

Discrimination between *Onchocerca volvulus* and *O. ochengi* filarial larvae in *Simulium damnosum* s.l. and their distribution throughout central Ghana using a versatile high-resolution speciation assay

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Abstract

Transmission of the human filarial nematode *Onchocerca volvulus* is typically monitored using molecular pool screening techniques and dissection of the Simuliid blackfly vector. Black flies from disease endemic regions also co-transmit a range of other *Onchocerca* spp, which can be difficult to distinguish from the human parasite based on morphological characters alone. Here we describe a versatile molecular approach that exploits mitochondrial DNA sequence variation to discriminate between *O. volvulus* and *O. ochengi* dissected from black flies. We validated these tools on 185 *Onchocerca* larvae dissected from black flies captured from 14 communities in Ghana throughout 2011-13, which revealed (i) a higher than expected prevalence of *O. ochengi*, (ii) evidence for differential migration of both species within different tissues of the fly, and (iii) a non-uniform distribution of the two parasites, with 25%, 47%, and 93% of *O. volvulus* being found in the western-most (Black Volta, Tain and Tombe), the central Pru and eastern-most Daka river basins, respectively. The tools presented provide a simple and cost-effective approaches to determine the identity and distribution of two *Onchocerca* species, and will be valuable for future genetic studies that focus on parasites collected from blackflies. The results emphasise the need for molecular identification of parasites collected from blackflies, particularly if inferences regarding transmission of the disease-causing *O. volvulus* are made.