The ancestor of the \textit{S. japonicum} complex diversity rapidly colonized Central, Eastern, and South East Asia. Mt genome gene order is the same as all other trematodes and cestodes.

The ancestor of the \textit{S. mansoni} clade rapidly colonized Central, Eastern, and South East Asia. Mt genome gene order is the same as all other trematodes and cestodes.

Population bottleneck occurred marked by a change in mt genome gene order and in sex chromosome size, and it gave rise to the proto-\textit{S. mansoni} clade.

Second invasion of Africa by ancestors that were similar to \textit{Orientobilharzia turkestanicum} and \textit{S. incognitum}.

First invasion of Africa by \textit{Schistosoma} giving rise to the \textit{S. hipposotomi} clade. This is basal to the rest of the non-African/non-\textit{S. japonicum} group species and assumed to have the same mt gene genome order as the Asian \textit{Schistosoma} species.

\textit{S. haematobium} is the only species in Africa with this karyotype but shares homology with the other African species in mt gene order.


Reinvasion of Asia from the Africa giving rise to the \textit{S. indicum} group.

Both species, \textit{S. bovis} and \textit{S. mattheei} primarily found in cattle and appear to have the same karyotype even though the mtDNA shows them to be phylogenetically distinct.