

SUPPLEMENTARY MATERIAL

Multilocus coalescent species delimitation reveals widespread cryptic differentiation among Drakensberg mountain-living freshwater crabs (Decapoda : *Potamonautes*)*Ethel Emmarantia Phiri^A and Savel Regan Daniels^{A,B}*^ADepartment of Botany and Zoology, Stellenbosch University, Private Bag X1, Matieland 7602, South Africa.^BCorresponding author. Email: srd@sun.ac.za

Table S1. The molecular markers and primer pairs used in this study with their respective polymerase chain reaction conditions. Temperatures in bold under PCR profile indicate the annealing temperatures. The final extension was at 72 °C for 10 minutes (7 min. for DecapANT). * Protein coding. ** Exon-priming, intron-crossing

| Molecular markers | Product size (pb) | PCR | Primer sequence (5'-3' direction) | PCR profile | Reference |
|-------------------------------|-------------------|------------------------|--|--|--------------------------------|
| Mitochondrial (mt) | | | | | |
| 12S rRNA | 353 | 12Sai 12Sb | AAACTAGGATTAGATACCCTATTAT GAGAGTGACGGGCGATGTGT | 95 °C (5 min.), [95 °C (30 s), 50 °C (40 s), 72 °C (1 min.)] x 34 | Kocher <i>et al.</i> , (1989) |
| 16S rRNA | 536 | 16Sa-1471 16Sb-1472 | ACTTGATATATAATTAAGGGCCG CTGGCGCCGCTCTGAACTCAAATC | 95 °C (5 min.), [95 °C (30 s), 50 °C (40 s), 72 °C (1 min.)] x 34 | Palumbi <i>et al.</i> , (1991) |
| *Cytochrome oxidase subunit I | 625 | LCOI-1490 HCOI-2198 | GGTCAACAAATCATAAAGATATTG TAAACTTCAGGGTGACCAAAAAATCA | 94 °C (4 min.), [94 °C (30 s), 42 °C (40 s), 72 °C (45 s)] x 36 | Folmer <i>et al.</i> , (1994) |

Nuclear (nu)

| | | | | | | |
|---------------------------------------|-----|--------------------------|---|------|---|---|
| 28S rRNA | 620 | 28Sa-modified 28Sb | GACCCGTCTTGAARCACGGA GAAGGAACCAGCTAC | TCG- | 94 °C (4 min.), [94 °C (45 s), 50 °C (1 min.), 72 °C (1 min.)] x 40 | Jesse <i>et al.</i> , (2010) |
| **Adenine nucleotide transporter | 455 | DecapANT-F DecapANT-R | CCTCTTGAYTTTCGCKCGAAC TCATCATGCGCCTACGCAC | | 94 °C (3 min.), [94 °C (30 s), 60 °C (30 s), 72 °C (30 s)] x 35 | Teske & Beheregaray, (2009); Teske <i>et al.</i> , (2009) |
| *Phosphoenolpyruvate carboxykinase | 493 | PEPCK-for PEPCK-rev | GTAGGTGACGACATTGACYTG- GATGAAGAACCAGTTGACGTGGAA- GATC | | 94 °C (3 min.), [94 °C (30 s), 60 °C (45 s), 72 °C (1 min. 30 s)] x 35 | Tsang <i>et al.</i> , (2008) |

Table S2. Model parameters for each locus used in this study, where (a) represents the best-fit model for the Bayesian analyses as obtained in jModelTest v. 2.1.3 and (b) is nucleotide substitution models as obtained in MEGA5 v. 2.2 (* for Maximum Likelihood analyses only, obtained from MEGA 5 v. 2.2)

| Gene fragment | Model | Base pair frequencies (%) | Gamma (G) distribution parameter | Proportion invariable (I) sites |
|---------------|---|--|----------------------------------|---------------------------------|
| 12S rRNA | (a) TPM3uf + G (nst = 6; -lnL = 879.95; AIC = 1975.91) | A = 36.98 C = 8.63 G = 18.35 T = 36.04 | 0.013 | N/A |
| | (b) T92 + I; -ln L = 899.90; AIC = 2009.10) | A = 36.12 C = 13.88 G = 13.88 T = 36.12 | N/A | 0.779 |
| 16S rRNA | (a) TPM2uf + G (nst = 6; -lnL = 1722.17; AIC = 3660.35) | A = 37.32 C = 9.50 G = 16.39 T = 36.79 | 0.208 | N/A |

| | | | | |
|----------|--|--|-------|-------|
| | (b) TN93 + I; $-\ln L = 1741.12$; AIC = 3697.10) | A = 37.70 C = 9.90 G = 17.0 T = 35.4 | N/A | 0.660 |
| COI | (a) TIM2 + G + I (nst = 6; $-\ln L = 2446.72$; AIC = 5113.44) | A = 28.81 C = 19.05 G = 15.30 T = 36.84 | 1.095 | 0.603 |
| | (b) TN93 + G + I ($-\ln L = 2463.18$; AIC = 5143.11) | A = 29.30 C = 19.30 G = 15.80 T = 35.60 | 0.720 | 0.570 |
| 28S rRNA | (a) TIM3 + G (nst = 6; $-\ln L = 1263.51$; AIC = 2745.01) | A = 14.95 C = 31.15 G = 34.89 T = 19.02 | 0.157 | N/A |
| | (b) T92 ($-\ln L = 1286.30$; AIC = 2779.40) | A = 16.89 C = 33.11 G = 33.11 T = 16.89 | N/A | N/A |
| DecapANT | (a) TPM2uf + G (nst = 6; $-\ln L = 844.78$; AIC = 1903.556) | A = 23.34 C = 20.82 G = 26.24 T = 29.60 | N/A | N/A |
| | (b) K2 ($-\ln L = 849.85$; AICc = 1904.80) | A = 25.00 C = 25.00 G = 25.00 | N/A | N/A |

| | | | | |
|------------------|--|---|-------|-------|
| PEPCK | (a) HKY + G + I (nst = 2; -lnL = 1059.05; AIC = 2334.09) | T = 25.00 A = 19.51 C = 35.73 G = 27.99 | 0.396 | 0.824 |
| | (b) T92 + G + I (-lnL = 1261.09; AIC = 2733.11) | T = 16.77 A = 18.20 C = 31.80 G = 31.80 T = 18.20 | 3.590 | 0.930 |
| *cmtDNA | T92 + G (-lnL = 5220.92; AIC = 10642.13) | A = 34.67 C = 15.33 G = 15.33 T = 34.67 | 0.129 | N/A |
| *cnuDNA | T92 + G + I (-lnL = 3677.55; AIC = 7565.40) | A = 19.80 C = 30.20 G = 30.20 T = 19.80 | 0.430 | 0.830 |
| *cmtDNA + cnuDNA | T92 + G + I (-lnL = 10430.85; AIC = 21071.84) | A = 27.30 C = 22.70 G = 22.70 T = 27.30 | 0.760 | 0.750 |
