The complete mitochondria genome of *Chrysomya phaonis* (Seguy, 1928) (Diptera: Calliphoridae)

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**ABSTRACT**

*Chrysomya phaonis* (Seguy, 1928) is one of the blowflies of great medical and forensic importance. In this paper, we report that the entire genome of mitochondrial DNA of *C. phaonis* is 15,831 bp in length, which consists of 39 genes including 13 protein-coding genes, 24 tRNA genes, 2 mitochondrial ribosomal RNA genes, and a 992 bp non-coding A+T-rich region. The overall base compositions of A, G, C, and T are 38.79%, 9.75%, 14.15%, and 37.31%, respectively. We provide the first complete mitochondrial genome of *C. phaonis*, and should provide useful information for phylogenetic and species identification for *C. phaonis*.

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Table 1. Mitochondrial gene profile of\n\n| Gene | Direction | Nucleotide number | Size (bp) | OL | Non | Anticodon | Codon | Start | Stop |
|------|-----------|------------------|---------|----|-----|-----------|-------|-------|------|
| tRNA^{Met} | J | 1–64 | 64 | 4 | GAT | \n| tRNA^{Val} | N | 69–137 | 69 | 8 | TTG | \n| tRNA^{Trp} | J | 146–214 | 69 | CAT | \n| ND2 | J | 215–1229 | 1015 | \n| tRNA^{Ile} | J | 1230–1297 | 68 | 8 | TCA | \n| tRNA^{lys} | N | 1290–1353 | 64 | 7 | GCA | \n| tRNA^{Pro} | J | 3030–3717 | 688 | \n| COI | J | 1425–2958 | 1534 | \n| tRNA^{A0} | J | 2959–3024 | 66 | TAA | \n| COII | J | 3030–3717 | 688 | \n| tRNA^{Val} | J | 3718–3788 | 71 | 1 | GTG | \n| tRNA^{Ile} | J | 3788–3854 | 67 | GTC | \n| ATP8 | J | 3855–4019 | 165 | 7 | ATT | TAA | \n| ATP6 | J | 4013–4690 | 678 | 4 | ATG | TAA | \n| COIII | J | 4695–5483 | 789 | 6 | ATG | TAA | \n| tRNA^{Ile} | J | 5490–5554 | 65 | TCC | \n| ND3 | J | 5555–5908 | 354 | 2 | ATT | TAA | \n| tRNA^{Asp} | J | 5911–5975 | 65 | 1 | TGC | \n| tRNA^{Val} | J | 5975–6038 | 64 | 6 | TCG | \n| tRNA^{lys} | J | 6045–6110 | 66 | 1 | GTT | \n| tRNA^{Arg} | J | 6110–6179 | 70 | GCT | \n| tRNA^{pro} | J | 6180–6247 | 68 | 18 | TTC | \n| tRNA^{Pro} | N | 6266–6332 | 67 | GAA | \n| NDS | N | 6333–8052 | 1720 | 15 | ATT | T | \n| tRNA^{A0} | N | 8068–8133 | 66 | GTG | \n| ND4 | N | 8134–9472 | 1339 | 7 | ATG | T | \n| ND4L | N | 9466–9762 | 297 | 2 | ATG | TAA | \n| tRNA^{Pro} | J | 9765–9829 | 65 | TGT | \n| tRNA^{Ile} | N | 9830–9895 | 66 | 2 | TGG | \n| ND6 | J | 9898–10,422 | 525 | 1 | ATT | TAA | \n| CytB | J | 10,422–11,556 | 1135 | \n| tRNA^{A0} | J | 11,557–11,624 | 68 | 16 | TGA | \n| ND1 | N | 11,641–12,579 | 939 | 10 | ATA | TAA | \n| tRNA^{Met} | N | 12,590–12,654 | 65 | 1 | TAG | \n| tRNA^{Val} | N | 12,656–13,983 | 1328 | \n| tRNA^{A0} | N | 13,984–14,055 | 72 | TAC | \n| sRNA | N | 14,056–14,839 | 784 | \n| A + T rich | J | 14,840–15,831 | 992 | 66 | \n| tRNA^{Met} | J | 14,929–14,994 | 66 | GAT | \n
Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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References

DeBry RW, Timm A, Wong ES, Stamper T, Cookman C, Dahlem GA. 2013. DNA-based identification of forensically important Lucilia (Diptera: Calliphoridae) in the Continental United States. J Forensic Sci. 58:73–78.

Desmetrier S, Gosselin M. 2009. COI sequence variability between Chrysomyinae of forensic interest. J Forensic Sci Int. 3:89–95.

Fan ZD. 1992. Key to the common flies of China. 2nd ed. Beijing (China): Science Press. p. 992.

Fan ZD, Chen ZZ, Fang JM, Zheng SS, Tao ZL. 1997. Fauna Sinica Insecta: Vol. 6, Diptera: Calliphoridae. Beijing (China): Science Press. p. 186.

Ghandour AM. 1988. Health hazards in humans and animals caused by imported livestock diseases in Saudi Arabia. Fauna Saudi Arabia. 9:468–477.

Greenberg B. (1971). Flies and disease. In: Ecology, classification and biotic associations, vol. 1. Princeton, (NJ): Princeton University Press. p. 856

Greenberg B. 1973. 447. Flies and diseases, biology and disease transmission. Princeton, (NJ): Princeton University Press.

Harvey ML, Gaudieri S, Villet MH, Dadour IR. 2008. A global study of forensically significant calliphorids: implications for identification. Forensic Sci Int. 177:66–76.

Kuhlhorn F. 1983. Verbreitung der Toxoplasmore. Katzenkot Un Dipteren. Tierarzt, Prax. 11:385–392.
Kurahashi H, Thapa VK, Shinonaga S, Iwasa M. 1994. Notes on the Nepalese calliphorid flies (Insecta: Diptera). Jap J Sanit Zool. 45:179–252.
Norris KR. 1965. The bionomics of blow flies. Annu Rev Entomol. 10:47–68.
Tamura K, Stecher G, Peterson D, Filipski A, Kumar S. 2013. MEGA6: molecular evolutionary genetics analysis version 6.0. Mol Biol Evol. 30:2725–2729.
Yan J, Liao H, Xie K, Cai J. 2014. The complete mitochondria genome of *Chrysomya pinguis* (Diptera: Calliphoridae). Mitochondrial DNA. http://dx.doi.org/10.3109/19401736.2014.958675.
Wells JD, Williams DW. 2007. Validation of a DNA-based method for identifying Chrysomyinae (Diptera: Calliphoridae) used in a death investigation. Int J Legal Med. 121:1–8.
Zhong M, Wang X, Liu Q, Luo B, Wu C, Wen J. 2016. The complete mitochondrial genome of the flesh fly, *Boettcherisca peregrine* (Diptera: Sarcophagidae). Mitochondrial DNA Part A. 27:106–108.
Zumpt F. 1965. Myiasis in man and animals in the old world: a textbook for physicians veterinarians and zoologists. London (UK): Butterworth. p. 267.