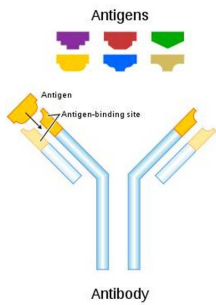


30 June 2009

By: Tudor Vieru, Science Editor



Each antibody binds only one specific antigen
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MIT Innovation Benefits Antibody Drugs

They could endure on the shelves for longer

Antibody drugs are among the most potent forms of medication that the world has ever seen, but their efficiency is counteracted by a built-in deficiency - the fact that the actual antibodies inside the drugs tend to clump together if they spend too much time on the shelves, causing them to become ineffective. Drug companies have been trying to work around this limitation for quite some time now, but it would appear that it's the private sector that gets the job done.

Researchers at the Massachusetts Institute of Technology (MIT), working together with experts from pharmaceutical company Novartis, have developed a method of understanding what exactly causes the antibodies to clump up.

There are currently two ways in which these drugs can be administered. The patients themselves can do it, but this requires small packages and higher concentrations, which have to be taken as soon after they are manufactured as possible, or doctors can. However, in the case of intravenous administration, with shots given by a physician, concentrations are regularly low, and this tends to cause instability within the antibodies, again forcing them to become less efficient.

But getting these drugs to work is fundamental to the development of modern medicine, considering that they have the potential to stop the spread or to cure cancer, arthritis and other chronic, inflammatory and infectious diseases.

At this point, there are some 200 such drugs undergoing clinical trials in other parts of the world, while a considerable number of them is already in public circulation. However, despite their relative wide spread, there is currently no cheap or effective way of addressing the issue of clumping in the early developmental stages of the drugs' design.

"Drugs are usually developed with the criteria of how effective they'll be, and how well they'll bind to whatever target they're supposed to bind. The problem is there are all of these issues down the line that were never taken into account," MIT team leader Bernhardt Trout, who is also a professor of chemical engineering at the Institute, says.

The researcher and his team, working together with Novartis expert Bernhard Helk, have developed a new computer model, which they hope will be able to predict exactly which part of the antibodies attracts other molecules.

If the model is successful, then pharmaceutical companies could theoretically modify the antibodies from the get-go, preventing clumping altogether. The model is described in the latest online issue of the journal Proceedings of the National Academy of Sciences (PNAS).