

Characterization of 17 novel microsatellite loci in the Nile monitor (*Varanus niloticus*)
via 454 pyrosequencing

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Supplementary Material

Supplementary Table S1. Results of BLASTn searches of NCBI's 'nucleotide collection (nr/nt)' database using microsatellite containing 454 fragments as queries.

Query	Locus	Best hit accession ID	Best hit description	Alignment length (bp)	% identity	Bit score	E-value
HN7TS9H02DQAES	<i>Mon1</i>	AC154274	<i>Mus musculus</i> BAC clone RP24-298J16 from 17, complete seq.	70	84.0	73.4	5.0×10^{-9}
HN7TS9H02ELQ4D	<i>Mon2</i>	No significant hits	N/A	N/A	N/A	N/A	N/A
HN7TS9H02DEI2X	<i>Mon3</i>	No significant hits	N/A	N/A	N/A	N/A	N/A
HMEZZP203GE0BW	<i>Mon4</i>	No significant hits	N/A	N/A	N/A	N/A	N/A
HN7TS9H03GN69L	<i>Mon6</i>	No significant hits	N/A	N/A	N/A	N/A	N/A
HMEZZP203FKADE	<i>Mon8</i>	No significant hits	N/A	N/A	N/A	N/A	N/A
HMEZZP203GSD5W	<i>Mon9</i>	No significant hits	N/A	N/A	N/A	N/A	N/A
HN7TS9H03GXHKZ	<i>Mon10</i>	No significant hits	N/A	N/A	N/A	N/A	N/A
HN7TS9H03GPPOC	<i>Mon12</i>	HQ896229	<i>Varanus salvator</i> clone JX14 microsatellite sequence	185	87.0	233.1	3.5×10^{-54}
HN7TS9H03HA3NZ	<i>Mon13</i>	No significant hits	N/A	N/A	N/A	N/A	N/A
HN7TS9H02EIY13	<i>Mon14</i>	No significant hits	N/A	N/A	N/A	N/A	N/A
HN7TS9H02DDL5H	<i>Mon15</i>	No significant hits	N/A	N/A	N/A	N/A	N/A
HN7TS9H02DPRRL	<i>Mon16</i>	CR394571*	Zebrafish DNA seq. from clone CH211-180M12 in link. group 21	43	100.0	78.8	8.6×10^{-11}
HN7TS9H02C6YMJ	<i>Mon17</i>	LK064835	<i>Apteryx australis mantelli</i> genome assem. AptMant0 scaffold 233	110	85.0	138.0	8.5×10^{-25}
HN7TS9H02DG8XH	<i>Mon18</i>	No significant hits	N/A	N/A	N/A	N/A	N/A
HN7TS9H02DDW8V	<i>Mon19</i>	JX038444	<i>Micrurus fulvius</i> clone FQ6DGU405F3RTD microsatellite seq.	79	87.0	91.5	2.1×10^{-14}
HN7TS9H02EVHLU	<i>Mon20</i>	XM_003216189	PREDICTED: <i>Anolis carolinensis</i> follistatin, transcript variant X1	127	74.0	88.0	3.5×10^{-11}

N/A = not applicable

* = Alignment nearly entirely corresponds to microsatellite repeat region proper and is therefore unlikely to be of biological significance

Supplementary Data File 1: Zip archive containing FASTA files of the 454 sequences generated during the course of our study.

Supplementary Data File 2: Excel spreadsheet containing the primers associated with the potentially amplifiable loci identified during the course of our study.