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Venom-gland transcriptome and venom proteome of the Malaysian king cobra (*Ophiophagus hannah*)

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King cobra (*Ophiophagus hannah*) is widely distributed and divergent throughout Asia. To elucidate the venom complexity of Malaysian species (MOH), venom gland was extracted from a 190-cm MOH (central-west Peninsula), 4 days post-venom milking. Venom-gland transcriptome was investigated with Illumina HiSeq™ platform; proteome was profiled using in-gel-nano-ESI-LCMS/MS. Transcriptomic result reveals high redundancy of toxin transcripts (3578.82 FPKM/transcript) despite small cluster number, implying gene duplication of restricted protein families in the accelerated MOH-venom evolution. Twenty-three toxin families were identified; three-finger toxins (3FTXs) and snake-venom metalloproteases (SVMPs) genes are the most diversified. The relative gene abundances decreases from 3FTXs, SVMPs, phospholipases A_2, cysteine-rich secretory proteins (CRiSPs), kunitz-type inhibitors, L-amino oxidases (LAOs) to >10 low-abundance genes. The toxin abundance estimated through transcriptome generally correlates with the proteomic findings based on protein families (r^2=0.968). The proteome reveals 3 long-chain neurotoxin, 2 short-chain neurotoxin and 2 non-conventional 3FTXs identified through mapping to 14 unique 3FTX transcripts, categorised based on the number and position of disulphide bonds. The venom proteome also reveals substantial SVMP, CRiSP, LAOs, vespryn etc. typically little or lacking in cobras (*Naja*), indicating their possible role in the ophiophagic behaviour of king cobra that preys on neurotoxin-resistant species. This is the first report on toxin abundances and variations based on both venom-gland transcriptome and venom-proteome of a Malaysian *Ophiophagus hannah*, providing insights into venom diversity of different localities. The findings may explain the low cross-neutralising potency of regional cobra-antivenom against MOH, and serve to optimise the design of a pan-regional broad-spectrum antivenom.