In this issue

How many HIV positives in India by 2016: A statistical projection

Of the many recent agents of human misery, the AIDS virus is probably the most powerful. Apart from the high mortality rate due to the virus itself, the social stigma associated with the disease greatly magnifies the trauma. Less conspicuously but more dangerously, the weakened immune response of the victim makes it an ideal host for a lot of other pathogens, which may in turn spread into the general population. Fortunately, there is increasing awareness both about the magnitude of the problem, and about the urgency of making all-out efforts on many fronts to contain the threat to manageable proportions. However, for devising any concrete action plan, it is essential to have realistic estimates of the expected number of HIV positive cases in the years to come. C. Nagaraja Rao and T. Srivenkataramana describe a practical and robust method of obtaining these estimates on **page 1302** of this issue, wherein they have suggested a judicious and optimal use of the data collected under the existing HIV/AIDS sentinel surveillance system.

As pointed out by the authors, the approach generally used for making such estimates relies on the back-calculation method. Though based on sound theoretical foundations, the application of this method requires a model for the distribution of infections, a knowledge of the distribution of incubation periods and the observed counts of AIDS cases over time. Unfortunately, for a country as large and diverse as India, many of these key parameters are bound to vary considerably from place to place, and amongst different socioeconomic groups. More importantly, both due to the confidentiality issues associated with HIV in particular and due to poor record keeping practices in general, the critical information necessary for using the back-calculation method is simply not available.

Nagaraja Rao and Srivenkataramana have neatly circumvented these limitations by making use of the existing seropositivity data, collected under the HIV/AIDS sentinel surveillance system for the last many years. Under this program, blood samples from high and low risk groups, obtained from many clinics in the country, are screened for HIV, and the results are expressed as seropositivity rates – numbers infected per 1000 individuals. Though the first AIDS case was detected in India in 1986, the seroprevalence figures are available for every year from 1989 onwards (and have climbed up from a value of 4.9 in 1989 to an alarmingly high 29.0 in 2000). The authors have successfully used (and validated) a power-law relationship between time and the seroprevalence rates. They have also described how one can make allowance for the heterogeneity of the population (e.g., males are twice as likely as females to be HIV positive, urbanites are thrice as likely compared to the rural people, etc.) while using their approach for making statistical projections for the country as a whole. Though the authors have been rather candid about the possible limitations of the method (and have suggested ways of obtaining more accurate projections), their findings are quite shocking. Within the next 15 years, the seropositivity rates are likely to increase threefold (from 29 per thousand to almost 90 per thousand). More alarmingly, almost one in every ten adult Indians is likely to be infected by HIV virus by the year 2016. For anyone wanting a more detailed picture of this frightening scenario, the article on **page 1302** of this issue is a must.

N. V. Joshi

Transcriptional regulation of fertility and repeat sequences

Earlier, repeat sequences were thought to be a redundant entity in the genome despite their conspicuous and sizeable presence. Subsequent genome analysis, however, has provided ample evidence on their biological roles in general and regulatory functions in particular. That GATA/GACA repeats transcribe in normal males, but not in the infertile ones, reported in a simple but exquisite study by Gangadharan *et al.* (**page 1320**) substantiate this view. Ever since their discovery, these repeats have been suspected to be involved in regulation of sex determination. However, direct evidence was never provided. The study by Gangadharan *et al.* seems to be the first one showing transcriptional breakdown of these sequences in the infertile animals. The GATA/GACA repeats could be part of several transcriptionally active ORFs present exclusively on the Y chromosome or the same may be shared by several critical genes on the autosomes involved in regulation of sex determination and perhaps spermatogenesis. It may be noted that spermatogenesis involves more than thousand genes and a sizable number of them may harbour different types of repeat elements. In a wide spectrum of molecular events leading to sex determination and spermatogenesis, critical regulatory roles of the repeat elements may be ascertained employing the present approach. Therefore, this work has much wider ramification, providing impetus to systematically isolate and characterize genes having different types of repeat motifs as part of their ORFs. This would also enable to assess overall number of such genes and prioritization of their tissue and stage-specific expression.

S. E. Hasnain