Studi in silico pengaruh mutasi protein vp35 terhadap reaktivitas virus ebola di zaire = In silico mutation study of viral protein vp35 on zaire ebola virus / Tika Wulandari

Tika Wulandari, author

Abstrak

[Ebola adalah penyakit endemik yang telah terjadi selama tiga puluhan tahun setelah pertama kali ditemukan di daerah Afrika Barat pada tahun 1976. Penyakit ini disebabkan oleh virus ebola (EBOV) yang adalah salah satu bagian dari famili Filovoridae atau filovirus. Kasus ebola tidak dilaporkan secara intens, karena sifatnya yang endemik, namun tidak dapat dipungkiri, penyakit ini tetap memakan korban. Beberapa tahun terakhir, wabah ini merebak dan kembali menjadi pebincangan hangat. Penyebaran tersebut dikhawatirkan terjadi akibat adanya mutasi virus. Beberapa bagian lain mengkhawatirkan penggunaan virus tersebut dalam tindakan bioterorisme. Perkembangan virus dipengaruhi juga oleh proses replikasi, sehingga replikasi menjadi salah satu faktor penentu terjadinya penyakit. Pada ebola, replikasi dipengaruhi oleh protein VP35. Ilmu bioinformatika dianggap mampu menjadi salah satu cara menganalisis mutasi protein tersebut secara in silico, sehingga diharapkan para ilmuwan mampu menemukan desain inhibitor potensial untuk melawan ebola secara in vivo. Secara in silico telah diketahui perubahan yang terjadi pada VP35 virus ebola saat ini dibandingkan dengan yang ditemukan pertama kali pada tahun 1976. Perbedaan tersebut terjadi dalam hal susunan residu asam amino penyusun protein, terbukti dengan analisis pohon filogenetik, dan analisis lanjutan.
;Ebola is an endemic disease which has been happened about thirty years after its first discovered in West Africa at 1976. It caused by ebolavirus (EBOV), member of Filoviridae. The ebola cases were not intensely reported, because it’s endemic disease, but the it still causes many deaths. Lately, ebola has been the headline, since its outbreak in West Africa, March 2014, and caused more than 50% mortality. Replication is one of the virulence factor. In ebolavirus, VP35 plays role in replication system, so the in silico study of VP35 ebolavirus is required, before the in vivo. Using bioinformatics tools, the differences between the 1976’s ebolavirus and 2014’s ebolavirus has been discovered. The differences are analyzed using phylogenetic tree, and advanced analyzing.
;Ebola is an endemic disease which has been happened about thirty years after its first discovered in West Africa at 1976. It caused by ebolavirus (EBOV), member of Filoviridae. The ebola cases were not intensely reported, because it’s endemic disease, but the it still causes many deaths. Lately, ebola has been the headline, since its outbreak in West Africa, March 2014, and caused more than 50% mortality. Replication is one of the virulence factor. In ebolavirus, VP35 plays role in replication system, so the in silico study of VP35 ebolavirus is required, before the in vivo. Using bioinformatics tools, the differences between the 1976’s ebolavirus and 2014’s ebolavirus has been discovered. The differences are analyzed using phylogenetic tree, and advanced analyzing.
, Ebola is an endemic disease which has been happened about thirty years after its first discovered in West Africa at 1976. It caused by ebolavirus (EBOV), member of Filoviridae. The ebola cases were not intensely reported, because it’s endemic disease, but the it still causes many deaths. Lately, ebola has been the headline, since its outbreak in West Africa, March 2014, and caused more than 50% mortality. Replication

is one of the virulence factor. In ebolavirus, VP35 plays role in replication system, so the in silico study of VP35 ebolavirus is required, before the in vivo. Using bioinformatics tools, the differences between the 1976’s ebolavirus and 2014’s ebolavirus has been discovered. The differences are analyzed using phylogenetic tree, and advanced analyzing.
]