

Fig.6 Sequence analysis of Cytochrome b (cytb) of LAH2 and LAH3 (The region of cytb to distinguish subspecies of Pelophylax in Fig.4)

- ①cytb sequence of *Pelophylax nigromaculatus* <https://www.ncbi.nlm.nih.gov/nuccore/KT878718.1>
- ②RCB1735 LAH2 Lot.1 :Result of distributed LAH2 cells (Lot.1): deposited as *Pelophylax nigromaculatus* origin
- ③RCB1735 LAH2 TK :Result of LAH2 cells immediately after deposition
- ④RCB1734 LAH3 Lot.1 :Result of distributed LAH3 cells (Lot.1): deposited as *Pelophylax porosus brevipodus* origin
- ⑤RCB1734 LAH3 TK :Result of LAH3 cells immediately after deposition
- ⑥cytb sequence of *Pelophylax porosus brevipodus* <https://www.ncbi.nlm.nih.gov/nuccore/AB980777.1>

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① 1 CCTCCTCGGAGTCTGCTTAATTGCTCAAATCGCCACCGGCTTATTCCTAGCCATGCACATAACAGCCGATACATCCCGTGCATTTCATCTATTGCCCATATCTGCCGAGAGTTAATAACGGTTGACTCCTACGAAACCTTCATGCCAA 150
② 1 CCTCCTCGGGGTCTGCTTAATTGCTCAAATCGCCACCGGCTTATTCCTAGCCATGCACATACACAGCCGACACATCCCTTGCATTTTCATCTATTGCCCATATCTGCCGAGACGTTAATAACGGTTGACTCCTACGAAACCTTCATGCCAA 150
③ 1 CCTCCTCGGGGTCTGCTTAATTGCTCAAATCGCCACCGGCTTATTCCTAGCCATGCACATACACAGCCGACACATCCCTTGCATTTTCATCTATTGCCCATATCTGCCGAGACGTTAATAACGGTTGACTCCTACGAAACCTTCATGCCAA 150
④ 1 CCTCCTCGGGGTCTGCTTAATTGCTCAAATCGCCACCGGCTTATTCCTAGCCATGCACATACACAGCCGACACATCCCTTGCATTTTCATCTATTGCCCATATCTGCCGAGACGTTAATAACGGTTGACTCCTACGAAACCTTCATGCCAA 150
⑤ 1 CCTCCTCGGGGTCTGCTTAATTGCTCAAATCGCCACCGGCTTATTCCTAGCCATGCACATACACAGCCGACACATCCCTTGCATTTTCATCTATTGCCCATATCTGCCGAGACGTTAATAACGGTTGACTCCTACGAAACCTTCATGCCAA 150
⑥ 1 CCTCCTCGGGGTCTGCTTAATTGCTCAAATCGCCACCGGCTTATTCCTAGCCATGCACATACACAGCCGACACATCCCTTGCATTTTCATCTATTGCCCATATCTGCCGAGACGTTAATAACGGTTGACTCCTACGAAACCTTCATGCCAA 150

① 151 CGGCGCATCTTTTCTTCTTATCTGCATCTACTTCCACATTGGCCGGTCTTACTATGGCTCCTACCTCTAATAAGAAACCTGAAACATTGGCGTCTCTCTGTGTTCTTAGTCATAGCCACGGCCTTTGTAGGCTATGTCCCTCCCTTG 300
② 151 CGGCGCATCTTTTCTTCTTATCTGCATCTACTTCCACATTGGACGAGGTCTCTACTACGGCTCCTACCTCTATAAAGAAACCTGAAACATTGGCGTTGTTCTACTGCTTTTAGTCATAGCCACTGCCTTTGTAGGCTACGTCCCTCCCTTG 300
③ 151 CGGCGCATCTTTTCTTCTTATCTGCATCTACTTCCACATTGGACGAGGTCTCTACTACGGCTCCTACCTCTATAAAGAAACCTGAAACATTGGCGTTGTTCTACTGCTTTTAGTCATAGCCACTGCCTTTGTAGGCTACGTCCCTCCCTTG 300
④ 151 CGGCGCATCTTTTCTTCTTATCTGCATCTACTTCCACATTGGACGAGGTCTCTACTACGGCTCCTACCTCTATAAAGAAACCTGAAACATTGGCGTTGTTCTACTGCTTTTAGTCATAGCCACTGCCTTTGTAGGCTACGTCCCTCCCTTG 300
⑤ 151 CGGCGCATCTTTTCTTCTTATCTGCATCTACTTCCACATTGGACGAGGTCTCTACTACGGCTCCTACCTCTATAAAGAAACCTGAAACATTGGCGTTGTTCTACTGCTTTTAGTCATAGCCACTGCCTTTGTAGGCTACGTCCCTCCCTTG 300
⑥ 151 CGGCGCATCTTTTCTTCTTATCTGCATCTACTTCCACATTGGACGAGGTCTCTACTACGGCTCCTACCTCTATAAAGAAACCTGAAACATTGGCGTTGTTCTACTGCTTTTAGTCATAGCCACTGCCTTTGTAGGCTACGTCCCTCCCTTG 300

① 301 AGGCCAAATATCTTCTGAGGCGCCACAGTCATTACAACTCTCTATCAGCCGCCCTTACATCGGCCAGATCTAGTTCAATGAATTTGAGGGGGTCTCAGTAGACAACCGCTACCCCTCACCCGGTTCTTACATTTCACTTCATCCT 450
② 301 AGGCCAAATATCTTCTGAGGCGCCACAGTCATTACTAACCTTCTATCAGCCGCCCTTACATCGGCCAGATCTAGTTCAATGAATTTGAGGGGGTCTCAGTAGACAACCGCTACCCCTCACCCGGTTCTTACATTTCACTTCATCCT 450
③ 301 AGGCCAAATATCTTCTGAGGCGCCACAGTCATTACTAACCTTCTATCAGCCGCCCTTACATCGGCCAGATCTAGTTCAATGAATTTGAGGGGGTCTCAGTAGACAACCGCTACCCCTCACCCGGTTCTTACATTTCACTTCATCCT 450
④ 301 AGGCCAAATATCTTCTGAGGCGCCACAGTCATTACTAACCTTCTATCAGCCGCCCTTACATCGGCCAGATCTAGTTCAATGAATTTGAGGGGGTCTCAGTAGACAACCGCTACCCCTCACCCGGTTCTTACATTTCACTTCATCCT 450
⑤ 301 AGGCCAAATATCTTCTGAGGCGCCACAGTCATTACTAACCTTCTATCAGCCGCCCTTACATCGGCCAGATCTAGTTCAATGAATTTGAGGGGGTCTCAGTAGACAACCGCTACCCCTCACCCGGTTCTTACATTTCACTTCATCCT 450
⑥ 301 AGGCCAAATATCTTCTGAGGCGCCACAGTCATTACTAACCTTCTATCAGCCGCCCTTACATCGGCCAGATCTAGTTCAATGAATTTGAGGGGGTCTCAGTAGACAACCGCTACCCCTCACCCGGTTCTTACATTTCACTTCATCCT 450

① 451 CCCCCTTATTTATTGCAGCGCAAGTATGATCACCTCTCTCTTTTCCACCAAAACGGTCTCCTTAACCCCAACAGGATTAATTCCTAACCTTGATAAAAGTCTCTTTTCAC 559
② 451 CCCCCTTATTTATTGCAGCGCAAGTATGATCACCTCTCTCTTTTCCACCAAAACGGTCTCCTTAACCCCAACAGGATTAATTCCTAACCTTGATAAAAGTCTCTTTTCAC 559
③ 451 CCCCCTTATTTATTGCAGCGCAAGTATGATCACCTCTCTCTTTTCCACCAAAACGGTCTCCTTAACCCCAACAGGATTAATTCCTAACCTTGATAAAAGTCTCTTTTCAC 559
④ 451 CCCCCTTATTTATTGCAGCGCAAGTATGATCACCTCTCTCTTTTCCACCAAAACGGTCTCCTTAACCCCAACAGGATTAATTCCTAACCTTGATAAAAGTCTCTTTTCAC 559
⑤ 451 CCCCCTTATTTATTGCAGCGCAAGTATGATCACCTCTCTCTTTTCCACCAAAACGGTCTCCTTAACCCCAACAGGATTAATTCCTAACCTTGATAAAAGTCTCTTTTCAC 559
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