Host-Pathogen Interaction (Immunology)
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Lecture-64
Influenza Virus and Disease-2

Hi all, so in previous session I have discussed about the structure of influenza virus and I have discussed about the pandemic. And in this session we will discuss about the naming, this is one of very important thing. Since the influenza virus is huge number, so people need to adopt some naming system. We will also discuss people made an attempt how to create this influenza virus in laboratory in order to understand the pandemic potential of this 1918 virus, the 1918 strain, so I will discuss all those things.

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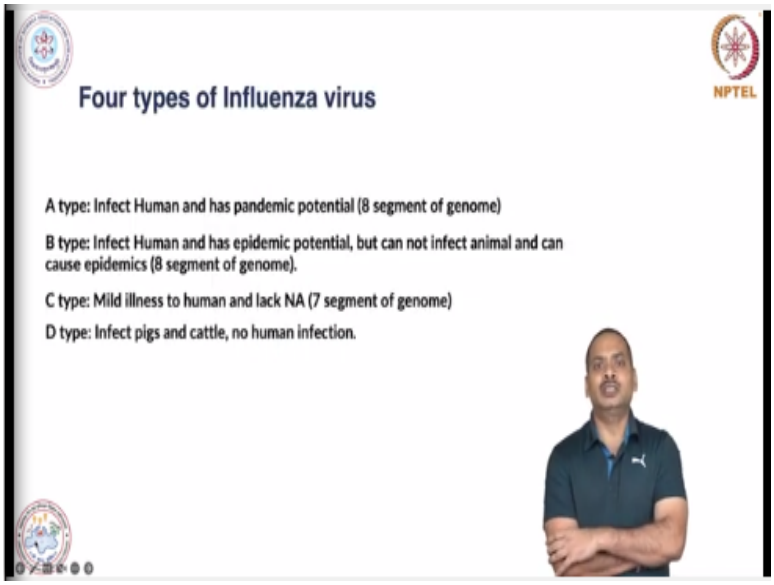

So, let us begin with the types of influenza virus, there are 4 types of influenza virus. The A type, A type basically infect human and has a pandemic potential, so A type is a most dangerous, so they can infect human and they can cause pandemic. And this A type is consists of 8 segments of genome as you have seen in a previous session. And another is B type, B type basically infect human and has epidemic potential, they have epidemic~~tome~~, they are not so dangerous.

Epidemic potential but cannot infect animal and can cause epidemic and this B type also has a 8 segments. Another is C type, C type is basically causes mild illness to human and lack neuraminidase enzyme and this lacks NA and therefore this has a only 7 genomic segment. The last is D type, so D type can infect pigs, cattles but this D type do not in fact human. So, these are the major type but as I told you there are so many kind of influenza virus, so there is a need of some naming system.

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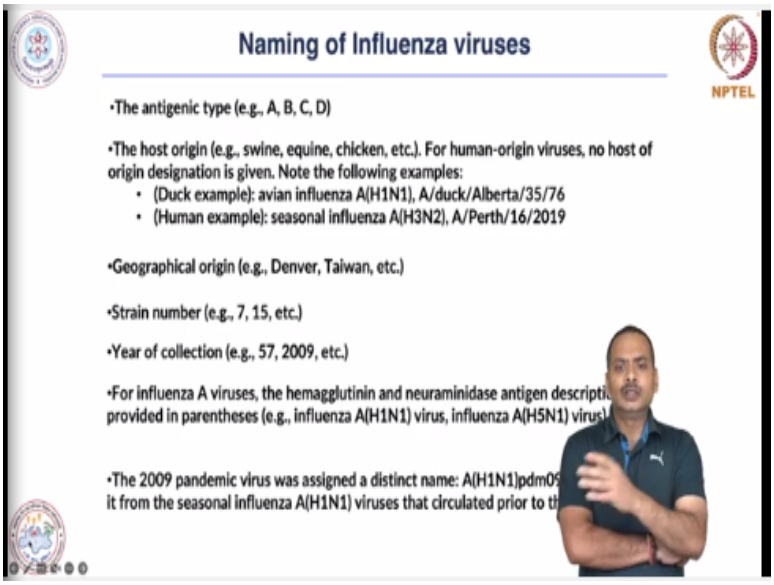

So, naming system of influenza is basically it is initiated with antigenic type like A, B, C, D, so they are antigenic type. The naming includes the host origin, host origin means if the virus is detected from pig then that is the host origin, the first detection, like pig, like horse, chicken. So, swine, equine and chicken, so these are the host origin, for human origin we generally do not write human, we just do not write any name for think we write swine for horse we will write equine.

If it is a human host then we do not write we just write A. So, here you can see there is example, so the virus originated from duck, so it is a avian Influenza A and you can see that A is written, A can infect the human and it is written duck. Another example, the human example it is a seasonal influenza A H3N2, so here is written but human is not written. So, you have seen that the type of influenza is written first the A, B, C, D then origin and then there will be geographical origin which part of the world it is originated.

If you see above the duck example that virus is originated from Alberta, so that is why Alberta is written, so geographical origin is written after the host origin. Then strain number, so strain number is nothing, it is order of discovery, this virus was discovered first, so that will receive first number, another influenza virus is discovered at 10th number, so we give the 10 number. Year of collection, when this sample was collected, so here you can see that 57, 2009 in above example there is a 76 written and 2019 is written, so year of collection is also included.

For influenza A virus the hemagglutinin HA and neuraminidase NA antigen description are also provided in bracket. Here you can see that influenza A H1N1 is written, so H1 and N1 is the hemagglutinin or N stand for neuraminidase. So, another example you can see that influenza A H5N1, so this is a numbering which number H is there, which number N is there, so that number is given H1N1, H5N1, H3N7 something like that.

In 2009 pandemic so after this pandemic the new naming system or some modification was done in this naming system. So, all those virus which caused the pandemic or which has a pandemic potential the letter and number was given that is PDM, PDM stand for pandemic and 09, here you can see there is example. To distinguish from this seasonal influenza virus, the viruses which have a pandemic potential they were given this PDM with number. And this is in order to distinguish between the virus which has a pandemic potential and compared to the virus which can cause seasonal flow.

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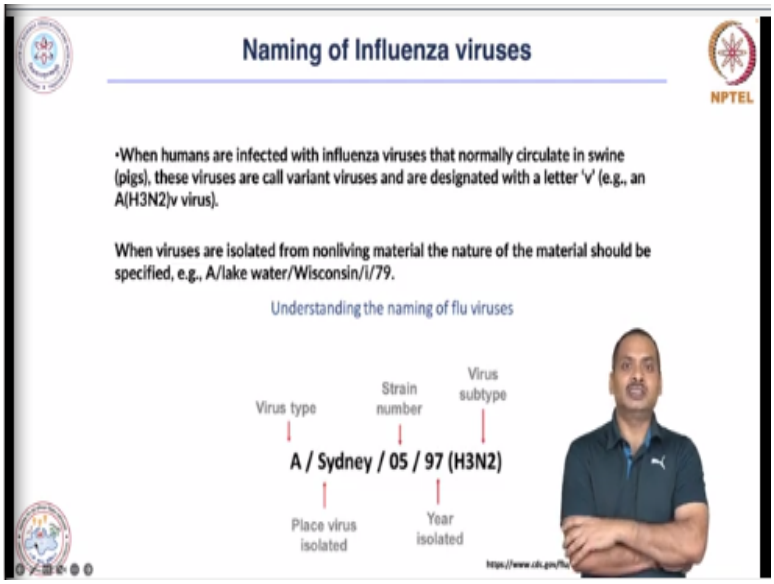

So, another is when human are infected with influenza virus that normally circulate in pigs and these viruses are called as a variant viruses and designated with a letter 'v'. Here you can see that there is an example A H3N2 v, so when you put the v then they are the variant and most likely they are present in that is pig. So, when viruses are isolated from non-living body, generally these viruses are present in a living host.

But when it is isolated from non-living places, for example the lake. So, in lake if you isolate the virus then we write it like the type of virus and lake water, here you can see there is example A/lake water/Wisconsin/i/79. So, here I have one example where you can see that A/Sydney/05/97/H3N2, so A stands for virus type and here you can see that after A the animal name is not given, it means this can infect the human.

It is isolated from Sydney that is why Sydney place of virus isolation is written, 05 is the strain number, 97 is the year of isolation, year isolated in this year it was isolated and H3N2 is a virus subtype. So, I hope you can understand this naming system because it is very much needed because we have a huge number of influenza virus in order to catalogue those viruses we have to have some appropriate naming system and here you can see that.

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Now I would again take you back to the 1918 Spanish Flu. So, there was a very much curiosity, why this virus caused so much in death at that time? So, there is a one very curious scientist who wanted to understand why it causes the so much death and his name is John Hultin. So, he at the age of 25 he decided to explore this thing why this virus caused so much death? And then he chose the site of mass grave, he went to the site where there is a mass grave of Brevig Mission, Alaska.

You can understand it is a frozen place; it is very cold, so here he went to John Hultin in 1951 at the age of 25. And he has excavated the places where the people are buried after this pandemic who are died by this pandemic.

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And here you can see that this John Hultin in 1951 at the age of 25, he went and he collected the samples.

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He performed some series of experiment in order to rescue that virus in order to isolate the virus but unfortunately he could not isolate any viable viral particle. Here you can see that this is I wrote it Hultin's fatal passion. He knows that this is a deadly virus but he is sucking using the mouth pipette. So, what I want to say that if it is alive then he can be infected and he may die but he has a huge passion in order to find out the virus.

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So, Hultin again he was not successful at that time but again John Hultin went to that site at the age of 72, from 25 to 72, he was a very persistent. Here I wrote his persistent fatal passion took him again to the site and again he tried because in that 46 years the technology was quite well developed but unfortunately he was not able to again isolate the virus.

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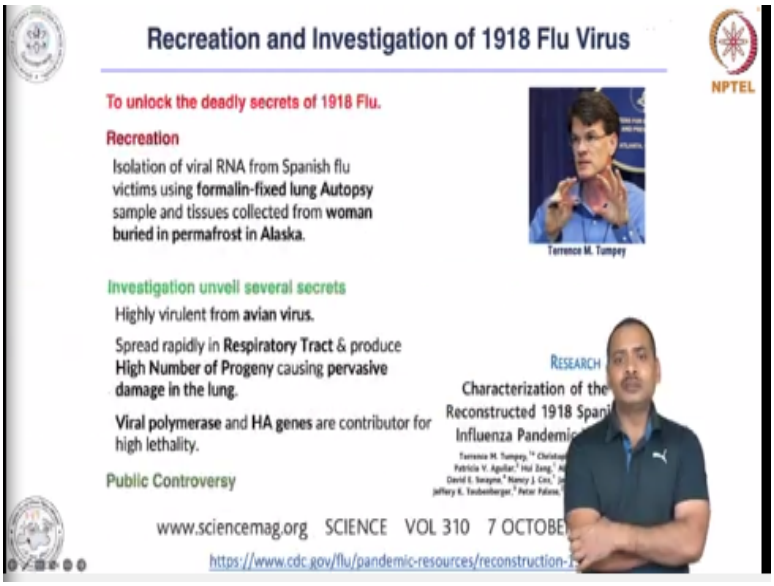

But he could help other here you can see that there is a group of M. Tumpey and with the help of genetic tools or molecular biology tool they can recreated the virus although there is a some contribution of John Hultin. But here you can see that his group can isolate the viral RNA from Spanish Flu victim using formally in fixed lung autopsy. So, there was some sample also kept

and from that sample the scientist could able to isolate the RNA molecule from a woman buried in the permafrost in Alaska.

You can you have seen from Alaska he went to the Alaska in order to rescue the virus. And finally this virus was recreated and investigation unveils several secrets of this 1918 Spanish Flu. So, they found out that this is a highly virulent avian virus came from birds, it is spread rapidly in the respiratory tract and produce high number of progeny causing permissive damage to the lungs, so that can create a massive damage in the lung.

And viral polymerase and HA gene are contributed for high lethality, that is the key factor which cause so much death. So, this work was very well done, everything is very good then they wanted to publish this work in scientific journals but there was a lot of public controversy, try to understand here the virus was recreated, it was recreated by scientific means. So, public controversy is that if this information, this recreation information or recreated virus somehow reached to the wrong people then they can create a biochemical weapon.

So, this public controversy was there and then this work was having a lot of resistance for publication. But on another hand there is another group of people they also said that if the scientific community knows this secret then they can be better prepared for future pandemic. So, eventually after long this battle this paper was published and this was published in science, here you can see that characterization of the reconstructed 1918 Spanish Flu influenza pandemic virus.

And here you can see that this work is published but in this work there is a no name of John Hultin, probably he was not one of key contributor maybe he has helped in one or another way, I do not know the real story.

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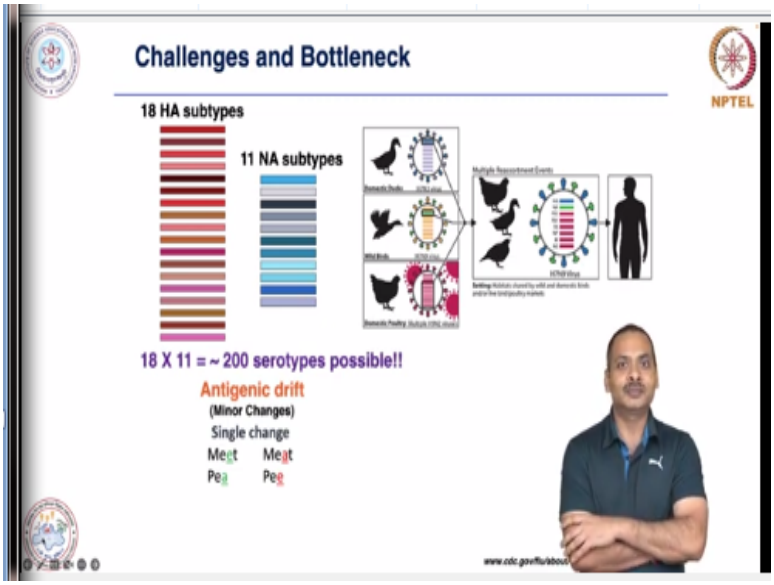

So, this is all about recreation of Spanish Flu, now I would like to discuss the challenges and bottleneck with influenza virus. So, as I told you there are so many kind of HA protein and so many kind of NA protein. And you have learned that this virus can this virus can infect different host and there is some host which can be infected by variety of influenza virus. So, if you take this as 18 HA and 11 NA then theoretically there is a possibility to create a 200 approximately 200 serotypes, and how it is created.

Here you can see, as I told you there are host which can be infected by different influenza virus. So, here you can see that there is a domestic duck, wild bird, domestic poultry they are having a different influenza virus and these influenza virus can also infect one host. And over there you can understand that when this host is infected with multiple influenza virus then there is a possibility of exchange of genomic segments.

And when this exchange of genomic segment will take place then there is a possibility of recreation of very dangerous virus which can infect human or which can cause pandemic. Actually all these things are happening by few simple phenomena which we call it as a antigenic drift. So, antigenic drift is simply it is a minor changes in the genome, here you can see there is a single change.

This single change meet change to the meat pea changed to the pee, so you can understand this word meaning is entirely changing pea, pea is that bean and pee is different, it is a process.

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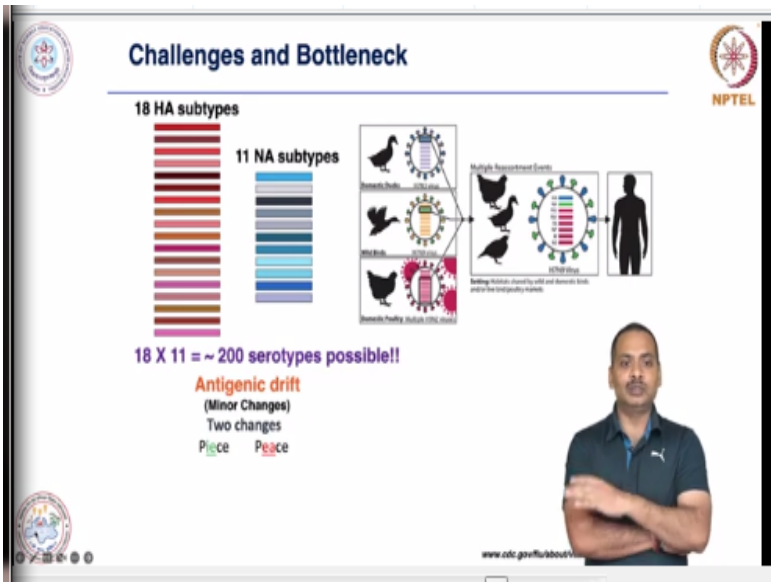

There could be a double changes, it is a 2 mutation kind of thing piece change to the peace.

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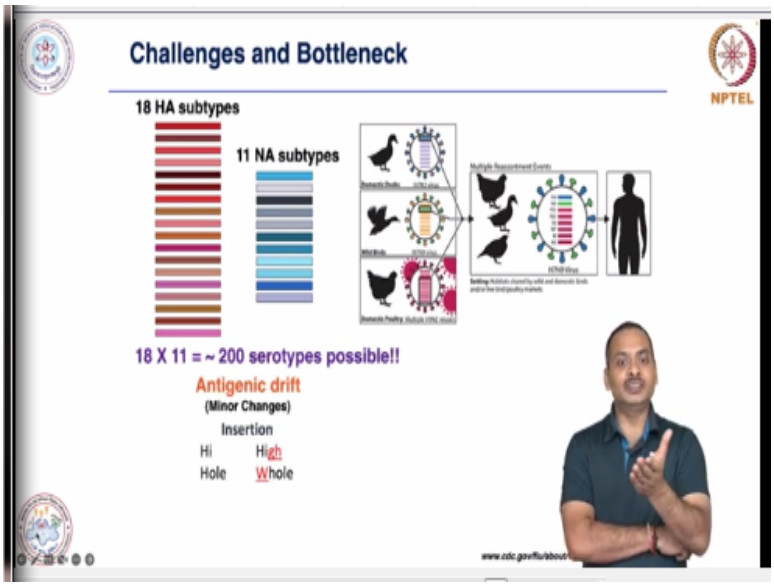

There could be an insertion hi change to the high, hole change to the whole.

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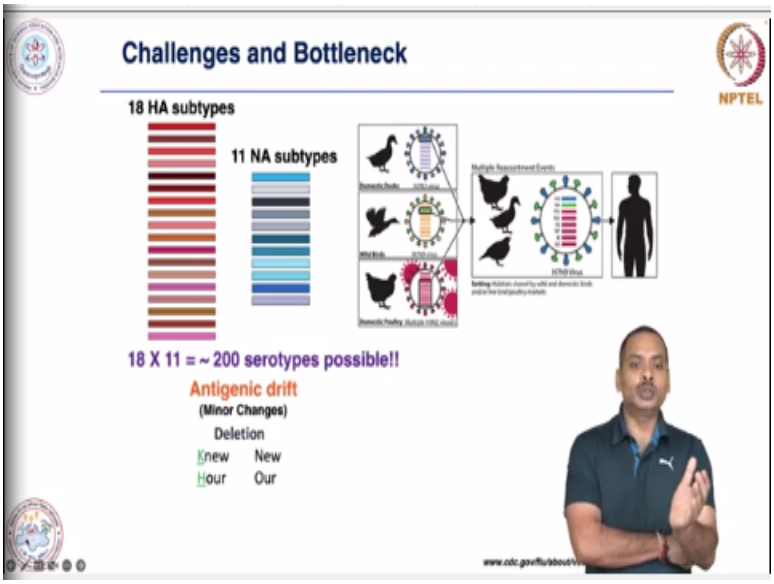

There could be a deletion, the knew can change to the new, k n e w, knew is different from n e w new, it is the same pronunciation but different word. So, I am just trying to give you the overview or perspective of this single change or double change or single addition or single deletion, how this change the word. So, similarly these small changes can change the polypeptide chain change in the viruses and that can create a highly pathogenic influenza virus.

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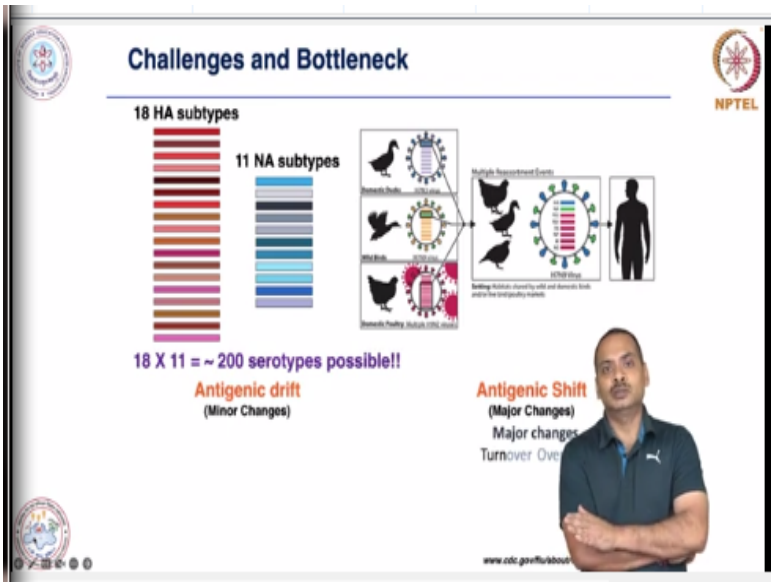

There could be a major change; major change like a turnover can change to the overturn.

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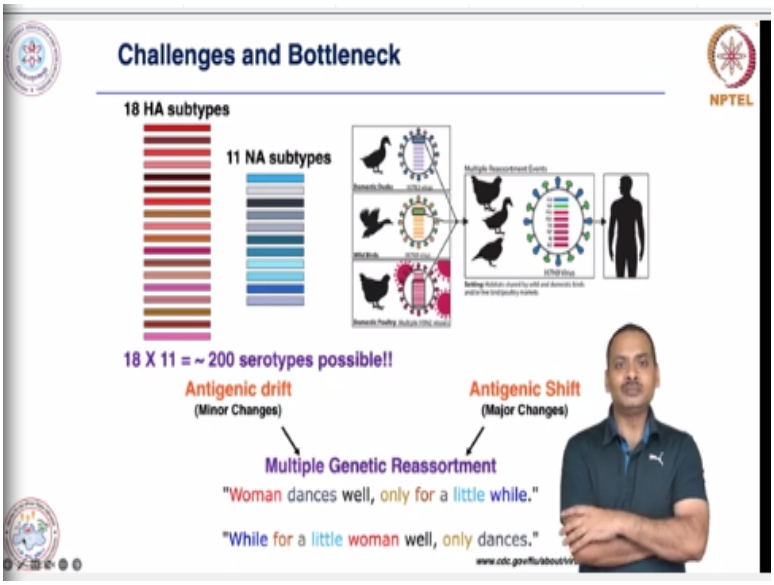

And all these changes basically can also be a much more bigger level, there is exchange of segments and that we call it as a multiple genetic reassortment. And this multiple genetic reassortment can be like that woman dances well, only for a little while, this sentence has these words. But they using the same word this whole meaning of sentence can be changed like while for a little woman well, only dances.

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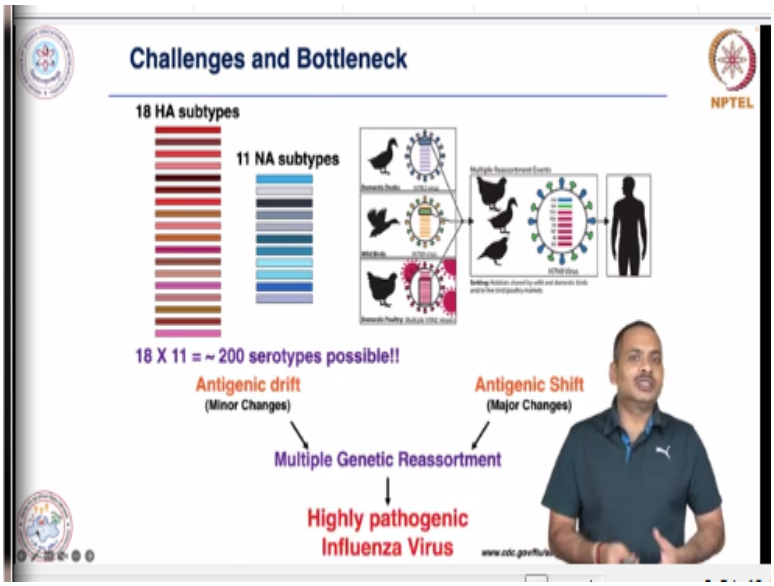

So, here I am just giving you a simple example in order to understand antigenic drift, antigenic shift and multiple genetic reassortment and all these things can result to the generation of highly pathogenic influenza virus. **(Video Starts: 22:01)** Here you can see this short video, where there

is a creation of a new virus. Here you can see different kinds of viruses came and then they are created. **(Video Ends: 22:22)** So, with this I will stop here and in next session I will again discuss more about the influenza virus what is the composition of this influenza virus and so on so forth, thank you.