identifying a potential target protein and then designing or screening compounds to identify those that inhibit the function of that target. This reductionist analysis has identified many potential drug targets and drugs, yet only when a drug is tested in animal models or humans are the systems consequences of the drug's action revealed; not uncommonly, so-called off-target effects may become apparent and be sufficiently adverse for researchers to cease development of the agent. A good example of this problem is the unexpected outcomes of the vitamin B–based regimens for lowering homocysteine levels. In these trials, plasma homocysteine levels were reduced effectively; however, there was no effect of this reduction on clinical vascular endpoints. One explanation for this outcome is that one of the B vitamins in the regimen, folate, has a panoply of effects on cell proliferation and metabolism that probably offset its homocysteine-lowering benefits, promoting progressive atherosclerotic plaque growth and its consequences for clinical events. In addition to these types of unexpected outcomes exerted through pathways that were not considered ab initio, conventional approaches to drug development typically do not take into consideration the possibility of emergent behaviors of the organism or the metabolic pathway or the transcriptional network of interest. Thus, a systems-based analysis of potential drugs (drug-target network analysis) can benefit the development paradigm both by enhancing the likelihood that a compound of interest will not manifest unforeseen adverse effects and by promoting novel analytic methods for identifying unique control points or pathways in metabolic or genetic networks that would benefit from drug-based modulation.

SYSTEMS PATHOBIOLOGY AND HUMAN DISEASE CLASSIFICATION: NETWORK MEDICINE

Perhaps most important, systems pathobiology can be used to revise and refine the definition of human disease. The classification of human disease used in this and all medical textbooks derives from the correlation between pathologic analysis and clinical syndromes that began in the nineteenth century. Although this approach has been very successful, serving as the basis for the development of many effective therapies, it has major shortcomings. Those shortcomings include a lack of sensitivity in defining preclinical disease, a primary focus on overtly manifest disease, failure to recognize different and potentially differentiable causes of common late-stage pathophenotypes, and a limited ability to incorporate the growing body of molecular and genetic determinants of pathophenotype into the conventional classification scheme.

Two examples will illustrate the weakness of simple correlation analyses grounded in the reductionist principle of simplification (Occam's razor) in defining human disease. Sickle cell anemia, the "classic" Mendelian disorder, is caused by a Val6Gln substitution in the β chain of hemoglobin. If conventional genetic teaching holds, this single mutation should lead to a single phenotype in patients who harbor it (genotype-phenotype correlation). This assumption is, however, false, as patients with sickle cell disease manifest a variety of pathophenotypes, including hemolytic anemia, stroke, acute chest syndrome, bony infarction, and painful crisis, as well as an overtly normal phenotype. The reasons for these different phenotypic presentations include the presence of disease-modifying genes or gene products (e.g., hemoglobin F, hemoglobin C, glucose-6-phosphate dehydrogenase), exposure to adverse environmental factors (e.g., hypoxia, dehydration), and the genetic and environmental determinants of common intermediate pathophenotypes (i.e., variations in those generic pathologic mechanisms underlying all human disease—inflammation, thrombosis/hemorrhage, fibrosis, cell proliferation, apoptosis/necrosis, immune response).

A second example of note is familial pulmonary arterial hypertension. This disorder is associated with over 100 different mutations in three members of the transforming growth factor β (TGF-β) superfamily: bone morphogenetic protein receptor-2 (BMPR-2), activin receptor-like kinase-1 (Alk-1), and endoglin. All these different genotypes are associated with a common pathophenotype, and each leads to that pathophenotype by molecular mechanisms that range from haploinsufficiency to dominant negative effects. As only approximately one-fourth of individuals in families that harbor these mutations manifest the pathophenotype, other disease-modifying genes (e.g., the serotonin receptor 5-HT2B, the serotonin transporter 5-HTT), genomic and environmental determinants of common intermediate pathophenotypes, and environmental exposures (e.g., hypoxia, infective agents [HIV], anorexigens) probably account for the incomplete penetrance of the disorder.

On the basis of these and many other related examples, one can approach human disease from a systems pathobiology perspective in which each "disease" can be depicted as a network that includes the following modules: the primary disease-determining elements of the genome (or proteome, if posttranslationally modified), the disease-modifying elements of the genome or proteome, environmental determinants, and genomic and environmental determinants of the generic intermediate pathophenotypes. **Figure 87e-2** graphically depicts these genotype-phenotype relationships as modules for the six common disease types with specific examples for each type. **Figure 87e-3** shows a network-based depiction of sickle cell disease using this kind of modular approach.

Goh and colleagues developed the concept of a human disease network **(Fig. 87e-4)** in which they used a systems approach to characterize the disease-gene associations listed in the Online Mendelian Inheritance in Man database. Their analysis showed that genes linked to similar disorders are more likely to have products that physically associate and greater similarity between their transcription profiles than do genes not associated with similar disorders. In addition, proteins associated with the same pathophenotype are significantly more likely to interact with one another than with other proteins not associated with the pathophenotype. Finally, these authors showed that the great majority of disease-associated genes are not highly connected genes (i.e., not hubs) and are typically weakly linked nodes within the functional periphery of the network in which they operate.

This type of analysis validates the potential importance of defining disease on the basis of its systems pathobiologic determinants. Clearly, doing this will require a more careful dissection of the molecular elements in the relevant pathways (i.e., more precise molecular pathophenotyping), less reliance on overt manifestations of disease for their classification, and an understanding of the dynamics (not just the static architecture) of the pathobiologic networks that underlie pathophenotypes defined in this way. **Figure 87e-5** illustrates the elements of a molecular network within which a disease module is contained. This network is first identified by determining the interactions (physical or regulatory) among the proteins or genes that comprise it (the "interactome"). These interactions then define a topologic module within which exists functional modules (pathways) and disease modules. One approach to constructing this module is illustrated in **Fig. 87e-6**. Examples of the use of this approach in defining novel determinants of disease are given in **Table 87e-1**.

TABLE 87e-1 EXAMPLES OF SYSTEMS BIOLOGY APPLICATION TO DISEASE

Disease	Analysis	Reference
Hereditary ataxias	Many ataxia-causing proteins share interacting partners that affect neurodegeneration	Lim et al: Cell 125:801-814, 2006
Diabetes mellitus	Metabolite-protein network analysis links three unique metabolite abnormalities in prediabetics to seven type 2 diabetes genes through four enzymes	Wang-Sattler et al: Mol Syst Biol 8:615, 2012
Ebstein-Barr virus infection	Viral proteome exerts its effects through linking to host interactome	Gulbahce et al: PLoS One 8:e1002531, 2012
Pulmonary arterial hypertension	Network analysis indicates adaptive role for microRNA 21 in suppressing rho kinase pathway	Parikh et al: Circulation 125:1520-1532, 2012