meta-analysis shows that mitochondrial mutations are not neutral

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\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{human_mito.png}
\caption{Sketch of the human mitochondrial genome and its gene products.}
\end{figure}

1. mitochrondial genome mutations: always neutral?

mt genome mutations affect life-history traits, metabolism and fitness. these effects can either be additive or be based on epistatic interactions between the mt genome and the nuclear genome. epistatic effects between co-evolved and non co-evolved genome combinations in animals appear to be moderate to strong\textsuperscript{4} (figure 2).

this indicates that the mt genome and the nuclear genome have co-evolved, likely selected for by maximising atp production. this resulted in an optimised interplay between the polypeptides form both genomes.

\begin{figure}[h]
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\includegraphics[width=\textwidth]{effect_size_2.png}
\caption{Effect-size estimates for combined additive and epistatic effects on mt genome mutations.}
\end{figure}

2. the effect (strength) of mitochondrial genome mutations depends on metabolic needs

hypothesised by lane, species with higher metabolic needs experience stronger effects by mt genome mutations\textsuperscript{5}. the higher the metabolic needs of an individual are, the more it hinges on a perfect interplay between the mitochondrial and nuclear encoded elements of the etc. this hypothesis got some first empirical support for twelve animal species in a meta analysis\textsuperscript{4} (figure 3).

metabolic needs are tissue-specific. more detailed knowledge about tissues and cell types prone to be affected by mt genome mutations could enhance our knowledge about and understanding of diseases caused by such mutations.

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{effect_size_3.png}
\caption{An increase in the basal metabolic rate (bmr) leads to stronger effects of mitochondrial genome mutations.}
\end{figure}

want to know more?