The WE*ome* of *Schistosoma mansoni* – a non-coding DNA resource shaping schistosome biology, variability, and evolution?

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A large part of eukaryote genomes consists of non-coding DNA. This part includes tandemly repeated sequences, which gained attention because they offers exciting insights into genome biology. We investigated satellite DNA-like elements, called W-elements (WEs), of the platyhelminth *Schistosoma mansoni*. Schistosomes are the only trematodes that have evolved separate genders, and the sexual maturation of the female depends on constant pairing with the male. The schistosome karyotype comprises eight chromosome pairs, males are homogametic (ZZ), females heterogametic (ZW). Former studies identified the WEs W1 and W2 in Puerto Rican isolates of *Schistosoma mansoni* as female-specific satellite DNAs, which are located in the heterochromatic block of the W-chromosome. Unexpectedly, W1 and W2 occurred in a Liberian strain of *S. mansoni* also in males. Subsequent studies based on genome version 5 of the *S. mansoni* genome described a total of 36 WE families (WEFs), and first evidence was obtained for WE transcripts in the free-living larval stages (miracidium, cercaria).
Based on new genome (version 7) and transcriptome data, we performed a comprehensive reanalysis of the WEFs of *S. mansoni*. Besides a new classification into 19 WEFs, we provide first evidence for stage-, gender-, pairing-, gonad-, and strain-specific/preferential transcript occurrence of WEs. Furthermore, we revealed their mobile nature, deduced from the identification of autosomal copies of full-length and partial WEs and sequence features typical for the activity of mobile elements. Advanced structural analyses suggested potential roles of WEFs as sources of non-coding RNAs like hammerhead ribozymes (HHRs). For the latter we obtained biochemical evidence. Finally, we also investigated WEF occurrence in different schistosome species and discovered remarkable divergence. From all obtained results we conclude that WEs exert enduring influence on the biology of *S. mansoni*. Their variable occurrence in different species, strains as well as among biological replicates and within clonal populations suggests that the WE*ome* of schistosomes represents one of the sources of heritable and spontaneuos variation associated with the evolution of sexual dimorphism and diversification of the family Schistosomatidae.