

## Detecting KHV variants for vaccine development

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Koi herpesvirus infection (KHV-I) is a notifiable disease according to OIE (World Organisation for Animal Health) and EU. It causes high mortalities in aquaculture of *Cyprinus carpio* L. worldwide. While there are genetic variants among the causative agent KHV, it remains unknown how these different variants of KHV have evolved and how they spread among carp populations. Therefore, a phylogenetic method based on variable number of tandem repeats (VNTR) has been adapted to get a deeper insight into the global phylogeny of KHV. During the last two decades a considerable number of aquaculture facilities had to be closed due to KHV. By reason of this high economic impact of KHV-I, there is an urgent need of a safe vaccine in Germany. Using classical and molecular methods we are aiming at a safe and robust vaccine, which does not spread from animal to animal and which is easy to administer.

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