European Journal of Human Genetics (2013) 21, 1191–1196

www.nature.com/ejhg

VIEWPOINT

Controlling complexity: the clinical relevance of mouse complex genetics

Klaus Schughart*[,1,2,3], Claude Libert[4,5], SYSGENET consortium[7] and Martien J Kas[6]

Experimental animal models are essential to obtain basic knowledge of the underlying biological mechanisms in human diseases. Here, we review major contributions to biomedical research and discoveries that were obtained in the mouse model by using forward genetics approaches and that provided key insights into the biology of human diseases and paved the way for the development of novel therapeutic approaches.

European Journal of Human Genetics (2013) **21,** 1191–1196; doi:10.1038/ejhg.2013.79; published online 1 May 2013

Keywords: Mouse model; forward genetics; review

INTRODUCTION

Developing treatments aimed at the causes of diseases such as cancer, infections and metabolic, autoimmune and psychiatric disorders requires knowledge of the underlying biological mechanisms. Such knowledge can only be obtained by functional studies in which the disease-relevant tissue and the course of disease are manipulated systematically, for example, pharmacologically, environmentally or genetically. Experimental models are fundamental for meeting these challenges, and biomedical scientists often select mice as models. That 'mice are not humans' is obvious and some studies claim that the mouse is not a good model for human diseases.[1] The use of experimental models in biomedical research serves two important functions: discovery of basic biological mechanisms and development of new drugs and treatments, both of which have been successfully employed for the development of novel clinical therapeutic concepts and treatments. In this article, the members of the SYSGENET network recount some seminal studies on mouse models that provided key insights into the biology of human diseases and paved the way for the development of novel therapeutic approaches. SYSGENET represents a network of European scientists who use mouse genetic reference populations (GRPs) to understand complex genetic factors influencing disease phenotypes.[2]

MOUSE STUDIES HAVE CONTRIBUTED TO MAJOR ADVANCEMENTS IN CLINICAL MEDICINE

One of the most important advances in immunology was the discovery of the major histocompatibility antigens, which turned out to be the key molecules in antigen recognition and tissue rejection. This landmark discovery came from studying tissue transplantations in different mouse strains and performing appropriate genetic studies, for which George Snell[3] was awarded the Nobel Prize in Physiology or Medicine in 1980. Four years later, research on mice was awarded another Nobel Prize in Physiology or Medicine: Köhler and Milstein[4,5] were given the prize for developing one of the most innovative therapeutic approaches, the generation of monoclonal antibodies.

THE VALUE OF FORWARD GENETICS USING MOUSE MODELS

Forward genetic studies rely on natural variations of the genomes to analyze complex genetic traits. They are generally performed on N2 backcross, F2 intercross mice or in mouse GRPs. These approaches resemble genome-wide association studies (GWAS) in humans. They allow detection of genomic regions (referred to as quantitative trait loci) with multiple genes that exert quantitative influences on the phenotype, an approach referred to as complex genetic trait analysis. The simplest GRP is a collection of inbred mouse strains, each of which generated by repeated brother–sister mating for at least 20 generations, rendering all members of a strain genetically identical and homozygous at all loci. In humans, such identity exists only between monozygotic twins.

The most advanced GRPs are the BXD recombinant inbred strains[6,7] and the newly generated Collaborative Cross population,[8] which covers a genetic diversity twice as large as that of the human population and enables high resolution mapping.[8–13] Furthermore, the frequency of functional mutations can be increased by treating inbred strains with mutagens such as *N*-ethyl-*N*-nitrosourea.[14–22] In this approach, a single gene determines the phenotypic alterations, which are generally referred to as Mendelian traits.

A typical forward genetics approach starts with the phenotyping of a GRP or a collection of mutagenized mice. Once a phenotypic difference is found, breeding and genotyping studies are performed to identify the genomic region, and eventually the gene locus, responsible for the phenotype. Below, we describe several examples in which forward genetics approaches led to important discoveries that are highly relevant for understanding human diseases.

Infection and immunity

The story started from a simple observation in mice and ended with the award of the Nobel Prize for Physiology or Medicine to Bruce Beutler in 2011. Injection of bacterial lipopolysaccharide (LPS) causes a lethal toxic shock in most mouse strains. However, C3H/HeJ mice are resistant to LPS.[23] By performing breeding experiments and genetic mapping, they discovered that a

[1]Department of Infection Genetics, Helmholtz Centre for Infection Research, 38124 Braunschweig, Germany; [2]University of Veterinary Medicine Hannover, Germany; [3]University of Tennessee Health Science Center, Memphis, TN, USA; [4]VIB Department for Molecular Biomedical Research, Ghent, Belgium; [5]UGent Department Biomedical Molecular Biology, Ghent, Belgium; [6]Division of Neuroscience, Department of Neuroscience and Pharmacology, Rudolf Magnus Institute, University Medical Center Utrecht, Utrecht, The Netherlands
*Correspondence: Professor K Schughart, Department of Infection Genetics, Helmholtz Centre for Infection Research, Inhoffenstrasse 7, D-38124 Braunschweig, Germany. Tel: +49 531 6181 1100; Fax: +49 531 6181 1199; E-mail: klaus.schughart@helmholtz-hzi.de
[7]Members of the SYSGENET consortium are listed at the end of the article.

defect in the *Tlr4* gene causes the resistance of C3H/HeJ mice to LPS.[24] *Tlr4* belongs to a family of genes that are essential for the detection of microbial pathogens and initiation of immune responses. TLR4 also has an essential role in sepsis, which causes >200 000 deaths annually in the USA.[25] Furthermore, *Tlr4* knockout mice are resistant to the development of neuropathic pain.[26] TLR genes also have roles in autoimmune disorders, and they are now used as therapeutic targets for the development of drugs.[27] The initial discovery of TLRs as pathogen-sensing molecules opened a new research avenue that led to the discovery of pathways in immune and non-immune cells that are crucial for the host defense.[28]

Wild-derived mouse strains are highly resistant to infection with West Nile virus, but many laboratory inbred strains are susceptible. Genetic analysis has revealed that the gene encoding the 2′-5′-oligoadenylate synthetase 1b isoform (*Oas1b*) contributes to this susceptibility.[29,30] The role of *Oas1b* was confirmed in laboratory mice by introducing the wild-derived allele into inbred mouse strains by generating knock-in and transgenic mice.[31,32] These studies paved the way to the discovery of genetic variants of the *OAS1* gene in humans as a risk factor for primary infections with West Nile virus.[33,34]

Metabolism

To identify non-invasive markers of non-alcoholic fatty liver disease (NAFLD), Barr *et al*[35] performed a metabolomics study on serum samples from a mouse model of this complex disease. Their work identified several disease markers, which were later also found in a cohort of patients with NAFLD. These markers have been developed as a standardized clinical assay for diagnosis and classification of NAFLD in humans.

The obese mutant mouse *ob/ob* arose spontaneously in The Jackson Laboratories, and genetic studies identified a mutation in the leptin (*Lep*) gene as the cause. Leptin is a satiety factor, and its absence in *ob/ob* mice results in uncontrolled eating.[36] Subsequent studies on humans also found an association between mutations in *LEP* in a subset of morbidly obese people, confirming leptin's function in the regulation of appetite in humans.[37,38] Since then, leptin has been demonstrated to have other functions in humans, including regulation of hematopoiesis, angiogenesis, wound healing, and immune and inflammatory responses.[39] Leptin level or leptin responsiveness is altered in humans affected by diabetes, renal failure, hypothyroidism and AIDS. Thus, the identification of leptin and its receptor (*Lepr*), which is mutated in the db/db mouse, has opened a whole new research field to understand the biology of obesity and its risk for several severe disorders in humans, including diabetes, cardiovascular diseases and cancer.

Cardiovascular system

Koutnikova *et al*[40] described the mapping of quantitative trait loci (QTLs) for blood pressure in the BXD recombinant inbred mouse population and found a QTL on chromosome 9. By using a combined genetic analysis of candidate genes from this QTL interval in mice and syntenic regions on chromosome 3 in humans, they discovered that a polymorphism in the *UBP1* gene is associated with hypertension in humans. The gene product of *UBP1* and the pathways in which it is active could serve as targets for treatment of hypertension in humans.

Atherosclerosis is a complex human disease involving both genetic and environmental risk factors. Polymorphisms in genes directing lipid metabolism, inflammation and thrombogenesis are thought to be responsible for the wide range of susceptibilities in the general population to myocardial infarction, a fatal consequence of atherosclerosis. Genetic linkage studies have been carried out on humans and mouse models to identify genetic polymorphisms controlling related phenotypic traits. Until now, ~40 quantitative trait loci for atherosclerotic disease have been found in humans, and ~30 in mice.[41] Follow-up studies identified genes that are causally involved in the development of atherosclerosis. For example, the *Tnfsf4* gene, encoding the OX40 ligand, has been identified by positional cloning as a gene that influences atherosclerosis formation in mice. Subsequent analysis in a human cohort identified a polymorphism in the *TNFSF4* gene associated with increased risk of myocardial infarction.[42]

Circadian rhythms

The first known mammalian gene regulating circadian behavior is *Clock*. It was discovered in mice in an ENU mutation screen.[43–45] These findings led to the discovery of a set of core circadian clock genes (*Bmal1, Npas2, Per1,2,* and *Cry1,2*), which function together with *Clock* in a negative feedback loop. They also paved the way to the concept of central and peripheral clocks regulating circadian biology. The discovery of *Clock* was the basis for genetic association studies in humans, which demonstrated an association of *CLOCK* and other circadian genes with sleep/wake cycles and disrupted circadian rhythms in familial cases of advanced sleep phase syndrome.[46,47] More importantly, the discovery of *Clock* and other circadian genes provided the basis for the investigation of circadian clock-controlled mechanisms in diverse physiological and pathological conditions in humans, such as the regulation of blood pressure, cardiovascular functions, ischemia, diabetes, metabolism syndrome and regulation of endocrine and immune functions.[48,49]

Central nervous system

Poot *et al*[50] studied the natural variation in the volume of the corpus callosum in mice from the BXD population. They found a QTL on chromosome 7 that influences this trait. Subsequently, they related the mouse genes located in this QTL interval to genetic data from patients with abnormal corpus callosum (ACC) development. Their analysis revealed that the *HNRPU* gene (*Hnrpul1* in mice) is strongly associated with corpus callosum abnormalities in humans. These results pinpointed a common genetic basis for corpus callosum development in the brain of mouse and man, and provided a foundation for using mouse models to elucidate the neurobiological mechanisms underlying behavioral disorders associated with abnormal development of the corpus callosum.

Narcolepsy is a rare human sleep disorder with a strong genetic component. However, genetic studies in humans only found a strong association with the human leukocyte antigen (HLA) system. Forward genetic studies in the dog and reverse genetics in the mouse found that the orexin/hypocretin system underlies this disease.[51,52] Subsequent studies on humans found that orexin-expressing neurons are lost in narcolepsy and are not detectable in cerebrospinal fluid. Orexin level in cerebrospinal fluid is now used to diagnose narcolepsy and to study the etiology of the loss of specific orexin neurons.[53,54]

Psychiatric abnormalities

Psychiatric disorders are very difficult to study in humans as well as in experimental animals due to the difficulty of defining and assessing disease phenotype. However, comparative genetics has contributed to the discovery of translational genotype–phenotype relationships in humans and mice that are relevant for starting to understand these complex brain disorders.[55]

De Mooij-van Malsen *et al*[56] studied chromosome substitution strains of mice

(CSS)[57] to dissect complex behaviors into separate components. Subsequent genetic mapping of these traits revealed a genetic locus for avoidance behavior on mouse chromosome 15 that is homologous to a human linkage region for bipolar disorder. By integrating the mouse QTL data with genotypes from a large genome-wide association data set for bipolar disorders, they identified novel genes, such as *Adcy8*, that provide new insights towards understanding the neurobiological mechanisms underlying this complex mood disorder.[56]

Hovatta *et al*[58] performed behavioral analysis in different inbred mouse strains and related them to gene expression profiles in various brain regions. They identified 17 genes with expression patterns correlating with anxiety-like phenotypes. Subsequently, they tested 13 known human homologs as candidate genes for human anxiety disorders and showed that several of them are associated with human anxiety disorders as well.[59]

Malki *et al*[60] treated mice from different inbred strains with antidepressant drugs and measured gene expression levels in the hippocampus. Gene expression analysis of strain-by-drug interactions revealed 17 differentially expressed genes. Subsequently, they searched for SNPs in the corresponding genes in a human cohort in which the response to antidepressant drugs was investigated. This comparison identified in the human *PPM1A* gene polymorphisms that are associated with differential responses to nortriptyline, a norepinephrine reuptake inhibitor.

REVERSE GENETICS AND THE MOUSE MODEL

In addition to forward genetic approaches, the mouse has been extensively used as a model for reverse genetics, that is, manipulating a gene and then determining the biological consequences. For the latter, the establishment of targeted mutagenesis in ES cells has made it possible to generate knockout (KO) mice in which a specific gene is deleted. The main advantage of KO models is studying the function of a single gene by comparing KO mice to wild-type mice, on a defined genetic background. KO models have contributed enormously to our understanding of gene functions.[61,62] Generation of a mouse KO for every mouse gene in combination with systematic phenotyping of these mutant lines by the International Mouse Phenotyping Consortium (IMPC) will be extremely important for future forward genetic approaches.[63]

Complex genetics studies in mice and genome-wide association studies in humans identify QTL regions in which the causative gene(s) can be identified. Subsequently, the combination of extensive knowledge of many genes and the availability of the KO models is extremely important to find the best candidates and to demonstrate causality. One example is the confirmation of the consequences of the *Tlr4* mutation for LPS resistance.[26]

KO mice are generated on a single genetic background. However, the phenotypic manifestation of a gene KO might differ between genetic backgrounds due to differences in modifier genes. Such variations have been observed in diabetic mice with mutations in the *db* or *ob* gene.[64] Similarly, the severity of the diabetes caused by disruption of the *Wfs1* gene depends on the mouse genetic background.[65] Further, the *clock* mutation was found in a ENU screen in a B6 background, but was lost when transferred onto a C3H background. A subsequent QTL study identified a modifier gene that is part of the melatonin synthesis pathway.[66] Thus, forward and reverse genetic approaches are not mutually exclusive but highly complementary.

'THE HUMAN IS THE BEST MODEL FOR HUMAN DISEASES'

One criticism leveled against the use of mouse models for human diseases is that they do not reflect the full complexity observed in humans.[67] We very much disagree with this view, because it does not appreciate the reasoning behind using models, which is to reduce the complexity of a system and not to reproduce it. Only then is it possible to study the effect of individual causal components. In humans, diseases are in most cases multifactorial. Both genetic and environmental factors influence the outcome, so it is often very difficult to identify the genetic influences because they are masked by too many confounding factors. Experimental models are extremely useful because they 'simplify' the study by keeping most of the environmental factors constant (no differences in medication, diets, socioeconomic factors, stress at work, pollution, etc).

It is also important to reflect on the term 'model' in biomedical research. In basic research, the main purpose is to discover and understand biological mechanisms. In this case, it is not necessary that a model reflects perfectly a human disease state. One should not always expect that a mutation in an orthologous gene in the mouse results in the same phenotype observed in humans. But even in these cases, one will obtain important insights into its biological functions. On the other hand, the expectations are different in drug research and development. In this case, a model should approximate as much as possible the human phenotype in order to reliably predict the outcome of clinical treatment. Here, many sophisticated disease models based on advances in mouse genetics have been developed. They include mouse lines with multiple gene knockouts and transgenic lines carrying human disease-associated alleles. An analysis of the 100 best-selling drugs showed that phenotypes of knockout mice correlate well with drug efficacy, and thus were crucial for target discovery and validation.[68,69] In addition, ~40% of animal studies could be reproduced in human trials. For those that failed, one of the reasons may have been inappropriate clinical trial design.[70,71] It should also be noted that using a single mouse strain and a single tissue for analysis may not be appropriate to draw general conclusions about the usefulness of the mouse model.[1] Thus, 'we should foster the possibilities of each model, not malign them'.[72]

Another argument against the validity of the mouse as a model system is that GWAS studies in humans make mouse genetics obsolete.[73] This may be true in some cases, but not in general. For obvious ethical reasons, experiments on humans are not possible for phenotypes such as susceptibility to infections, toxic substances, allergens or stress. Further, the regions identified in GWAS studies contain many genes and without prior knowledge of gene functions in the mammalian organism (described in experimental models) it will be impossible to find the causal gene variants. Once an association between genetic variations and disease states has been identified in human studies, it will be necessary to prove causal relationship. This is only possible in an animal model. Furthermore, environmental and other confounding factors are numerous and difficult to control in human studies. To address them, cohorts will have to be stratified into increasingly smaller groups, reducing the groups to sizes that do not allow any more significant associations. Last but not the least, studies in mouse models cost only a fraction of the cost of large-scale genetic studies in humans.

CONCLUSIONS

Granting agencies and policy makers as well as clinical researchers and practitioners should all realize that mouse models are essential to advance our understanding of human biology and, in this way, obtain a better knowledge of human disease pathomechanisms and how to best treat them. Yet, we do recognize the limitations of mouse models and that one-to-one translation to humans in clinical trials is not the norm. Thus, joint translational research involving clinicians and basic researchers using mouse models will always be vital for the success of clinical research.

Furthermore, one should not be shortsighted and dictate research approaches solely by current clinical needs. Even experts in their fields were way off the mark when predicting the future potential of their developments. Gottlieb Daimler presumed that 'There will be a maximum of 5000 automobiles being built, because there are not enough chauffeurs to drive them.' IBM chief Thomas Watson estimated in 1943 'a worldwide need of about five computers', and in 1981, Bill Gates thought that '640 K are enough for everybody'.[74] Thus, looking back, it is very clear that without broad basic research approaches, and the use of mouse model systems, in particular, many modern clinical treatments and therapies would simply not exist. Therefore, only continuous efforts to understand mammalian biology in experimental animal models will allow biomedical research to make major discoveries that will considerably advance the development of novel strategies to diagnose and treat human diseases.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

1 Seok J, Warren HS, Cuenca AG *et al*: Genomic responses in mouse models poorly mimic human inflammatory diseases. *Proc Natl Acad Sci USA* 2013; **110**: 3507–3512.
2 Schughart K: SYSGENET: a meeting report from a new European network for systems genetics. *Mamm Genome* 2010; **21**: 331–336.
3 Snell GD: Studies in histocompatibility. *Science* 1981; **213**: 172–178.
4 Kohler G, Howe SC, Milstein C: Fusion between immunoglobulin-secreting and nonsecreting myeloma cell lines. *Eur J Immunol* 1976; **6**: 292–295.
5 Kohler G, Milstein C: Derivation of specific antibody-producing tissue culture and tumor lines by cell fusion. *Eur J Immunol* 1976; **6**: 511–519.
6 Peirce JL, Lu L, Gu J, Silver LM, Williams RW: A new set of BXD recombinant inbred lines from advanced intercross populations in mice. *BMC Genet* 2004; **5**: 7.
7 Taylor BA, Wnek C, Kotlus BS, Roeme rN, MacTaggart T, Phillips SJ: Genotyping new BXD recombinant inbred mouse strains and comparison of BXD and consensus maps. *Mamm Genome* 1999; **10**: 335–348.
8 Collaborative Cross Consortium. The genome architecture of the collaborative cross mouse genetic reference population. *Genetics* 2012; **190**: 389–401.
9 Kelada SN, Aylor DL, Peck BC *et al*: Genetic analysis of hematological parameters in incipient lines of the collaborative cross. *G3 (Bethesda)* 2012; **2**: 157–165.
10 Bottomly D, Ferris MT, Aicher LD *et al*: Expression quantitative trait loci for extreme host response to influenza a in pre-collaborative cross mice. *G3 (Bethesda)* 2012; **2**: 213–221.
11 Aylor DL, Valdar W, Foulds-Mathes W *et al*: Genetic analysis of complex traits in the emerging Collaborative Cross. *Genome Res* 2011; **21**: 1213–1222.
12 Durrant C, Tayem H, Yalcin B *et al*: Collaborative Cross mice and their power to map host susceptibility to *Aspergillus fumigatus* infection. *Genome Res* 2011; **21**: 1239–1248.
13 Philip VM, Sokoloff G, Ackert-Bicknell CL *et al*: Genetic analysis in the Collaborative Cross breeding population. *Genome Res* 2011; **21**: 1223–1238.
14 Nolan PM, Hugill A, Cox RD: ENU mutagenesis in the mouse: application to human genetic disease. *Brief Funct Genomic Proteomic* 2002; **1**: 278–289.
15 Cox RD, Brown SD: Rodent models of genetic disease. *Curr Opin Genet Dev* 2003; **13**: 278–283.
16 Beier DR, Herron BJ: Genetic mapping and ENU mutagenesis. *Genetica* 2004; **122**: 65–69.
17 Clark AT, Goldowitz D, Takahashi JS *et al*: Implementing large-scale ENU mutagenesis screens in North America. *Genetica* 2004; **122**: 51–64.
18 Sung YH, Song J, Lee HW: Functional genomics approach using mice. *J Biochem Mol Biol* 2004; **37**: 122–132.
19 Acevedo-Arozena A, Wells S, Potter P, Kelly M, Cox RD, Brown SD: ENU mutagenesis, a way forward to understand gene function. *Annu Rev Genomics Hum Genet* 2008; **9**: 49–69.
20 Gondo Y, Fukumura R, Murata T, Makino S: ENU-based gene-driven mutagenesis in the mouse: a next-generation gene-targeting system. *Exp Anim* 2010; **59**: 537–548.
21 Fuchs H, Gailus-Durner V, Adler T *et al*: Mouse phenotyping. *Methods* 2011; **53**: 120–135.
22 Nguyen N, Judd LM, Kalantzis A, Whittle B, Giraud AS, van Driel IR: Random mutagenesis of the mouse genome: a strategy for discovering gene function and the molecular basis of disease. *Am J Physiol Gastrointest Liver Physiol* 2011; **300**: G1–11.
23 Freudenberg MA, Keppler D, Galanos C: Requirement for lipopolysaccharide-responsive macrophages in galactosamine-induced sensitization to endotoxin. *Infect Immun* 1986; **51**: 891–895.
24 Poltorak A, Smirnova I, He X *et al*: Genetic and physical mapping of the Lps locus: identification of the toll-4 receptor as a candidate gene in the critical region. *Blood Cells Mol Dis* 1998; **24**: 340–355.
25 Cohen J: The immunopathogenesis of sepsis. *Nature* 2002; **420**: 885–891.
26 Tanga FY, Nutile-McMenemy N, DeLeo JA: The CNS role of Toll-like receptor 4 in innate neuroimmunity and painful neuropathy. *Proc Natl Acad Sci USA* 2005; **102**: 5856–5861.
27 O'Neill LA, Bryant CE, Doyle SL: Therapeutic targeting of Toll-like receptors for infectious and inflammatory diseases and cancer. *Pharmacol Rev* 2009; **61**: 177–197.
28 Beutler B, Goodnow CC: How host defense is encoded in the mammalian genome. *Mamm Genome* 2011; **22**: 1–5.
29 Mashimo T, Lucas M, Simon-Chazottes D *et al*: A nonsense mutation in the gene encoding 2'-5'-oligoadenylate synthetase/L1 isoform is associated with West Nile virus susceptibility in laboratory mice. *Proc Natl Acad Sci USA* 2002; **99**: 11311–11316.
30 Perelygin AA, Scherbik SV, Zhulin IB, Stockman BM, Li Y, Brinton MA: Positional cloning of the murine flavivirus resistance gene. *Proc Natl Acad Sci USA* 2002; **99**: 9322–9327.
31 Scherbik SV, Stockman BM, Brinton MA: Differential expression of interferon (IFN) regulatory factors and IFN-stimulated genes at early times after West Nile virus infection of mouse embryo fibroblasts. *J Virol* 2007; **81**: 12005–12018.
32 Simon-Chazottes D, Frenkiel MP, Montagutelli X, Guenet JL, Despres P, Panthier JJ: Transgenic expression of full-length 2',5'-oligoadenylate synthetase 1b confers to BALB/c mice resistance against West Nile virus-induced encephalitis. *Virology* 2011; **417**: 147–153.
33 Yakub I, Lillibridge KM, Moran A *et al*: Single nucleotide polymorphisms in genes for 2'-5'-oligoadenylate synthetase and RNase L inpatients hospitalized with West Nile virus infection. *J Infect Dis* 2005; **192**: 1741–1748.
34 Lim JK, Lisco A, McDermott DH *et al*: Genetic variation in OAS1 is a risk factor for initial infection with West Nile virus in man. *PLoS Pathog* 2009; **5**: e1000321.
35 Barr J, Vazquez-Chantada M, Alonso C *et al*: Liquid chromatography-mass spectrometry-based parallel metabolic profiling of human and mouse model serum reveals putative biomarkers associated with the progression of nonalcoholic fatty liver disease. *J Proteome Res* 2010; **9**: 4501–4512.
36 Friedman JM, Halaas JL: Leptin and the regulation of body weight in mammals. *Nature* 1998; **395**: 763–770.
37 Montague CT, Farooqi IS, Whitehead JP *et al*: Congenital leptin deficiency is associated with severe early-onset obesity in humans. *Nature* 1997; **387**: 903–908.
38 Farooqi IS, Jebb SA, Langmack G *et al*: Effects of recombinant leptin therapy in a child with congenital leptin deficiency. *N Engl J Med* 1999; **341**: 879–884.
39 Farooqi IS, Matarese G, Lord GM *et al*: Beneficial effects of leptin on obesity, T cell hyporesponsiveness, and neuroendocrine/metabolic dysfunction of human congenital leptin deficiency. *J Clin Invest* 2002; **110**: 1093–1103.
40 Koutnikova H, Laakso M, Lu L *et al*: Identification of the UBP1 locus as a critical blood pressure determinant using a combination of mouse and human genetics. *PLoS Genet* 2009; **5**: e1000591.
41 Chen Y, Rollins J, Paigen B, Wang X: Genetic and genomic insights into the molecular basis of atherosclerosis. *Cell Metab* 2007; **6**: 164–179.
42 Wang X, Ria M, Kelmenson PM *et al*: Positional identification of TNFSF4, encoding OX40 ligand, as a gene that influences atherosclerosis susceptibility. *Nat Genet* 2005; **37**: 365–372.
43 Vitaterna MH, King DP, Chang AM *et al*: Mutagenesis and mapping of a mouse gene, Clock, essential for circadian behavior. *Science* 1994; **264**: 719–725.
44 Antoch MP, Song EJ, Chang AM *et al*: Functional identification of the mouse circadian Clock gene by transgenic BAC rescue. *Cell* 1997; **89**: 655–667.
45 King DP, Zhao Y, Sangoram AM *et al*: Positional cloning of the mouse circadian clock gene. *Cell* 1997; **89**: 641–653.
46 Toh KL, Jones CR, He Y *et al*: An hPer2 phosphorylation site mutation in familial advanced sleep phase syndrome. *Science* 2001; **291**: 1040–1043.
47 Xu Y, Padiath QS, Shapiro RE *et al*: Functional consequences of a CKIdelta mutation causing familial advanced sleep phase syndrome. *Nature* 2005; **434**: 640–644.
48 Huang W, Ramsey KM, Marcheva B, Bass J: Circadian rhythms, sleep, and metabolism. *J Clin Invest* 2011; **121**: 2133–2141.
49 Yu EA, Weaver DR: Disrupting the circadian clock: gene-specific effects on aging, cancer, and other phenotypes. *Aging (Albany NY)* 2011; **3**: 479–493.
50 Poot M, Badea A, Williams RW, Kas MJ: Identifying human disease genes through cross-species gene mapping of evolutionary conserved processes. *PLoS ONE* 2011; **6**: e18612.
51 Chemelli RM, Willie JT, Sinton CM *et al*: Narcolepsy in orexin knockout mice: molecular genetics of sleep regulation. *Cell* 1999; **98**: 437–451.
52 Lin L, Faraco J, Li R *et al*: The sleep disorder canine narcolepsy is caused by a mutation in the hypocretin (orexin) receptor 2 gene. *Cell* 1999; **98**: 365–376.

53 Peyron C, Faraco J, Rogers W *et al*: A mutation in a case of early onset narcolepsy and a generalized absence of hypocretin peptides in human narcoleptic brains. *Nat Med* 2000; **6**: 991–997.
54 Kornum BR, Faraco J, Mignot E: Narcolepsy with hypocretin/orexin deficiency, infections and autoimmunity of the brain. *Curr Opin Neurobiol* 2011; **21**: 897–903.
55 Kas MJ, Kahn RS, Collier DA *et al*: Translational neuroscience of Schizophrenia: seeking a meeting of minds between mouse and man. *Sci Transl Med* 2011; **3**: 102mr103.
56 de Mooij-van Malsen AJ, van Lith HA, Oppelaar H *et al*: Interspecies trait genetics reveals association of Adcy8 with mouse avoidance behavior and a human mood disorder. *Biol Psychiatry* 2009; **66**: 1123–1130.
57 Singer JB, Hill AE, Burrage LC *et al*: Genetic dissection of complex traits with chromosome substitution strains of mice. *Science* 2004; **304**: 445–448.
58 Hovatta I, Tennant RS, Helton R *et al*: Glyoxalase 1 and glutathione reductase 1 regulate anxiety in mice. *Nature* 2005; **438**: 662–666.
59 Donner J, Pirkola S, Silander K *et al*: An association analysis of murine anxiety genes in humans implicates novel candidate genes for anxiety disorders. *Biol Psychiatry* 2008; **64**: 672–680.
60 Malki K, Uher R, Paya-Cano J *et al*: Convergent animal and human evidence suggests a role of PPM1A gene in response to antidepressants. *Biol Psychiatry* 2011; **69**: 360–365.
61 Rosenthal N, Brown S: The mouse ascending: perspectives for human-disease models. *Nat Cell Biol* 2007; **9**: 993–999.
62 Masih-ul A, Müller W: Studying immunology in mice; in Hedrich H (eds). *The Laboratory Mouse*. London, UK: Academic Press, 2012; pp 349–362.
63 Brown SD, Moore MW: Towards an encyclopaedia of mammalian gene function: the International Mouse Phenotyping Consortium. *Dis Model Mech* 2012; **5**: 289–292.
64 Coleman DL: Diabetes-obesity syndromes in mice. *Diabetes* 1982; **31**: 1–6.
65 Ishihara H, Takeda S, Tamura A *et al*: Disruption of the WFS1 gene in mice causes progressive beta-cell loss and impaired stimulus-secretion coupling in insulin secretion. *Hum Mol Genet* 2004; **13**: 1159–1170.
66 Shimomura K, Lowrey PL, Vitaterna MH *et al*: Genetic suppression of the circadian Clock mutation by the melatonin biosynthesis pathway. *Proc Natl Acad Sci USA* 2010; **107**: 8399–8403.
67 Seok J, Warren HS, Cuenca AG *et al*: Genomic responses in mouse models poorly mimic human inflammatory diseases. *Proc Natl Acad Sci USA* 2013; **110**: 3507–3512.
68 Zambrowicz BP, Turner CA, Sands AT: Predicting drug efficacy: knockouts model pipeline drugs of the pharmaceutical industry. *Curr Opin Pharmacol* 2003; **3**: 563–570.
69 Zambrowicz BP, Sands AT: Knockouts model the 100 best-selling drugs—will they model the next 100? *Nat Rev Drug Discov* 2003; **2**: 38–51.
70 Hackam DG, Redelmeier DA: Translation of research evidence from animals to humans. *JAMA* 2006; **296**: 1731–1732.
71 van der Worp HB, Howells DW, Sena ES *et al*: Can animal models of disease reliably inform human studies? *PLoS Med* 2010; **7**: e1000245.
72 Baldarelli RM: Drug discovery: in defence of the animal model. *Nature* 2012; **485**: 309.
73 Aitman TJ, Boone C, Churchill GA, Hengartner MO, Mackay TF, Stemple DL: The future of model organisms in human disease research. *Nat Rev Genet* 2011; **12**: 575–582.
74 Hans J: Delphi-Methode; in Harting JM, Kerstan T (eds). *Wissen to go. Ein Studium generale in 100 Begriffen*. München, Germany: Piper, 2008.

APPENDIX

Members of the SYSGENET network

1. Penelope Andreux, Ecole Polytechnique Fédérale de Lausanne, AI 1351—Station 15, 1015 Lausanne, Switzerland
2. Ana Maria Aransay, CIC bioGUNE & CIBERehd, Bizkaia Tecnology Park, Building 801-A, 48160 Derio, Spain
3. Johan Auwerx, Ecole Polytechnique Federale de Lausanne, SV-IBI1—NCEM1, AI 1151, Station 15, 1015 Lausanne, Switzerland
4. Rudi Balling, Luxembourg Centre for Systems Biomedicine (LCSB), University of Luxembourg, 7, avenue des Hauts-Fourneaux, L-4362 Esch-sur-Alzette, Luxembourg
5. Sreeparna Banerjee, Department of Biological Sciences, Middle East Technical University, Z-16, 06800 Ankara, Turkey
6. Anastasios Bezerianos, Biosignal Processing Lab. Department of Medical Physics, ASCLIPIOU 2, School of Medicine, University of Patras, 26500 Patras, Greece
7. Alessandra Desj Bragonzi, San Raffaele Scientific Institute, via Olgettina 58, 20132 Milano, Italy
8. Gudrun A Brockmann, Humboldt-Universität, Breeding Biology and Molecular Genetics, Invalidenstraße 42, D-10115 Berlin, Germany
9. Steve Brown, MRC Mammalian Genetics Unit, Harwell, Oxfordshire OX11 0RD, UK
10. Joan Campbell-Tofte, Department of Clinical Biochemistry, Frederiksberg Hospital, DK-2000 Frederiksberg, Denmark
11. Jan Cendelin, Department of Pathophysiology, Faculty of Medicine in Pilsen, Charles University, Lidicka 1, 301 66 Plzen, Czech Republic
12. Aristotelis Chatziioannou, Ethniko Idryma Erevnon National Hellenic Research Foundation, 48 Vassileos Constantinou Ave, 11635 Athens, Greece
13. Duan Chen, Norwegian University of Science and Technology, NO-7491 Trondheim, Norway
14. Wim Crusio, Institut de Neurosciences Cognitives et Intégratives d'Aquitaine, CNRS UMR 5287, Bat B2—Avenue des Facultés, 33405 Talence, France
15. Konstantina Dimitrakopoulou, University of Patras, Rio, 26500 Patras, Greece
16. Juan M Falcon, CIC bioGUNE, Bizkaia Tecnology Park, Building 801-A, 48160 Derio, Spain
17. Jiri Forejt, Institute of Molecular Genetics, Academy of Sciences of the Czech Republic, Videnska 1083, 142 20 Prague, Czech Republic
18. Paul Franken, University of Lausanne, Center for Integrative Genomics, Genopode building, CH-1015 Lausanne-Dorigny, Switzerland
19. Leopold F Fröhlich, Medical University of Graz, Institute of Pathology, Auenbruggerplatz 25, A-8036 Graz, Austria
20. Yann Herault, ICS, TAAM, PHENOMIN, IGBMC, Inserm, CNRS, UdS, GIE-CERBM, 1 Rue Laurent Fries, BP 10142 Parc d'Innovation, 67404 Illkirch, France
21. Iiris Hovatta, University of Helsinki, Research Program of Molecular Neurology, 00014 Helsingin yliopisto, Finland
22. Fuad A Iraqi, Sackler Faculty of Medicine, Tel-Aviv University, 69978 Tel-Aviv, Israel
23. Ritsert C Jansen, University of Groningen, Kerklaan 30, 9751 NN Haren (GN), Netherlands
24. Leszek Kaczmarek, Polish Academy of Sciences Nencki Institute of Experimental Biology, Pasteura 3, 02-093 Warsaw, Poland
25. Martien Kas, Rudolf Magnus Institute of Neuroscience, University Medical Centre Utrecht, Universiteitsweg 100, 3584CG Utrecht, The Netherlands
26. Ewelina Knapska, Nencki Institute, Pasteur 3, 02-093 Warsaw, Poland
27. Sulev Koks, Faculty of Medicine, University of Tartu, 19 Ravila Street, 50411 Tartu, Estonia
28. Fragiskos Kolisis, NTUA, 9 Iroon Polytechneiou, 15700 Athens, Greece
29. Michal Korostynski, Institute of Pharmacology, Polish Academy of Sciences, Smetna 12, 31-343 Krakow, Poland
30. Frank Lammert, Department of Medicine II, Saarland University Hospital, Saarland University, Kirrberger Street 1, 66421 Homburg, Germany
31. Hans Lehrach, Max Planck Institute for Molecular Genetics, Ihnestrasse 73, 14195 Berlin, Germany
32. Andreas Lengeling, The Roslin Institute and Royal Dick School of Veterinary Studies, University of Edinburgh, Easter Bush Campus, EH25 9RG Roslin, United Kingdom
33. Claude Libert, VIB, Rijvisschestraat 120, 9052 Gent, Belgium

34. Xavier Montagutelli, Institut Pasteur, 25 rue du Docteur Roux, 75724 Paris cedex 15, France
35. Grant Morahan, The Western Australian Institute for Medical Research, University of Western Australia, Perth WA, Australia
36. Richard Mott, University of Oxford, Wellcome Trust Centre for Human Genetics, Roosevelt Drive, OX3 7BN Oxford, United Kingdom
37. Jean-Jacques Panthier, Institut Pasteur, Mouse functional Genetics Unit, 75015 Paris, France
38. Ryszard Przewlocki, Institute of Pharmacology, Smetna 12, 31-343 Krakow, Poland
39. Annamari Ranki, Institute of Clinical Medicine, PL 22 (Meilahdentie 2), University of Helsinki, Helsinki, Finland
40. Javier Santos, Centro de Biología Molecular Severo Ochoa, Nicolás Cabrera, 1, Campus de la Universidad Autónoma de Madrid, 28049 Madrid, Spain
41. Feride Severcan, Department of Biological Sciences, Middle East Technical University, Inonu Caddesi, 06531 Ankara, Turkey
42. Leonard Schalkwyk, King's College London, Institute of Psychiatry PO82, London SE5 8A3, UK
43. Klaus Schughart, Department of Infection Genetics, Helmholtz Centre for Infection Research, Inhoffenstr 7, D-38124 Braunschweig, Germany
44. August B Smit, Department of Molecular and Cellular Neurobiology, Research Institute Neurosciences Vrije Universiteit, Faculty of Biology, De Boelelaan 1087, 1081 HV Amsterdam, The Netherlands
45. Anton Terasmaa, Department of Physiology, University of Tartu, 50411 Tartu, Estonia
46. Eero Vasar, Department of Physiology, University of Tartu, 19 Ravila Street, 50411 Tartu, Estonia
47. Kurt Zatloukal, Medical University of Graz, Institute of Pathology, Auenbruggerplatz 25, A-8036 Graz, Austria