HIV strains and types

KEY POINTS

- There are two main types of HIV – HIV-1 (the most common) and HIV-2 (relatively uncommon and less infectious).
- Like many viruses, HIV has the ability to mutate and change over time - within the main types of HIV there are many genetically distinct subgroups.
- Tests to diagnose HIV and monitor the level of virus in the body that are sensitive to the full range of subtypes (and to group O and HIV-2) do exist, but may not be readily available in all settings.

Explore this page to find out more about HIV-1 and HIV-2, groups within HIV-1, subtypes within HIV-1, and whether differences in subtypes matter.

HIV-1 and HIV-2

HIV-1 and HIV-2 are two distinct viruses. Although tests which are sensitive to both types of viruses are widely available, only one antibody test currently available can specifically distinguish between antibodies to HIV-1 or HIV-2.

Worldwide, the predominant virus is HIV-1. HIV-1 accounts for around 95% of all infections worldwide. HIV-2 is estimated to be more than 55% genetically distinct from HIV-1.1

The relatively uncommon HIV-2 virus is concentrated in West Africa but has been seen in other countries with links to West Africa. It is less infectious and progresses more slowly than HIV-1,
resulting in fewer deaths. However, without treatment, most people living with HIV-2 will eventually progress to AIDS and die from the disease.  

While many commonly used antiretroviral drugs are active against HIV-2, non-nucleoside reverse transcriptase inhibitors (NNRTIs) like nevirapine and efavirenz do not work against it. The best way to treat HIV-2 has been less clearly defined than HIV-1. 

Groups within HIV-1

HIV Types and Strains

The strains of HIV-1 can be classified into four groups. Of these, M is the ‘major’ group and is responsible for the majority of the global HIV epidemic. The other three groups - N, O and P - are quite uncommon. Group O represents up to 5% of infections in several west and central African countries, and Group N and P have been rarely identified in Cameroon. All groups can be detected by HIV-1 antibody tests.

Subtypes within HIV-1 group M

Within group M there are known to be at least nine genetically distinct subtypes of HIV-1. These are subtypes A, B, C, D, F, G, H, J and K.

Additionally, different subtypes can combine genetic material to form a hybrid virus, known as a ‘circulating recombinant form’ (CRFs). Around 89 of these are known to exist.

The dominant HIV subtype in the Americas, Western Europe and Australasia is subtype B. As a result, the great majority of HIV clinical research has been conducted in populations where subtype B predominates, despite this subtype representing only 12% of global HIV infections.

In contrast, less research is available for subtype C, although nearly 50% of all people living with HIV have subtype C. It is very common in the high prevalence countries of Southern Africa, as well as in the horn of Africa and India.

The greatest diversity of subtypes is found in Cameroon and the Democratic Republic of Congo - the region where the HIV-1 epidemic originated. But migration and population mixing means geographical patterns in the distribution of subtypes are changing over time, and predicting transmission patterns in particular areas has also become more difficult.
Do differences in subtypes matter?

Some studies suggest that certain subtypes have a greater risk of transmission or faster disease progression than others - but more recent research suggests that this may not be the case. On the other hand, antiretroviral drugs (ARVs), although largely tested in people with subtype B, have generally proven to be effective against a wide range of subtypes (although there is conflicting evidence about the effectiveness of protease inhibitors against subtype C virus.

A more practical concern are the tests used to diagnose HIV and monitor the level of virus in the body (viral load). Tests that are sensitive to the full range of subtypes (and to group O and HIV-2) do exist but may not be readily available in all settings. This is a concern in places where diverse subtypes are prevalent.

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7. HIV sequence database (2017), ‘HIV Circulating Recombinant Forms (CRFs)’

Last full review:
25 January 2019
Next full review:
22 January 2022