nature genetics

The germinating seed of Arab genomics

Recent studies and a new database indicate that investment in genetics could bring practical health benefits to the states of the Eastern Mediterranean.

Mention Arab genetics and most people will immediately think of the origins and regional pre-eminence in thoroughbred horse racing in North Africa and the Arabian Peninsula. However, it is the diverse people across this geographical area who present one of the greatest opportunities for the application of medical genetics. In turn, the study of their constituent regional populations can form a new research resource from which their scientists can bring fresh insights to the world genomics community.

The 23 member states of the Arab League are bound by the aim of cooperation for the health of their peoples, who comprise over 323 million from Mauritania to Oman. Their economies grossed some $\$1.5 \times 10^{12}$ in 2005, with significant economic growth. So there now exists the declared intent, the human capital and the financial potential for considerably greater investment in research and development across the entire region. In addition, some 30 million people worldwide can trace their ancestry to this region.

Editorials in *Nature* (**441**, 1027, 2006) and *The Lancet* (**367**, 959, 2006) earlier this year have reviewed the prospects for international funding of regional research and for the restructuring of medical education and practice in response to the three United Nations Arab Human Development Reports, respectively. For recommendations to become reality, practical examples are needed that can be sustained, copied and amplified by the efforts of others. From this journal's perspective, an excellent example of such a seed is provided by the Centre for Arab Genomic Studies (CAGS: http://www.cags.org.ae/index.html) established in Dubai by the Sheikh Hamdan Bin Rashid Al Maktoum Award for Medical Sciences.

Ghazi O. Tadmouri and colleagues (*Nucl. Acids Res.* **34**, D601–D606, 2006) have assembled the CAGS database, CTGA, that at the time of that publication listed 692 phenotypes for some 235 genes that have been found to be mutated in people living in Arab countries. About a third of the genes responsible for these genetic conditions have not yet been identified, so even in its current state, the CTGA database indicates that the populations it covers constitute a considerable resource for understanding single-gene disorders. Another useful feature of the database is that it assembles links to a large number of regional English-language medical journals that may be unfamiliar to an international readership.

Close-kin marriage and large families are cultural factors in the Eastern Mediterranean region that have drawn the attention of geneticists; their implications increase as development progressively reduces the mortality resulting from poor childhood nutrition and infectious disease. Ahmad S. Teebi and Hatem I. El-Shanti (*Lancet* **367**, 970–971, 2006) estimate the rates of consanguinity (marriages between second cousins or more closely related family members) at between 20% and 70% in the Middle East excluding Israel and Cyprus. They estimate that a first-cousin couple has a twofold higher risk of a child with a major birth defect and also point out the utility of consanguineous pedigrees for homozygosity mapping of rare autosomal recessive disorders.

It is unlikely that consanguinity contributes significantly to polygenic or multifactorial diseases once socioeconomic variables have been controlled for. However, in light of the high, and increasing, prevalence of cardiovascular diseases and diabetes with economic development in the region, it is important to consider the genetic component of common and complex diseases. The existence of diverse highly localized populations suggests that genetic characterization of a range of populations within the region would be particularly rewarding in this respect. Indeed, in much of the rest of the world it is very hard to make sense of population structure because of migration, admixture or lack of historical records.

The Arab world, possessing its own funding sources, geneticists and particular populations, is well placed to be a leader in demonstrating the type of cooperation between resource-rich and less well resourced countries that will characterize the next phase of human genomics, exemplified by the Human Variome Project (http://www.humanvariomeproject.org/). There is much that can be done to build the impetus provided by CAGS, to coordinate clinical genetic reporting and to disseminate existing genetic knowledge within the context of improving literacy and educational opportunity, particularly for women.

An "Eastern Mediterranean Variome Project" would build upon the sense of common purpose inherent in these distinctive populations and provide an appreciation of their place in the history of the human population. The knowledge gained could be immediately used to address urgent health needs. It would also offer an opportunity to promote education and knowledge drawing upon local examples, constructive engagement of global research efforts in human health from a position of strength, and opportunities to build sustainable post-petroleum economic activity based upon education and the improvement of human health. ■