Introgression of a block of genome with many weakly selected variants

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Most traits are \textit{highly} polygenic

- $O(10^5)$ common SNPs $\rightarrow$ causal effects on height. [Boyle \textit{et al}, 2017]
- infinitesimal model \textit{with linkage}. 

Innitesimal model with linkage

Inheritance of blocks of genome:

\[ y_O (1 - y_O y_P) \]

\[ V_0 \approx \text{heterogeneity along the genome.} \]

[Robertson, 1977]
Inheritance of blocks of genome:

\[ P(z_O) = \mathcal{N} \left[ \frac{y_O}{y_P} z_P, V_0 y_O \left(1 - \frac{y_O}{y_P}\right) \right]. \]

[Robertson, 1977]

\[ V_0 \approx \text{heterogeneity} \] along the genome.
Approaching the infinitesimal limit

\[ \sigma^2 \]

\( r \)

\( L \) loci (uncorrelated effects) spread uniformly.

\[ V_0 = \frac{\sigma^2}{r} \rightarrow \text{genic variance per unit map length} \]

When can selection ‘see’ discrete loci?
Spread of a genome with linked, weakly selected variants

- Introgression due to **weakly selected, linked** loci vs. **neutral** introgression?
- What determines ‘success’ of different fragments of a block?

\[
\text{fitness } \propto e^{\beta z}
\]

NO new mutations
Initial spread of introduced genome: snapshots

Model as a *branching process*: at most 1 introduced fragment per individual

\[ \beta \sqrt{V_0} = 0.1 \]

\[ t=20 \]

\[ t=80 \]
Initial spread of introduced genome: snapshots

Model as a branching process: at most 1 introduced fragment per individual
Rate of introgression

![Graph showing the rate of introgression over time with different values of \( \beta \sqrt{V_0} \).]

- \( \beta \sqrt{V_0} = 0.2 \)
- \( \beta \sqrt{V_0} = 0.1 \)
- \( \beta \sqrt{V_0} = 0.05 \)
- \( \beta \sqrt{V_0} = 0.0 \)

Exponentially fast vs. \( \sim t \) spread

Weakly selected variants \( \approx \) neutral variants?

Not if linked
Medium-sized fragments drive exponential introgression

Fragment with map length $y_*$ and trait value $z_*$:  
- Typical $z_* \sim \pm \sqrt{V_0 y_*}$, assuming uncorrelated loci.  
- $\beta z_* > y_* \implies$ successful fragment that increases intact exponentially.  
- Successful fragments: typical map length and growth rate $\propto \beta^2 V_0$.  

$\beta \to$ strength of selection on trait; $V_0 = \sigma^2 / r \to$ variance per unit map length
Introgression of individual variants: initial vs. long-term

80 copies of 40 cM block with 2048 loci ($\beta\sigma = 0.0007$) introduced into population ($N = 4000$).

Analytical solution for short-term dynamics

\[ \text{Expected growth rate of variant} \approx \beta z - y \text{ for fastest-growing containing fragment.} \]
Introgression of individual variants: initial vs. long-term

80 copies of 40cM block with 2048 loci ($\beta\sigma = 0.0007$) introduced into population ($N = 4000$).

Analytical solution for short-term dynamics

$\Rightarrow$

Expected growth rate of variant $\approx \beta z - y$ for fastest-growing containing fragment.
Long-term introgression: role of individual effects

Own effect → fine-scale variation at long times in large populations.
Conclusions

- **Linked variants** crucial to polygenic adaptation.
- **Exponential spread** of genetic material even under infinitesimal selection.
- Successful fragments are **medium-sized**.
- **Two phases** of introgression: short-term (hitchhiking with single successful fragments) vs. long-term (partial purging of deleterious variants).
- Individual variants with high introgression probability **may not be adaptive**.
Understanding heterogeneous genomic landscapes

Neutral

Beneficial

Deleterious
Understanding heterogeneous genomic landscapes

Neutral  
Beneficial  
Deleterious

2-tiered description: Weak pairwise associations between linkage blocks?
Sweep signatures: one vs. multiple adaptive variants?

Graphs showing haplotype diversity along the genome with different adaptive variants.
Sweep signatures: one vs. multiple adaptive variants?
Response from standing variation

- Spread of a single genome into a heterogeneous population?
- When does selection see discrete loci?
- Heterogeneity along the genome in the infinitesimal limit?
Wide distribution of fragment lengths

$P(l)$

$t = 100$ generations after the introduction event.
Introgression of a beneficial block

Long vs. short introduced blocks

Average length of surviving fragments.

Medium-sized blocks have longest descendant fragments.
To be a long block or not to be?

Depends on the initial advantage of the block.

![Graph showing the average number of descendants at different initial advantages](chart.png)