

Vaccine to cope with viral diversity in HIV

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The ability of HIV-1 to develop high levels of genetic diversity and acquire mutations to escape immune pressures contributes to our difficulties in producing a vaccine. David Nickle et al present here an efficient algorithm to develop vaccines that cope with the diversity of HIV or other variable pathogens.

This computational method clarifies and analyzes the variation found in the strains of the virus by describing the molecules which stimulate the immune response to HIV (immunogens) that have multiple forms of variable elements of the virus. These antigens compress the variation found in many viral strains into lengths suitable for vaccine immunogens. "We can capture 62% of the variation found in the Nef protein and 81% of the variation in the Gag protein into immunogens of three gene lengths", says Nickle.

These short-length immunogens are potentially useable in a vaccine, as they reflect the diversity of features in HIV-1 strains. These immunogens should elicit immune responses against high frequency viral strains as well as against most mutant forms of the virus.

Source: Public Library of Science

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