From mitochondrial markers to reference genomes: Evolutionary history of African and Arabian horned and sand vipers

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This thesis adds new knowledge to the evolutionary history of the genus *Cerastes*, a group of understudied venomous snakes highly adapted to the arid conditions of North Africa and Arabia. Using several genomic approaches, we disentangled new and unexpected evolutionary relationships within this group, contradicting previous evolutionary hypothesis based on morphology and mitochondrial markers. Then, we assembled one of the first high-quality chromosome-level reference genomes for true vipers, highlighting the absence of chromosomal rearrangements within vipers. Moreover, using RNA-seq and proteomics, we identified the main toxins in the venom of *C. gasperettii*, identifying their genomic location and comparing the gene copy number variation among venomous species. Using genomic data, we inferred several conservation genomic parameters for the genus *Cerastes* and unravelled how structural variance is an important mechanism driving venom variation in the main toxin families. Finally, we assessed the effectiveness of the genomic methods applied in this thesis and analysed their strengths and limitations in addressing both the study of venom and the evolutionary history of non-model species.