TECHNICAL NOTE

## Buccal swabbing as a source of DNA from squamate reptiles

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Received: 8 October 2007 / Accepted: 6 November 2007 © Springer Science+Business Media B.V. 2007

**Abstract** Buccal swabbing was compared with other tissues as a source of DNA for microsatellite genotyping from two squamate reptiles. For both species, the lizard *Lacerta agilis* and the snake *Coronella austriaca*, buccal swabbing proved more reliable than tissues including tail tips, toe clips and ventral scale clips.

Keywords Lizard · Snake · Microsatellites

Buccal swabbing has become a routine non-invasive technique for the DNA sampling of many species including amphibians (Pidancier et al. 2003; Broquet 2007), chelonian reptiles (Poschadel and Moller 2004) and the tuatara (Miller 2006). I investigated whether buccal swabbing provides a reliable source of DNA from sand lizards *Lacerta agilis* and smooth snakes *Coronella austriaca*, two rare reptiles in Britain (Beebee and Griffiths 2000), and compared it with relatively invasive methods.

Ten lizards and 10 snakes provided the samples. Toetips from a hind foot were taken using sharp scissors from five lizards, and 10 mm tail tips were gently broken off from the remaining five. Pieces of ventral scale (c. 4 mm<sup>2</sup>) were cut from five snakes, and 10 mm tail tips were cut from the other five. All animals were also buccal-swabbed using BuccalAmp<sup>TM</sup> extraction kits (Cambio, Cambridge, UK), as prescribed by the manufacturer. Each animal was allowed to bite/chew on the swab for about 1 min, after which the swabs were briefly air-dried. All samples were

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DNA was obtained from the various tissues using a standard proteinase K digestion and phenol/chloroform extraction procedure. Swabs were extracted according to the manufacturer's instructions. Approximately 100 ng of DNA from the tissue samples, and 4  $\mu$ l of swab extract DNA, were used in PCRs of final volumes 20  $\mu$ l or 40  $\mu$ l respectively. For *L. agilis*, primers the eight microsatellite loci *La-1, La-2, La-3, La-4, La-5, La-8, La-9* and *La-10* were used (Gullberg et al. 1997); For *C. austriaca*, the eight microsatellite loci *Ca16, Ca19, Ca20, Ca26, Ca30, Ca40, Ca45* and *Ca47* were used (Bond et al. 2005). Genotypes were analysed as described elsewhere (Rowe et al. 1997). In the event of failure to obtain a genotype on the first attempt, a second attempt was always made.

Table 1 summarises the results. Lizard toe clips were significantly more successful than tail tips (Wilcoxon signed rank test, WSRT, two-tailed exact P = 0.031). There was no significant difference in the success rates of snake scale clips and tail tips (WSRT, P = 0.688). However, for both species buccal swabbing was by far the most successful method. For the lizard, buccal swabbing generated 68 genotypes (85% of the possible total of 80) compared with the tissue methods (combined) that yielded 41 genotypes (51% success), a highly significant difference (WSRT, P = 0.008). For the snake, buccal swabbing generated 73 genotypes (91% success) whereas the combined tissues generated 55 genotypes (69% success), again a highly significant difference (WSRT, P = 0.016).

In the lizard, there were no significant differences among the loci but highly significant differences (Kruskal–Wallis ANOVA, KWA, P < 0.001) among individuals. In the snake, there were differences among loci (KWA, P = 0.043) because one locus, *Ca16*, worked very poorly for tissue

Locus	La-1	La-2	La-3	La-4	La-5	La-8	La-9	La-10
L. agilis								
Tail tip (/5)	1	2	3	3	1	2	3	2
Toe clip(/5)	2	3	3	4	3	3	3	3
Total: tip + clip (/10)	3	5	6	7	4	5	6	5
Buccal swab (/10)	9	9	9	9	9	8	9	6
Locus	Cal6	Ca19	Ca20	Ca26	Ca30	Ca40	Ca45	Ca47
C. austriaca								
Tail tip (/5)	2	2	4	5	4	4	3	3
Scale clip(/5)	0	4	4	3	5	4	5	4
Total: tip + clip (/10)	2	6	8	8	9	8	8	7
Buccal swab (/10)	8	10	9	9	10	10	8	9

 Table 1 Summary of genotyping results

Numbers are of successful genotypes obtained after up to two attempts

samples. There were also differences among individuals (KWA, P = 0.016).

Observed heterozygosity averaged 0.561 in the lizard tissue samples and 0.588 in the lizard buccal extracts. For the snake, the values were 0.473 (tissue) and 0.507 (buccal). Genotypes agreed well between tissue and buccal DNA samples, with only four differences in the lizard and two in the snake.

Buccal swabbing therefore worked well as a technique for producing PCR-quality DNA in both the reptiles studied here. Tissue extracts obtained by more destructive methods were less satisfactory, perhaps because contaminants interfered with the PCR. Buccal swabbing was easy to do (all specimens of both species were easily induced to chew on the swabs), produced no obvious signs of stress or tissue damage, and yielded good results. It seems likely that buccal swabbing will prove a good method for obtaining DNA from many species of squamate reptiles.

Acknowledgements Many thanks M. Beebee for sampling assistance, to Dave Bird, and to Nick Moulton of the Herpetological Conservation Trust (HCT), for their help in obtaining specimens and to the British Ecological Society for financial support. All this work was under licence from Natural England and the UK Home Office.

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