is increasing global interdependency of access to genetic resources. Its main finding is that formalization of exchange practices as such is not necessarily leading to more restrictive licensing conditions.

FAO (2009). "Scoping Study on Micro-organisms Relevant to Food and Agriculture."

The objective of the study was to identify the critical challenges to the EU food safety and nutrition framework, their future evolution up to 2050, their impacts on its current structure and the potential critical changes to the current framework necessary to maintain the prevailing high standards. The intention was to provide insight and guidance for the development of future policy response scenarios and future analysis and research necessary for their development. The study describes the key drivers of food safety and nutrition identified, presents the scenarios developed on the basis of an innovative and participative approach, summarises the results of the stakeholder consultation, draws conclusions on how high levels of food safety and nutrition can be safeguarded in the future, and finally indicates related research needs.

Fritze, D., D. Martin, et al. (2012). Final report on the GBRCN Demonstration Project. Germany, GBRCN Secretariat.

The GBRCN Demonstration Project is a response to the OECD initiative on Biological Resource Centres. A Task Force, including experts from OECD and Non-OECD countries, recommended that governments, scientific policy makers and other stakeholders should implement policies to ensure that high quality biological material is made available for research and development worldwide, and that the challenges of safe and legitimate access to it are tackled. Five main points of action were formulated: 1 establish national BRCs 2 develop an accreditation system for BRCs based on international criteria 3 create international linkages among BRCs 4 coordinate standards, rules and regulations, taking BRCs into account 5 establish a global BRC network.

Fritze, F. (2006). "The European initiatives MINE, CABRI, EBRCN and ENBI." Microbiology Australia March: 28-30.

Worldwide development of biotechnology results increasingly in the recognition of the importance of microbial culture collections and their holdings. In particular, it is recognised that the knowledge on these holdings accumulated in culture collections should be put more easily at the use of researchers. Far sighted scientists, under the leadership of the late VBD Skerman, had set up, already from the mid 1960s on, activities to catalogue culture collections and their holdings.

Fujisaka, S., D. Williams, et al. (2009). The Impact of Climate Change on Countries' Interdependence on Genetic Resources for Food and Agriculture. Rome, FAO.

With respect to climate change, the most relevant prediction for this paper is that, on average, global temperatures will increase worldwide by 0.2 degrees per decade. There will be both increases and decreases in precipitation. Droughts and floods will increase. The areas with climates that are now suited to a particular suite of crops, forages, livestock, trees, microbes, and aquaculture will shift in ways that are more favourable to a minority of countries and less favourable to the majority

Groenewald, M. (2007). Molecular characterization of *Cercospora beticola* and its relatives. Wageningen Wageningen University.

Various types of molecular techniques have been developed in an attempt to unravel some of the questions regarding diversity among species and populations. Some of these techniques allow a great number of polymorphic loci to be detected in individuals for direct assessment of genetic variation in populations and can thus be used to study the genetic variability at species and population levels with great reliability. The amount of genetic variation that is present within a single population is measured in terms of genotype or gene diversity and may indicate how rapidly a pathogen can evolve and adapt to changing environments.

Guizani, N. and A. Mothershaw (2007). Handbook of Food Preservation. New York, CRC Press.

The processing of food is no longer simple or straightforward, but is now a highly inter-disciplinary science. A number of new techniques have developed to extend shelf-life, minimize risk, protect the environment, and improve functional, sensory, and nutritional properties. The ever-increasing number of food products and preservation techniques creates a great demand for an up to date handbook that will facilitate understanding of the methods, technology, and science involved in the manipulation of these conventional and sophisticated preservation methods.

Hawksworth, D. L., P. W. Crous, et al. (2011). "The amsterdam declaration on fungal nomenclature." IMA Fungus 2 105–112.

The Amsterdam Declaration on Fungal Nomenclature was agreed at an international symposium convened in Amsterdam on 19-20 April 2011 under the auspices of the International Commission on the Taxonomy of Fungi (ICTF). The purpose of the symposium was to address the issue of whether or how the current system of naming pleomorphic fungi should be maintained or changed now that molecular data are routinely available. Possible amendments to the Draft BioCode (2011) to allow for the needs of mycologists are suggested for further consideration, and a possible example of how a fungus only known from the environment might be described is presented.

Jinnah, S. and S. Jungcirt (2009). "Global biological resources. Could access requirements stifle your research?" Science 323: 464-465.

The CBD aims not only to conserve biological diversity but also to address sustainable development-related conservation issues. Specifically, the CBD aims to negotiate rules that facilitate foreign access to genetic resources in biodiversity-rich countries and to ensure that local communities and governments that provide access to those resources are protected from commercial exploitation by powerful foreign interests. Providers of resources would also be fairly compensated under the future

regime. They focus on issues such as the following: (1) how to ensure prior informed consent from knowledge holders or provider countries before accessing genetic resources and associated traditional knowledge; (2) how to access genetic resources based on mutually agreed terms between the user and provider countries; and (3) how sharing benefits arising from the use of these resources could take place.

Kamper, J., R. Kahmann, et al. (2006). "Insights from the genome of the biotrophic fungal plant pathogen *Ustilago maydis*." *Nature* 444: 97-101.

Ustilago maydis is a ubiquitous pathogen of maize and a well-established model organism for the study of plant-microbe interactions. Here the authors report on the genome sequence for a member of this economically important group of biotrophic fungi. The 20.5-million-base despite years of research into the mechanism of pathogenicity in *U. maydis*, no 'true' virulence factors had been previously identified. Thus, the discovery of the secreted protein gene clusters and the functional demonstration of their decisive role in the infection process illuminate previously unknown mechanisms of pathogenicity operating in biotrophic fungi. Genomic analysis is, similarly, likely to open up new avenues for the discovery of virulence determinants in other pathogens.

Kurtzman, C. P. and D. P. Labeda (2009). *Type Culture Collections and Their Databases*. Oxford, United Kingdom, Elsevier.

Microbial culture collections, also known as Biological Resource Centers, are primary suppliers of microbial cultures (germplasm) for medical, agricultural and biotechnological research and development. Many countries have one or more culture collections, which may specialize in certain microbial groups or may offer a broad coverage of many different microbial groups. Many of the larger collections are International Depository Authorities under the Budapest Treaty and in this capacity accept patent cultures. A major goal of culture collections is long-term preservation of strains without genetic change. Methods for preservation include freeze-drying (lyophilization), L-drying and ultra cold freezing with liquid nitrogen. Culture collections are also centers of taxonomic and microbiological expertise.

Lebonah, D. E., A. Dileep, et al. (2014). "DNA Barcoding on Bacteria: A Review " *Advances in Biology* 2014: 9.

Bacteria are omnipotent and they can be found everywhere. The study of bacterial pathogens has been happening from olden days to prevent epidemics, food spoilage, losses in agricultural production, and loss of lives. Modern techniques in DNA based species identification are considered. So, there is a need to acquire simple and quick identification technique. Hence, this review article covers the efficacy of DNA barcoding of bacteria. Routine DNA barcoding involves the production of PCR amplicons from particular regions to sequence them and these sequence data are used to identify or "barcode" that organism to make a distinction from other species.

Ma, J. and H. Sugawara (2011). "Activities of World Federation of Culture Collections (WFCC) World Data Centre for Microorganisms (WDCM)." *Microbiol. Cult. Coll* 27: 79-81

WDCM is subordinate to World Federation of Culture Collection (WFCC) and UNESCO Microbial Resources Centers Network (MIRCEN). It is a vehicle for networking microbial resource centers of various types of microbes. It also serves as an information resource for the customers of the microbial resource centers. Until now, 684 culture collections from 70 countries have registered in WDCM. UPM was established in 1931 which is covering the area of 1200 hectares in Malaysia. UNiCC is subordinate to Institute of Bioscience, UPM. It is in charge of microbial resource preservation and management; also provide strains and related services to the researchers and scientific research institutions.

McCluskey, K., M. Wiest A Fau - Plamann, et al. (2010). "The Fungal Genetics Stock Center: a repository for 50 years of fungal genetics research." J Biosci 35: 119–126.

The Fungal Genetics Stock Center (FGSC) was established in 1960 to ensure that important strains used in early genetics research were available to subsequent generations of fungal geneticists. Originally, only mutant strains were held. At present, any organism that has had its genome sequenced is a genetic system and so the FGSC has added many new organisms. Many of these strains were seldom requested over many years, but became among our most popular resources following the demonstration of their utility in studying fungicide resistance. This exemplifies why materials need to be preserved without regard to their immediate perceived value and reinforces the need for long-term support for preservation of a broad variety of genetic resources.

Mora, C., D. P. Tittensor, et al. (2011). "How many species are there on Earth and in the ocean?" PLoS Biol 9: e1001127.

The answer to this question remains enigmatic, as efforts to sample the world's biodiversity to date have been limited and thus have precluded direct quantification of global species richness, and because indirect estimates rely on assumptions that have proven highly controversial. In this overview it is show that the higher taxonomic classification of species follows a consistent and predictable pattern from which the total number of species in a taxonomic group can be estimated. In spite of 250 years of taxonomic classification and over 1.2 million species already catalogued in a central database, the results suggest that some 86% of existing species on Earth and 91% of species in the ocean still await description.

Morgan, C. A., N. Herman, et al. (2006). "Preservation of micro-organisms by drying. A review." Journal of Microbiological Methods 66: 183-193.

The preservation of micro-organisms by different drying methodologies has been used for decades. Freeze drying in particular is the preferred method for transporting and storing vast culture collections of micro-organism strain types. The literature on drying and preserving micro-organisms is often specific to one particular strain. This review attempts to draw some similar concepts and findings together in one paper, to compare different drying techniques, with specific reference to microorganisms.

Nilsson, R. H., M. Kristiansson E Fau - Ryberg, et al. (2008). "Intraspecific ITS variability in the kingdom fungi as expressed in the international sequence databases and its implications for molecular species identification." *Evol Bioinform Online* 4: 193–201.

The ITS region of the nuclear ribosomal repeat unit is the most popular locus for species identification and subgeneric phylogenetic inference in sequence-based mycological research. The region is known to show certain variability even within species, although its intraspecific variability is often held to be limited and clearly separated from interspecific variability. The current results caution against simplified approaches to automated ITS-based species delimitation and reiterates the need for taxonomic expertise in the translation of sequence data into species names.

OECD (2007). *Best Practice Guidelines for Biological Resource Centres*. Paris, France, OECD Publications.

In order to meet modern demands for the further advancement of biotechnology and life sciences, the OECD in 2001 introduced a new concept of repositories and providers of high quality biological materials and information: Biological Resource Centres (BRCs). BRCs are considered to be one of the key elements for sustainable international scientific infrastructure, which is necessary to underpin successful delivery of the benefits of biotechnology, whether within the health sector, the industrial sector or other sectors, and in turn ensure that these advances help drive growth. This report presents the outcome of discussions held by the OECD member countries.

Prado, F. C., J. L. Parada, et al. (2008). "Trends in non-dairy probiotic beverages." *Food Res. Int.* 41: 111-123.

The development of probiotics in the last two decades has signaled an important advance in the food industry. The number of scientific publications on probiotics has increased a lot stimulated by factors as exciting scientific and clinical findings using well-documented probiotic organisms. Some concerns over the limitations and side effects of the pharmaceutical agents and consumers demand for the natural products exist.

Rambold, G., M. Stadler, et al. (2013). "Mycology should be recognized as a field in biology at eye level with other major disciplines – a memorandum." *Mycological Progress* 12: 455–463.

Mycologists are often accused of using terminologies that are not immediately understood by biologists as a whole. A topical example is that of anamorph and teleomorph, rather than either the immediately understood asexual and sexual, or the now less-used alternative mitotic and meiotic. In descriptions, there is also a tendency to follow tradition. Some commonly used adjectives likely to be understood by those with some knowledge of Latin or Greek, but not so readily by others.

Ranadheera, R., S. Baines, et al. (2010). "Importance of food in probiotic efficacy." *Food Res. Int.* 43: 1-7.

Foods are carriers for the delivery of probiotics to the human body. In addition, foods help to buffer the probiotic through the gastrointestinal tract, regulate their colonization and contain other functional ingredients, such as bioactive components, which may interact with probiotics to alter their

functionality and efficacy. Nowadays, there is an increasing trend toward using probiotics in different food systems despite its original sources and even as nutraceuticals, such as in capsules. Selection of suitable food systems to deliver probiotics is a vital factor that should be considered in developing functional probiotic foods. This review focuses on information related to the effect of processed food products on functional efficacy of probiotics.

Robert, R., S. Szöke, et al. (2011). "The Quest for a General and Reliable Fungal DNA Barcode." The Open Applied Informatics Journal 5: 45-61.

DNA sequences are key elements for both identification and classification of living organisms. Mainly for historical reasons, a limited number of genes are currently used for this purpose. From a mathematical point of view, any DNA segment, at any location, even outside of coding regions and even if they do not align, could be used as long as PCR primers could be designed to amplify them. This paper describes two methods to search genomic data for the most efficient DNA segments that can be used for identification and classification.

Santivarangkna, C., U. Kulozik, et al. (2011). Storing Lactic Acid Bacteria: Current Methodologies and Physiological Implications. New York, Springer Science and Business Media.

The established methods for preservation of lactic acid bacteria (LAB) are freezing and freeze-drying, in which cells are maintained in frozen and dried forms. The physiological state of LAB plays a crucial role, and an increased viability can be obtained by the sublethal stress treatment of cells. Exposing LAB cells to a mild stress triggers cells' protective mechanisms to subsequent stresses occurring during the preservation processes. These stresses are, for example, the entry of cells to the stationary phase; osmotic, heat, cold, and acid shock; as well as genetic modification of genes related to those stresses.

Schoch, C. L., K. A. Seifert, et al. (2012). "Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi." Proc Natl Acad Sci U S A. 109: 6241-6246.

Six DNA regions were evaluated as potential DNA barcodes for Fungi by a multinational, multilaboratory consortium. Among the regions of the ribosomal cistron, the internal transcribed spacer (ITS) region has the highest probability of successful identification for the broadest range of fungi, with the most clearly defined barcode gap between inter- and intraspecific variation. The nuclear ribosomal large subunit, a popular phylogenetic marker in certain groups, had superior species resolution in some taxonomic groups, such as the early diverging lineages and the ascomycete yeasts, but was otherwise slightly inferior to the ITS. ITS will be formally proposed for adoption as the primary fungal barcode marker to the Consortium for the Barcode of Life, with the possibility that supplementary barcodes may be developed for particular narrowly circumscribed taxonomic groups.

Schüngel, M., E. Stackebrandt, et al. (2013). "MIRRI - The Microbial Resource Research Infrastructure: managing resources for the bio economy." EMBnet.journal 19.1: 5-8.

Starting its Preparatory Phase in November 2012, MIRRI aims to develop strategies to establish a pan-European infrastructure for microbial resources, their associated data and expertise. 16

renowned European partners work together to build a One-Stop-Shop for microbial raw material, expertise and legal advice to fulfil the users' needs. This includes developing the future governance structure, identifying the users' needs and expectations regarding the infrastructure as well as defining the legal operational framework for access to microbial resources. Implementation of the prepared strategies will start in 2015.

Siro, I., E. Kopolna, et al. (2008). "Functional food. Product development, marketing and consumer acceptance--a review." *Appetite* 51: 456-467.

Functional foods are found virtually in all food categories. Besides potential technological obstacles, legislative aspects, as well as consumer demands need to be taken into consideration when developing functional food. In particular, consumer acceptance has been recognized as a key factor to successfully negotiate market opportunities. This paper offers a brief overview of the current functional food market situation in USA, Japan and some European countries completed with some comments on functional food future potential. It explores the main challenges of such product development focusing on the different factors determining the acceptance of functional food. Furthermore it discusses some prominent types of these food products currently on the market.

Sly, I. (2010). Biodiversity and the Role of Microbial Resource Centres.

Micro-organisms have evolved into the most ecologically, genetically and metabolically diverse species known. Micro-organisms belong to all three Domains of life: The Bacteria, Archaea and Eukarya as well as the Viruses. They have shaped the evolution of the planet and continue to nurture and sustain the environment, plants and animals on which human society depends. Micro-organisms are major sources of important pharmaceutical and industrial products for worldwide community benefits in health, agriculture and industry. Cultures of micro-organisms have been essential for the production of enzymes, fermentation products and metabolites. With advances in molecular biology, genes of micro-organisms and whole natural communities are being exploited and fuelling accelerated interest in biodiscovery.

Smith, D. (2007). The implementation of OECD best practice in WFCC member culture collections. Goslar, WFCC and DSMZ.

The aim is to enhance the efficiency in collections of laboratory held, living biological material, by coordinating and driving activities to meet user needs. A network designed to accommodate the future needs of biotechnology and biomedicine. The task of ex-situ conservation is enormous and exceeds the technical potential of an individual collection in any individual country. Adequate collection management of well preserved and authenticated organisms is essential to guarantee quality and safety in the various areas of application, to allow controlled access to potentially hazardous organisms and to ease and improve the advantageous utilisation of the materials for health and environment.

Smith, D. (2012). "Culture collections." *Adv Appl Microbiol* 79: 73-118.

Culture collections no matter their size, form, or institutional objectives play a role in underpinning microbiology, supplying the resources for study, innovation, and discovery. Their basic roles include providing a mechanism for ex situ conservation of organisms; they are repositories for strains subject to publication, taking in safe, confidential, and patent deposits from researchers. They supply strains for use; therefore, the microorganisms provided must be authentic and preserved well, and any associated information must be valid and sufficient to facilitate the confirmation of their identity and to facilitate their use.

Smith, D. and P. Day (2012). European Consortium of Microbial Resource Centres: Microbial resources success stories. UK, CABI.

Microorganisms are everywhere, on the ocean floor, in our soil and buried deep in rocks. They are vital to human life and the environment we live in. Microorganisms are the source of many useful products and provide many solutions to healthcare, food security and industrial problems. Medicines such as penicillin and cyclosporin have saved millions of lives. This highlights some of these success stories and advocates the long-term preservation of microorganisms for future use and the benefit of humankind and our threatened planet.

Smith, D., K. McCluskey, et al. (2014). "Investment into the future of microbial resources: culture collection funding models and BRC business plans for biological resource centres." Springerplus 3: 81.

Through their long history of public service, diverse mBRCs have enabled the maintenance of specimens isolated before antibiotics, made available strains showing the development and change of pathogenicity toward animals, humans and plants, and have maintained and provided reference strains to ensure quality and reproducibility of science. However, this has not been achieved without considerable financial commitment. Different collections have unique histories and their support is often tied to their origins. However many collections have grown to serve large constituencies and need to develop novel funding mechanisms. Moreover, several international initiatives have described mBRCs as a factor in economic development and have led to the increased professionalism among mBRCs.

Smith, D. and M. Ryan (2012). "Implementing best practices and validation of cryopreservation techniques for microorganisms." Scientific World Journal(1537-744X (Electronic)).

Authentic, well preserved living organisms are basic elements for research in the life sciences and biotechnology. They are grown and utilized in laboratories around the world and are key to many research programs, industrial processes and training courses. They are vouchers for publications and must be available for confirmation of results, further study or reinvestigation when new technologies become available. These biological resources must be maintained without change in biological resource collections. Cryopreservation is often the best preservation method available to achieve these aims, allowing long term, stable storage of important microorganisms. The paper discusses quality management options and reviews cryopreservation of fungi, describing how the reproducibility and quality of the technique is maintained in order to retain the full potential of fungi.

Spatafora, J. (2011). "1000 fungal genomes to be sequenced." IMA Fungus 2: 41.

The overarching goal of the 1000 Fungal Genome Project (F1000) is to inform all areas of fungal biology by providing broad, genomic coverage of Kingdom Fungi (Fungi). Currently there are approximately 140 orders of Fungi and over 550 families. The F1000 goal over the next five years is to facilitate the sampling of fungal genomes so that at least two representatives are sequenced from every family or family-level clade of Fungi. This focus on "family or family-level" clade is meant as a guiding principle with the understanding that deliberate discussions involving taxonomic experts will be required to best integrate the current understanding of evolutionary relationships of Fungi and to the best select realistic exemplars.

Stackebrandt, E. (2010). "Diversification and focusing: strategies of microbial culture collections." Trends Microbiol 18: 283-287.

Microbial culture collections provide resources for the emerging area of the knowledge-based bioeconomy. These measures have to be introduced side by side with the deposition of increasingly phylogenetically and physiologically diverse microbiological organisms. It appears obvious that in order to make available an even broader range of diversity to users and researchers, collections will have to decide whether to diversify on a broad taxon spectrum of the hierarchic system, holding a small number of representatives per species, or to follow the route of focusing on in-depth holdings of selected groups of organisms, depending on existing taxonomic expertise. These decisions require a worldwide coordinated activity with the outcome to be made transparent to users in an emerging global network.

Stackebrandt, E. (2011). "Towards a strategy to enhance access to microbial diversity." Int J Syst Evol Microbiol 61: 479-481.

The issue of strain selection needs careful consideration because of the possible reverse effect of the strategy if authors are told that strains they consider worth depositing will not be considered by some of the other stakeholders, or if authors omit strains from publications in order to minimize their obligations. It goes without saying that the uncritical deposition of each microbial strain isolated is not practical and is even nonsensical in the true meaning of the word. In times of prudent handling of resources and public awareness of biodiversity, a coordinated strategy should be put in place which would increase and facilitate access to valuable and irretrievable microbial resources.

Stackebrandt, E., D. Smith, et al. (2014). "Deposit of microbial strains in public service collections as part of the publication process to underpin good practice in science." Springerplus 3: 208.

Despite recommendations to release microbial resources to the community post-publication, the reality is far from satisfying. This report discussed the need for a coordinated and effective deposition policy for 'key' microbial strains and proposes a set of criteria to facilitate their deposition into public service collections. The majority of authors either contacted directly or during submission of manuscripts to several international, mainly European bacteriology journals agreed to this set of 'key strain' criteria and to the voluntarily deposition of resources into public resource centres.

WFCC (2010). World Federation for Culture Collections Guidelines for the Establishment and Operation of Collections of Cultures of Microorganisms, World Federation for Culture Collections.

The increasing demands on culture collections for authenticated, reliable biological material and associated information have paralleled the growth of biotechnology. Recently, the Organisation for Economic Co-operation and Development (OECD) has recognised the importance of taking culture collections to a higher level of quality and delivery to underpin biotechnology. The OECD Best Practice Guidelines for Biological Resource Centres set the standard for quality management and also covers biosecurity, building capacity, preservation of biological sources and data management. The WFCC guidance provides an excellent first step towards the implementation of the OECD Best Practice. It is anticipated that many member collections will be able to implement this guidance in full immediately but it is expected that each agrees to implement it in a reasonable time frame.

Preparatory Action on EU Plant and Animal Genetic Resources

