Question for written answer E-007015/2020
to the Commission
Rule 138
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Subject: SARS-CoV-2 mutation and vaccines

SARS-CoV-2 is an RNA virus, and mutations occur naturally as the virus replicates. Cases of a new variant of SARS-CoV-2 have been identified mainly in the south-east of England. Analysis of data on the virus genome sequence showed that a large number of cases belonged to a single new phylogenetic cluster. According to the ECDC report, the new variant of the virus is defined by multiple mutations of the virus's spike proteins (deletion of 69-70, deletion of 144, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H), as well as mutations in other genomic regions. One of the most significant mutations is the N501Y mutation in the spike protein, which the virus uses to bind to the human ACE2 receptor, which can theoretically lead to a change in this part of the spike protein resulting in the virus becoming more infectious and easier to spread among humans.

In the absence of phenotypic data on the new viral variant and the lack of data on the ability of newly developed and soon to be authorised vaccines to produce antibodies that can neutralise this particular viral variant, how does the Commission intend to obtain a greater knowledge base from vaccine manufacturers to address the growing concerns about the effective use of conditionally authorised vaccines in the context of viral mutation? To what extent will the trajectories of other potential mutations have a binding effect on the advance purchase agreement and production of future vaccines?