

## 2.2 Genotypes

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Pestiviruses

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As for the distinction of the two genotypes, BVDV-1 and BVDV-2, the region coding for the viral auto-protease Npro seems to be particularly well suited [30]. Other regions, too, have been used for genome analysis, for instance E2 (the most variable as well as the most important Pestivirus protein as far as the induction of neutralizing antibodies is concerned [31]), NS3 and 5'UTR (untranslated region, a highly conserved region). For a short time, the two genotypes were considered two separate species. These, in turn, are subdivided in subgenotypes or subgroups (BVDV-1a - k, BVDV-2a/b). Similarities

BVDV-1 and BVDV-2 have several features in common. Both BVDV-1 and BVDV-2 can trigger serious disease, the majority (70 -90 %) of the infections, however, are asymptomatic (i.e., differences in genetic structure do not account for virulence). Both genotypes occur as cytopathic as well as non-cytopathic biotypes. Non-cytopathic BVDVs of both genotypes can cause persistent infections.

Differences

BVDV-1 and BVDV-2 are antigenetically different; this has consequences for the production of vaccines - an effective vaccine should always contain both genotypes.

BVDV-1 is found more frequently than BVDV-2. It's the "classic" BVD pathogen, and as such it was the main constituent of the first vaccines. BVDV-2 was first isolated in 1981, but only in 1993, in the aftermath of a BVD outbreak in Ontario/Canada ("severe acute BVD") was the pathogen identified as BVDV-2.

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