Evolutionary analysis contributes to the health sciences by:

identifying the origins and ongoing adaptations of infectious diseases;

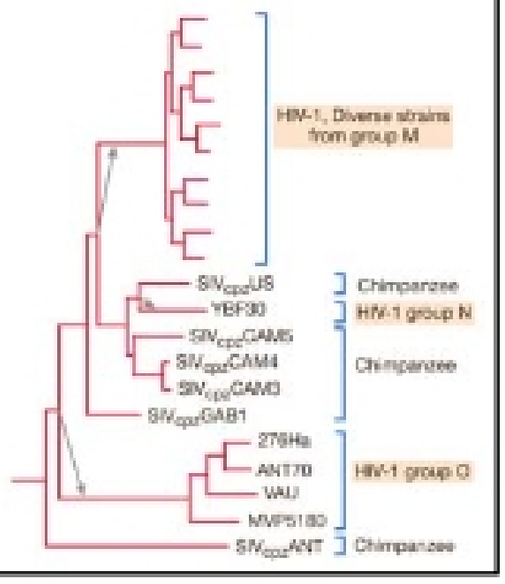
explaining human genetic variation in resistance (and other traits);

exploring the medical implications of human evolutionary history.

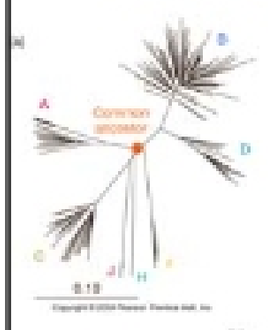
Where did HIV come from?

HIV belongs to a group of retroviruses that infect old-world monkeys and apes.

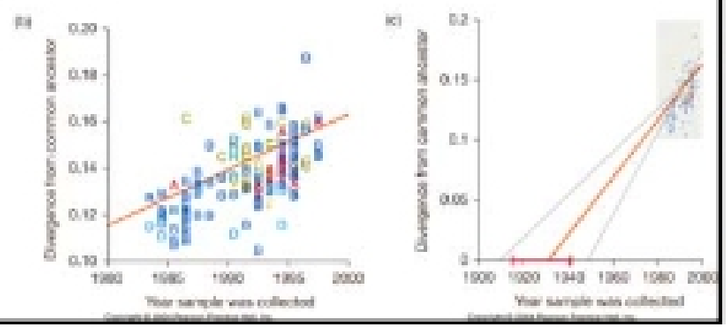
Phylogenetic analysis implies that HIV-1 (the highly virulent form that causes AIDS) jumped from chimpanzees to humans more than once.



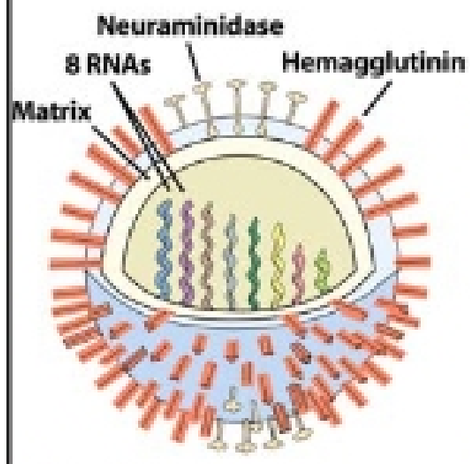
When did it arrive in the human population?



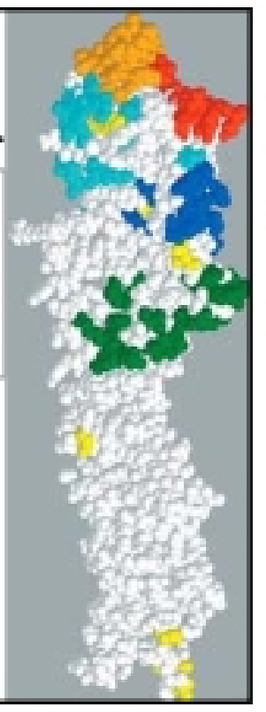
Most HIV-1 infections belong to the diverse "M" group. Bette Korber and colleagues (*Science* 288, 1789–1796, 2000) sequenced the envelope protein genes of 159 different viruses from this group, then inferred their evolutionary history (left) and used the *dates* when they were collected to estimate the *rate* at which the *env* gene evolves (below).



Where does influenza come from?



Antigenic sites (amino acids "seen" by the immune system) are colored in this space-filling molecular model.

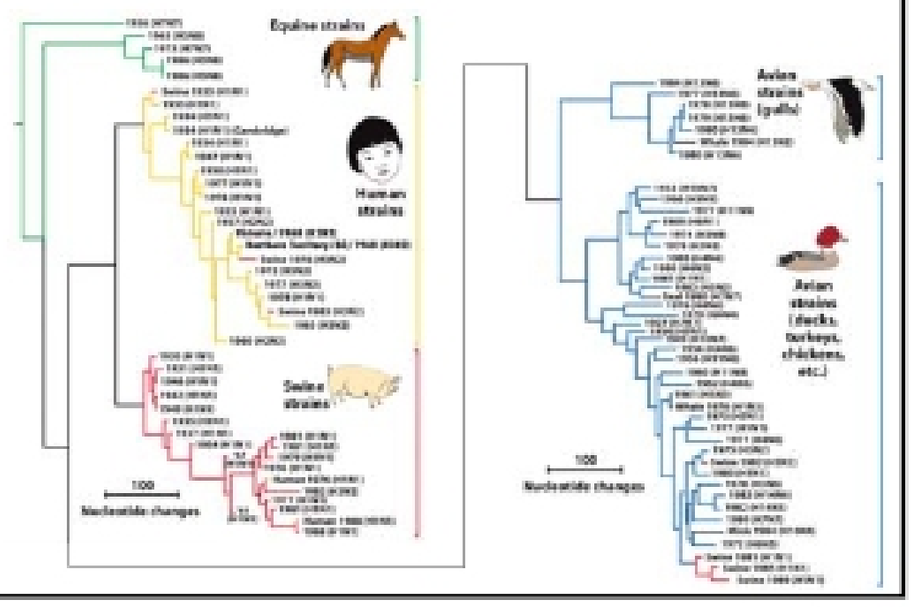


It's an RNA virus, with 8 chromosomes and 11 genes for polymerases, structural proteins and coat proteins.

Hemagglutinin initiates binding to host cells and is the primary target of the host's immune system.

Flu phylogeny based on a structural protein gene

All strains are closely related, and occasionally they jump between species.

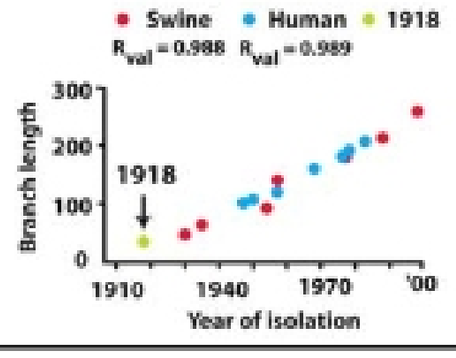


The super-deadly 1918 strain is near the base of the modern human/swine clade, but its origin is unclear.

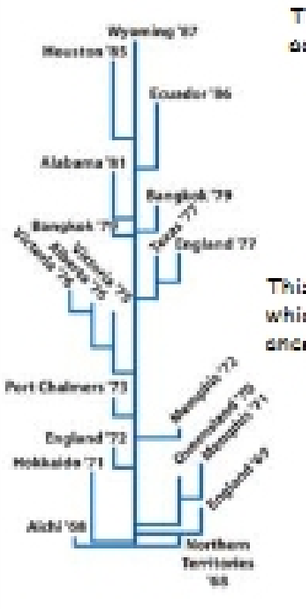
The amino-acid sequence of its nucleoprotein is similar to that of typical bird strains, suggesting that this whole clade may have come from a bird, several years earlier.

Broader surveys of bird-flu strains could confirm this idea.

Strains descended from the last common ancestor of the human/swine clade have evolved at a remarkably steady rate (shown here as estimated numbers of nucleotide substitutions).



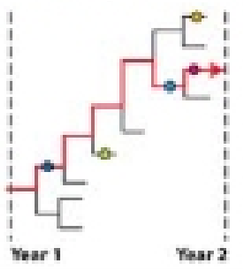
Most flu lineages go extinct. What's different about the survivors?



They have relatively more amino-acid substitutions in antigenic sites.

Lineages	Other Antigenic	Not
Surviving	33 (77%)	10
Extinct	21 (47%)	25

This principle can be used to predict which of *this year's* strains will be the ancestor of *next year's* strains!

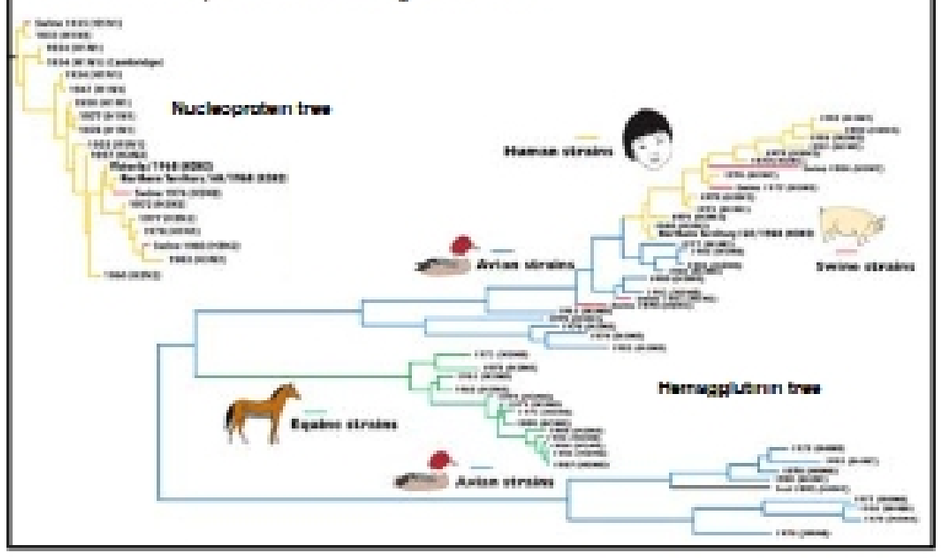


At least one pandemic strain (1968) arose through *recombination*.

The evidence is phylogenetic.

The 1968 (and later) *hemagglutinin* came from a *bird* flu strain.

But the nucleoprotein and *other genes did not*.

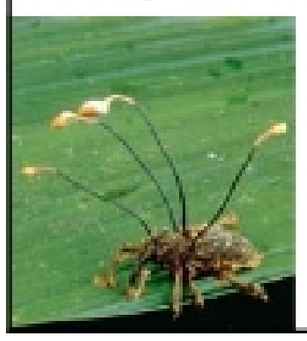


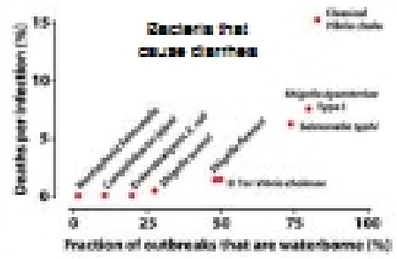
Why do pathogens vary so much in virulence? Three hypotheses:

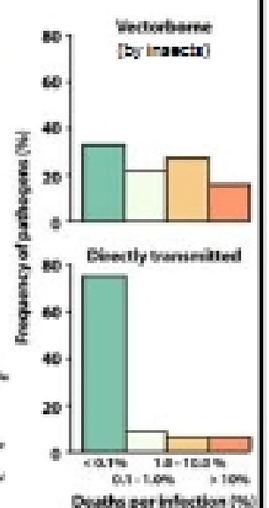
(1) ***Coincidental evolution*** (Tetanus is caused by a soil bacterium that is not a professional enemy of mammals.)

(2) ***Short-sighted evolution*** (Poliovirus lives in the intestine, occasionally invades the nervous system and adapts to growing there, but never transmits from there. And as we discussed previously, within-patient evolution of HIV also appears to be short-sighted.)

(3) ***Trade-offs among opportunities for transmission*** (Directly transmitted diseases need their hosts alive and mobile; water- and vector-borne diseases may not.)







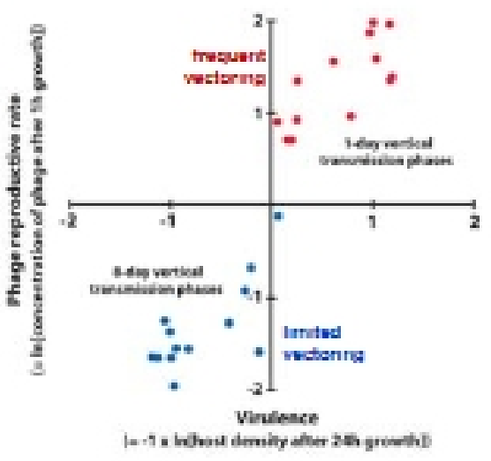
Nice theory. How about an experimental *test?*

Sharon Messenger, Ian Molineaux and James Bull cultured phage f1 (a relatively benign, vertically transmitted virus of *E. coli*) under conditions with two different levels of opportunity for horizontal transmission between unrelated bacteria.

(1) Horizontal transmission once every 8 days ("limited vectoring").

(2) Horizontal transmission once every day ("frequent vectoring").

Their prediction: phages in the limited-vectoring treatment would evolve to be nicer to their hosts (less virulent), because their own fitness would depend more on the reproduction (fitness) of their hosts.



Result: phages in the limited-vectoring treatment grew less and allowed their hosts to grow more, than those in the frequent-vectoring treatment.

Infectious diseases appear to maintain high frequencies of "broken" alleles at many genetic loci.

HIV uses a host cell-surface protein called CCR5 as the co-receptor (part of its "doorway" into the cell).

Some people have a mutant form of CCR5 (Δ32) which blocks entry of HIV.

This allele is common (up to 15%) in populations of European ancestry, and may have been favored by other diseases such as the Black Plague (14th Century), by conferring resistance to the plague bacillus.

Analogous resistance alleles exist at other loci. They too may have been favored by past epidemics, and are probably being favored again by HIV.

When did these mutations first arise and increase in frequency?

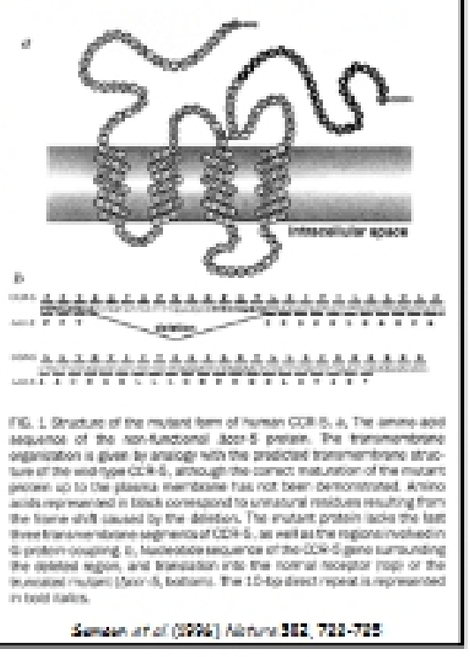
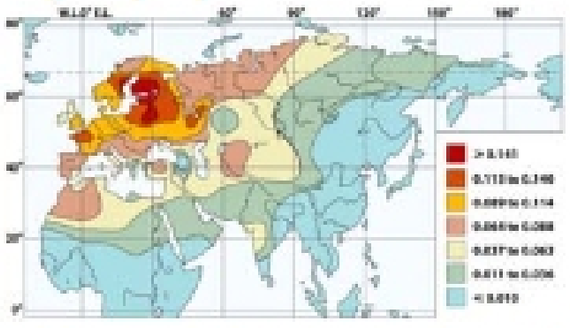


FIG. 1 Structure of the mutant form of human CCR-5. a, The amino-acid sequence of the non-functional Δccr-5 protein. The transmembrane organization is given by analogy with the predicted transmembrane structure of the wild-type CCR-5, although the correct maturation of the mutant protein up to the plasma membrane has not been demonstrated. Amino acids represented in black correspond to unnatural residues resulting from the frame shift caused by the deletion. The mutant protein lacks the last three transmembrane segments of CCR-5, as well as the regions involved in G-protein coupling. b, Nucleotide sequence of the CCR-5 gene surrounding the deleted region, and translation into the normal receptor (top) or the truncated mutant (Δccr-5, bottom). The 10-bp direct repeat is represented in bold italics.

Samson *et al* (1996) *Nature* **382**, 722-725

Δ32 is at high frequency in northern Europe, but not elsewhere.



Analysis of its linkage disequilibrium with genes on the same chromosome suggests that the Δ32 mutation occurred about 5,000 years ago (F&H, p. 299).

Four of 17 Bronze Age European skeletons (2,900 ybp, northwest Germany) are heterozygous carriers, giving an estimated allele frequency of 0.121

Population-genetic modeling suggests that Δ32's rise to high frequency could not have occurred by drift alone; there must have been positive selection.

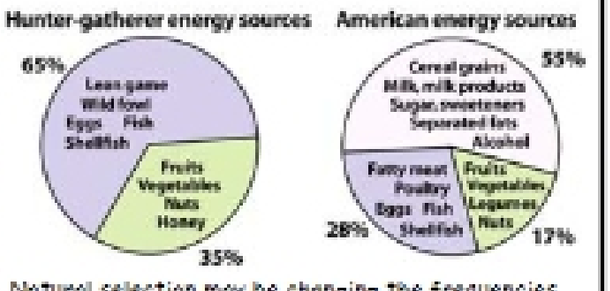
Similar analyses are being applied to other genes with medically significant polymorphisms (e.g., CFTR, Hb^S, GBA-Gaucher, G6PD deficiencies); in many such cases the "broken" alleles appear to be young and positively selected, implying that they may be evolutionary responses to diseases of "modern" life.

Many novel features of modern environments affect human health!

For example, our diets differ radically from those of hunter-gatherers.

We suffer from many diet-related diseases, and there is *considerable genetic variation* for susceptibility to those diseases. Why?

An analogy: myopia. Monozygotic twins are twice as concordant as dizygotic twins, and it's very common among younger Inuit, but not among their parents (F&H, page 551). Before WWII it didn't exist there, so wasn't heritable. Now it does, and is.



Natural selection may be changing the frequencies of more and less susceptible alleles at all such loci, with a mixture of "good" and "bad" consequences. This is a rich and important subject for future evolutionary research!

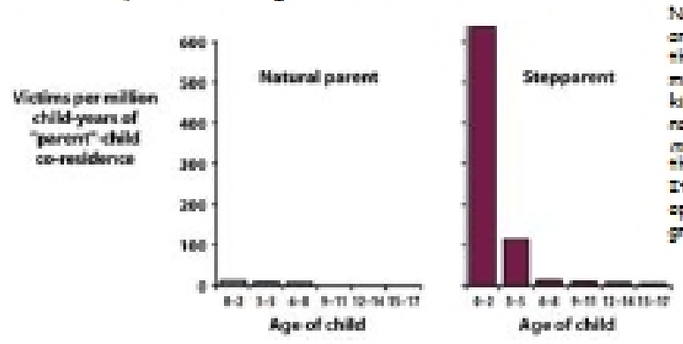
But there's much more to health than infectious diseases and food!

Social environments may also affect health profoundly, and in many respects they differ from the social environments of our recent evolutionary history.

An increasing number of studies suggest that kinship has public-health implications in modern societies (as inclusive-fitness theory might predict).

Most dramatically, Margo Wilson and Martin Daly found that infants and toddlers were 70 times more likely to be murdered by stepparents than by natural parents, in otherwise equivalent Canadian families.

To put this 70x relative risk in perspective, note that smokers are only 11 times more likely to die of lung cancer than non-smokers.



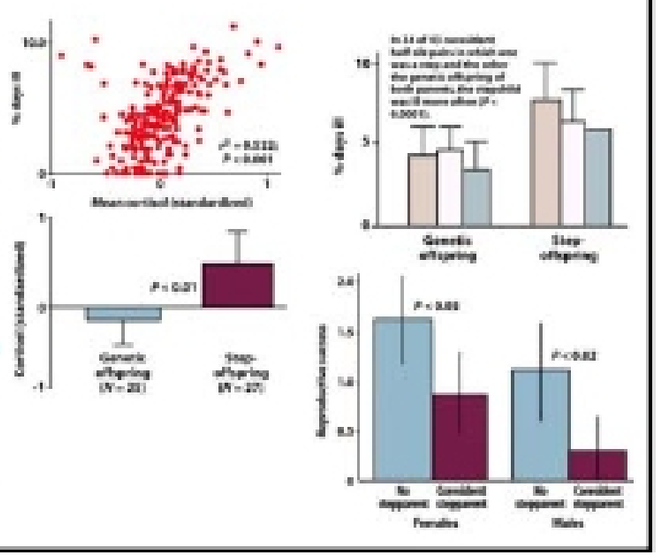
Note: The absolute risks are not very high (less than 1/1000 per year), and most of the victims were killed by biological parents, not stepparents, because *most children* live with their biological parents. It's the *relative risk* (per opportunity) that is much greater for stepchildren.

Subtle but pervasive effects of relatedness variation within families?

Mark Flinn and colleagues studied stress and illness among natural and stepchildren in a village in Dominica.

Levels of the stress hormone cortisol predicted how many days of school the children missed owing to illness, and stepchildren had higher cortisol levels.

Genetic offspring were ill on fewer days than step offspring. And remarkably, they ended up having more children of their own as young adults.



Homicide is also a serious public-health problem

Rates (victims/million/year) vary greatly among U.S. states, and there is a large average difference between southern and non-southern states.

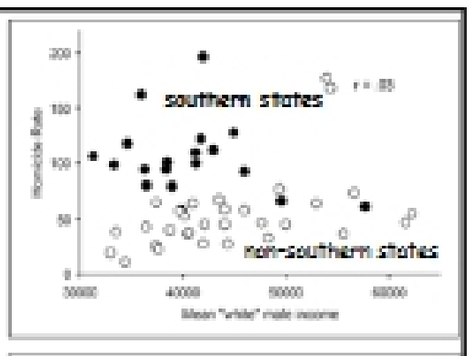
WHY?

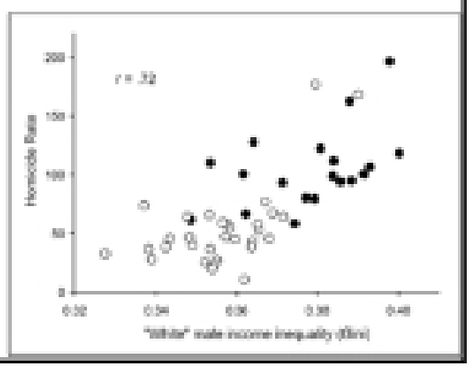
One popular theory: poverty.

Another popular theory: a southern "culture of honor" requires men to avenge insults to self or family.

Daly and Wilson asked, What about men's (unconscious) perceptions of their economic (fitness) prospects, and the degree to which risk-taking and violence might help them get ahead?

Income inequality ends up explaining *half* of the variation in homicide rates!! (More than any other variable.)





What about access to guns? What about violence on TV?

The Canadian provinces fall right on the regression for US states.

Canadians mostly don't own guns.

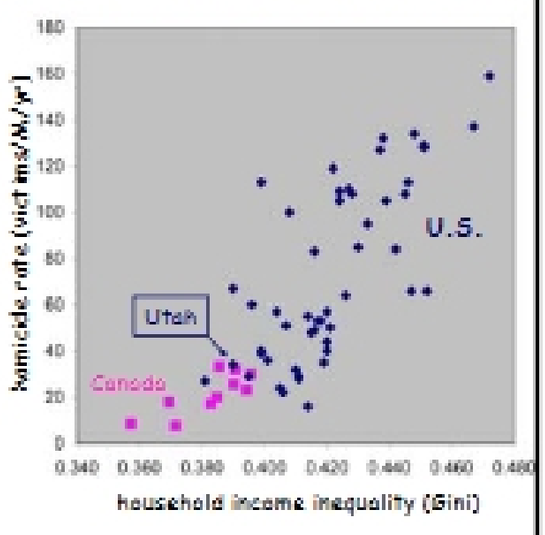
But they watch the same TV.

Again, the popular theories don't seem to explain the facts.

Daly & Wilson's theory proposes that psychological adaptations to *past* human environments incline us to adjust our perceptions and attitudes in certain ways that tended to increase fitness *then*.

Whether they do so now seems doubtful, even if the theory is substantially correct, which has not yet been shown.

But it certainly has led to some productive questions!



Summary

Many health-related issues can be illuminated by evolutionary analysis!

All of the properties of pathogens (infectiousness, virulence, etc.) have evolved, and many are still evolving *rapidly* under the influence of knowable tradeoffs. Identifying these processes may help us to fight the pathogens.

Pathogens appear to exert strong positive selection on many mutations that offer some degree of resistance, even when those mutations also have harmful side effects (especially in homozygotes, but also in heterozygotes).

The human gene pool contains many allelic variants that cause differential susceptibility to "diseases of civilization" and to other consequences of the highly novel environments that humans have created for themselves.

Human psychology may be adapted in some respects to past environments, and may include tendencies that need to be understood and managed creatively if our goal is to maximize health for everyone.