

## Genetic and epidemiological analysis of BRSV strains that circulate in the Wallonia region of Belgium

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Bovine respiratory syncytial virus (BRSV) is a virus belonging to the genus *Orthopneumovirus*, within the *Pneumoviridae* family (ICTV, 2020). BRSV is a major cause of bovine respiratory disease complex (BRD) as well as regular winter outbreaks of respiratory disease in cattle and is therefore responsible for important economic losses on the farming industry. The BRSV contains 11 viral proteins, among which the attachment glycoprotein (G). Displaying the highest reported mutation rate among BRSV strains, the G gene is commonly used as target during phylogenetic analysis and BRSV is classified to date into ten different subgroups (I to X). Recent studies achieved in different countries (Italy, Croatia and more recently Brasil and Japan) reported the circulation of new, genetically unique BRSV strains (groups VII to X) with mutations within essential immunodominant region. In this study, the genetic diversity of circulating BRSV strains in Belgium, which is unknown since end of 1990's, was investigated. Interestingly, our phylogenetic analyses revealed emergence and circulation of BRSV strains belonging to subgroup VIII, as observed elsewhere in Europe. The spatiotemporal distribution of BRSV isolates has been studied in different countries and should continue, as establishment of molecular surveillance of BRSV in different geographical regions can improve the identification of outbreaks, resulting in the implementation of preventive measures aimed to control the disease. Correlation between BRSV isolates circulating in Belgium and epidemiologic features like age, cattle breed, weather and geographical distribution has also been analysed here.