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A reassessment of explanations for discordant introgressions of mitochondrial and nuclear genomes

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Motivation

Examples of massive mitochondrial introgressions combined with no or very limited nuclear introgressions (i.e. **mito-nuclear discordance**) are accumulating, stimulating the development of various hypotheses to explain this pattern. On the one hand, **selective hypotheses** propose a selective advantage of the introgressing mitochondrial variants, or counter-selection of the nuclear genome; On the other hand, **neutral hypotheses** invoke sex-biased processes and/or drift and/or spatial invasions. The neutral hypotheses however are mostly verbal and have not been quantitatively evaluated. Here we reassess all these hypotheses using simulations under a wide range of demographic and genetic scenarios.

General simulation settings

▶ **Spatially explicit simulations of a secondary contact:**

▷ 2 habitats, each with 15 x 10 demes of N=10 diploid adult pairs ($N_1=N_2=3,000$)

▷ Forward individuals-based simulations of 6,000 generations of secondary contact considering **spatially limited dispersal** (IBD), **sex-biased processes**, **spatial invasion**, and **selection**

▷ Standard coalescent to simulate 80,000 generations of **divergence** between the ancestral populations
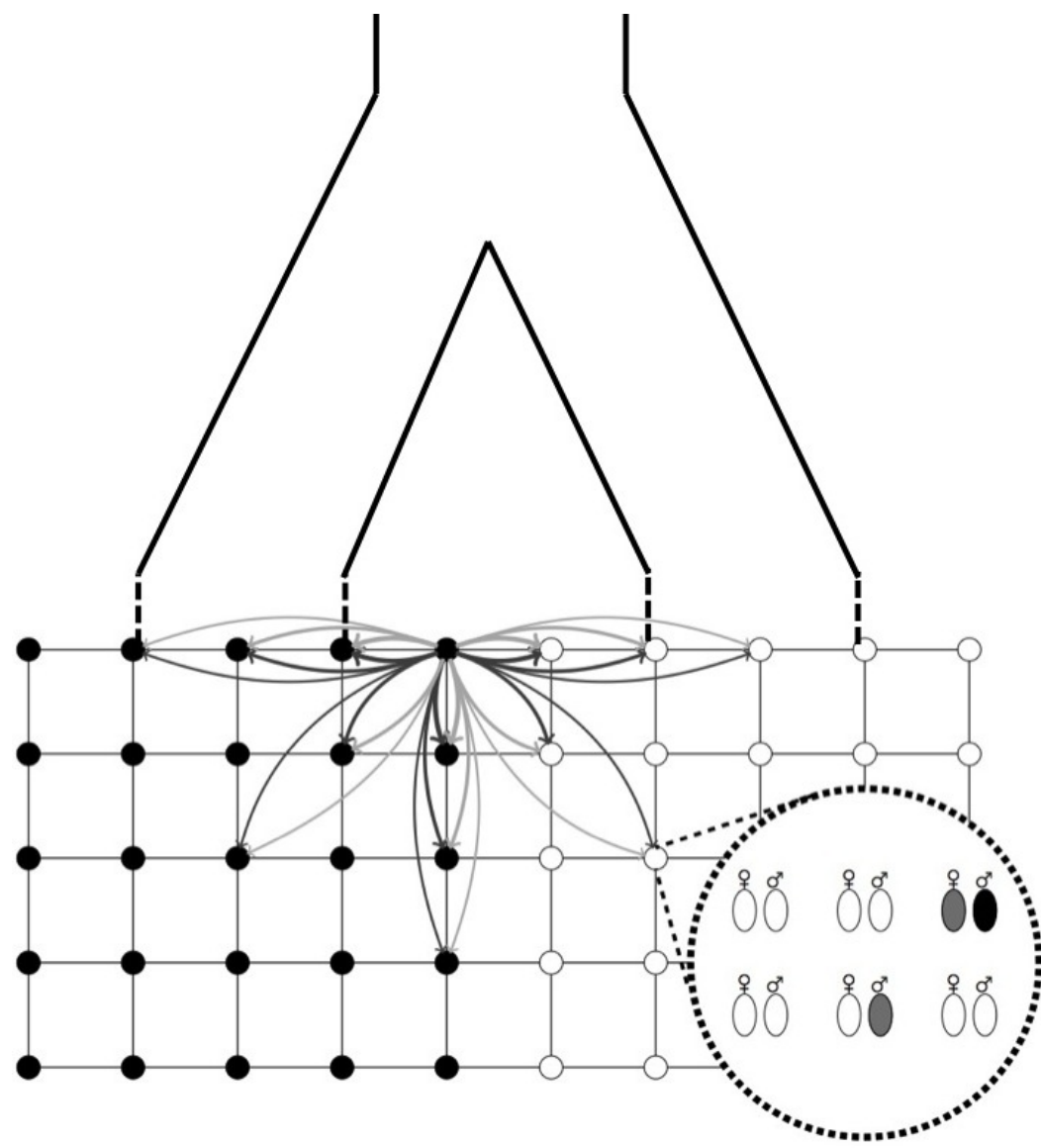
▶ Multi-locus **nuclear genome**:

▷ One chromosome with 20 pairs of loci (1 neutral & 1 selected)

▷ Recombination within and between pairs of loci

▶ **Mitochondrial genome**:

▷ One chromosome with one pair of linked loci (1 neutral + 1 selected)

▶ **Local adaptation** is modeled with one nuclear "speciation" locus (proxy for many co-adapted loci in LD):

▷ Lower fitness in the non-original habitat

▷ Lower fitness for hybrids in both habitats

Additional demographic and genetic processes explored

▶ **Sex-biased processes**:

▷ asymmetric crosses: one sex is preferred by both taxa e.g. the female cow in the Bison/Cow example

▷ sex-specific dispersal: one sex disperses more than the other

▷ sex-specific survival: one sex has higher mortality than the other

▶ **Spatial invasion combined with sex-biased dispersal**:

▷ One habitat expands over the other after secondary contact, gradually but completely.

▷ Direction and strength of sex-biased dispersal varies among different scenarios

▶ **Strong drift** (single hybridization event in small populations):

▷ Only 3 x 10 demes in each habitat ($N_1=N_2=600$)

▷ Single inter-taxa mating event allowed between two pure individuals

▷ Then no restrictions on matings between hybrids

▷ No sex-biased processes

For all scenarios, we considered **both high** (0.1) and **low migration rates** (0.001)

Outputs of the simulation study: introgression measures

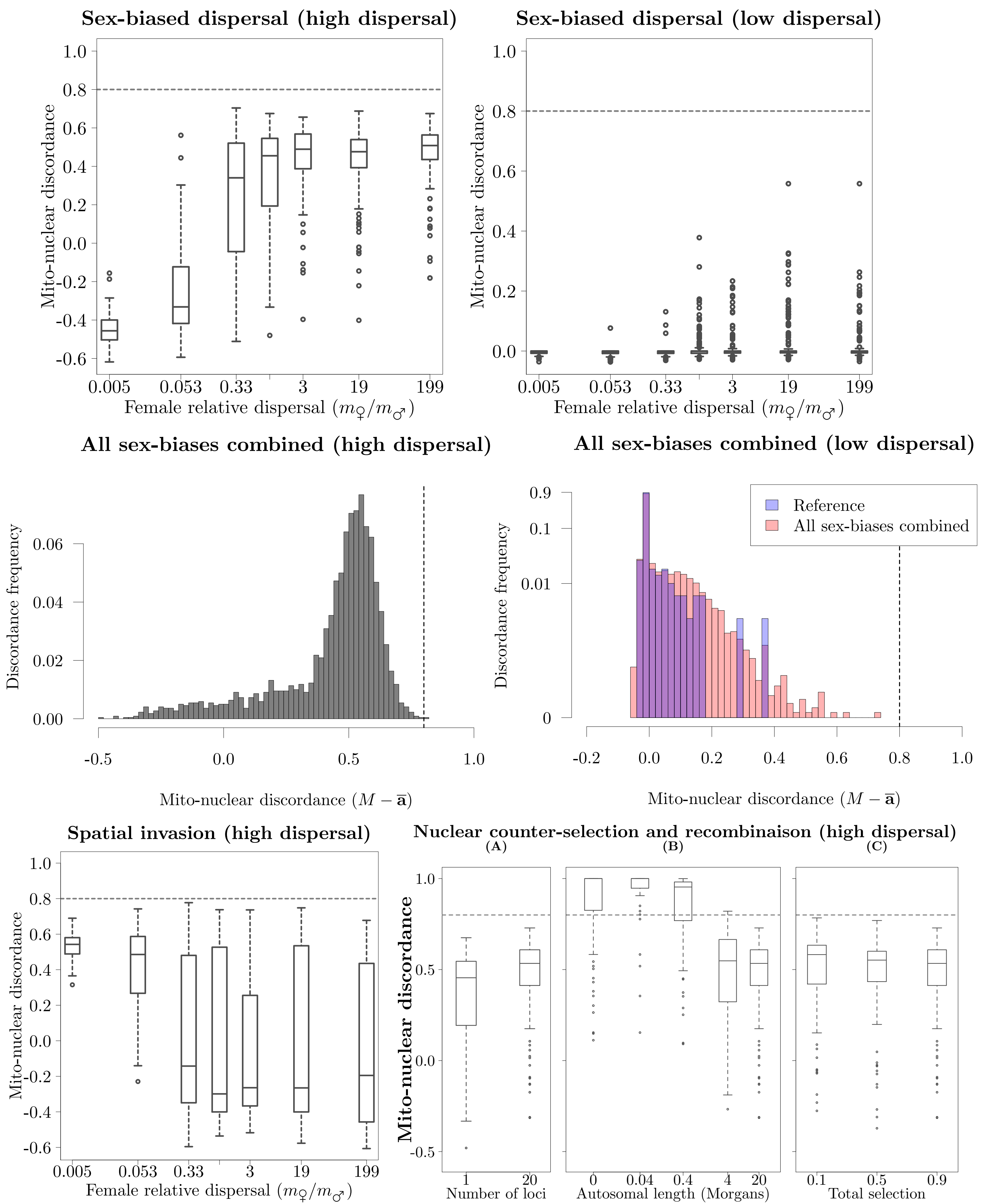M: proportion of introgressed Mt copies in the most introgressed taxon

$\mathbf{a}$: vector of proportions of introgressed nuclear gene copies

We are mostly interested in the following output:

▶ $M-\bar{\mathbf{a}}$ the **mito-nuclear introgression discordance**

and we define a Massively Discordant Mitochondiral Introgression (MDMI) when $M-\bar{\mathbf{a}} > 0.8$

Results

Sex-biased dispersal (high dispersal)

Sex-biased dispersal (low dispersal)

All sex-biases combined (high dispersal)

All sex-biases combined (low dispersal)

Spatial invasion (high dispersal)

Nuclear counter-selection and recombinaison (high dispersal)

Conclusions

Gene flow	Sex-biases	Invasion	Nu Selection	Mt Selection	MDMI
	-	-	-	-	No
	Yes	-	-	-	No[1]
High	-	Yes	-	-	No
	-	-	Yes	-	**Yes**
	-	-	-	Yes	No
	-	-	-	-	No
Low	Yes	-	-	-	No
	-	Yes	-	-	No
	-	-	-	Yes	**Yes**
Single hybridization	-	-	-	-	No[2]

▶ Neutral processes (sex-biases, strong drift and spatial invasion) fail to explain MDMI

▶ Only positive selection on Mt with low migration rates or counter selection on the whole nuclear genome can create MDMI

▶ but no detection of positive selection using Tajima's D or Fu' Fs on Mt polymorphism observed in the introgressed taxon

Take home message

▶ **Neutral processes can't dissociate nuclear and mitochondrial introgression**... .... because females too have nuclear genes!

▶ Our results are in line with recent and increasing evidence that **selection on Mt DNA** may be common

▶ Beware of verbal models, do not trust but **test** them **using models**