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The bug and the bridgehead: global colonisation patterns of the black soldier fly inferred from metapopulation genetic structure

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Athens, Greece
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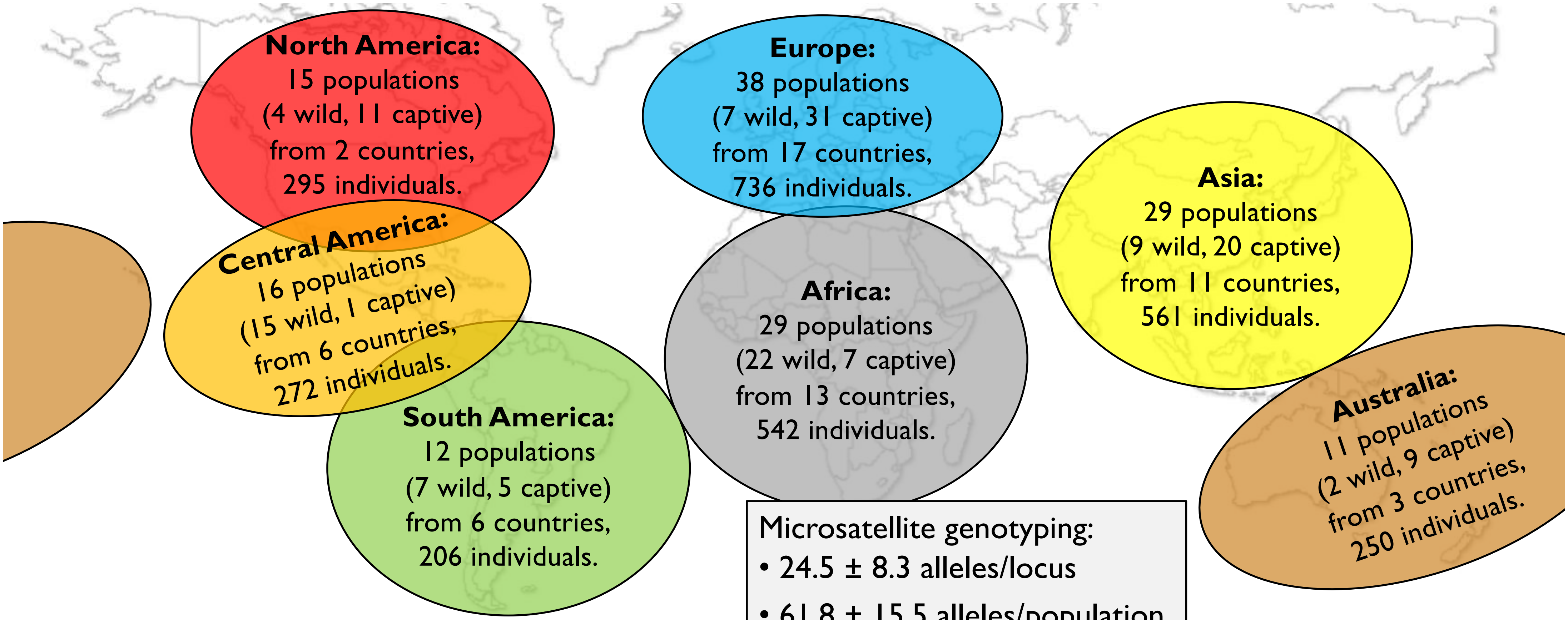
Global BSF samples

150 BSF populations (66 wild & 84 captive) from 57 countries on all relevant (sub-)continents, Ø 19 specimen per population → 2862 individuals in total.



North America:
15 populations
(4 wild, 11 captive)
from 2 countries,
295 individuals.

Central America:
16 populations
(15 wild, 1 captive)
from 6 countries,
272 individuals.

South America:
12 populations
(7 wild, 5 captive)
from 6 countries,
206 individuals.

Europe:
38 populations
(7 wild, 31 captive)
from 17 countries,
736 individuals.

Africa:
29 populations
(22 wild, 7 captive)
from 13 countries,
542 individuals.

Asia:
29 populations
(9 wild, 20 captive)
from 11 countries,
561 individuals.

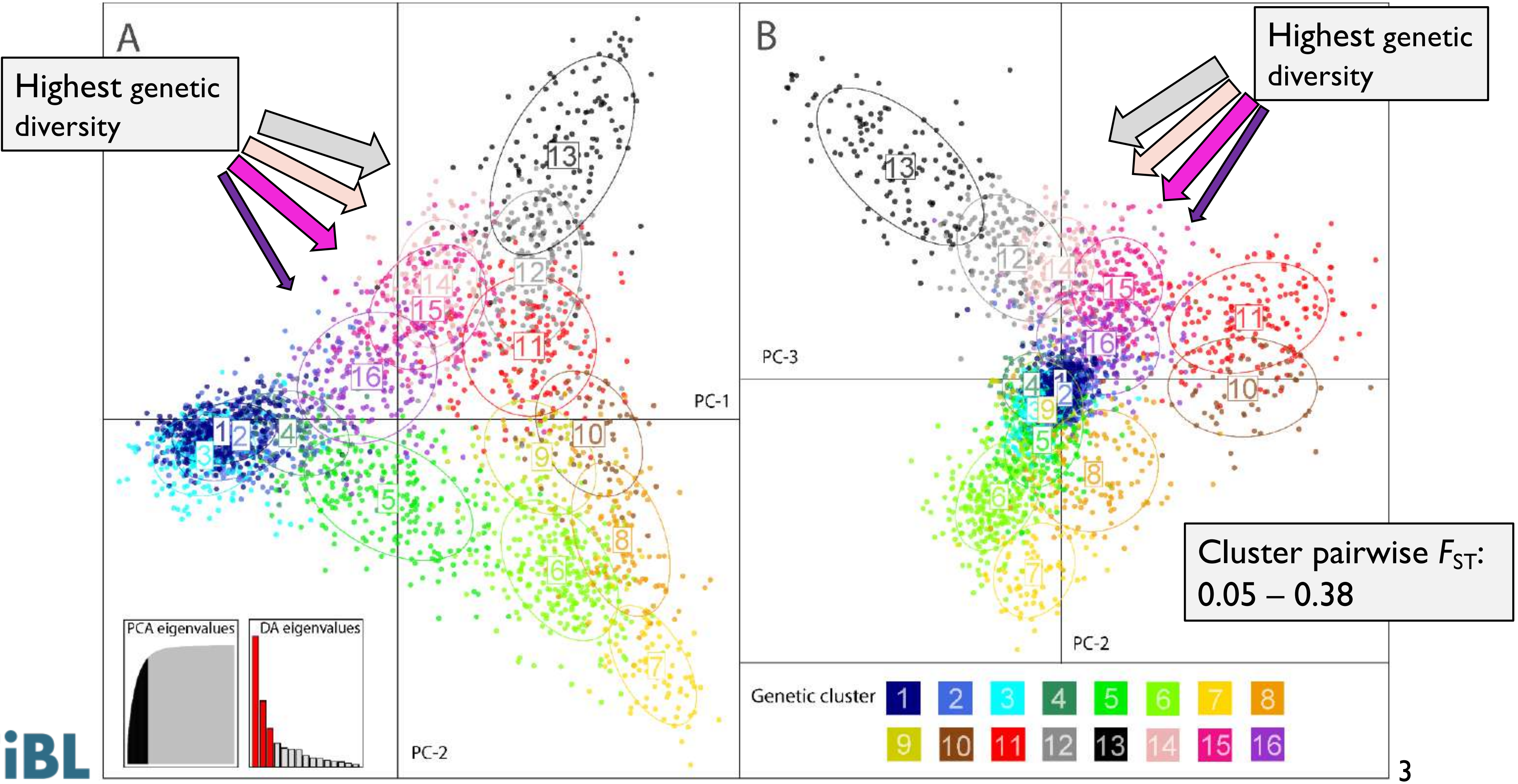
Australia:
11 populations
(2 wild, 9 captive)
from 3 countries,
250 individuals.

Microsatellite genotyping:

- 24.5 ± 8.3 alleles/locus
- 61.8 ± 15.5 alleles/population
- global F_{ST}: 0.24

BSF global population genetic structure

Genetic cluster analysis: discriminant analyses of principal components (DAPC)



Highest genetic diversity

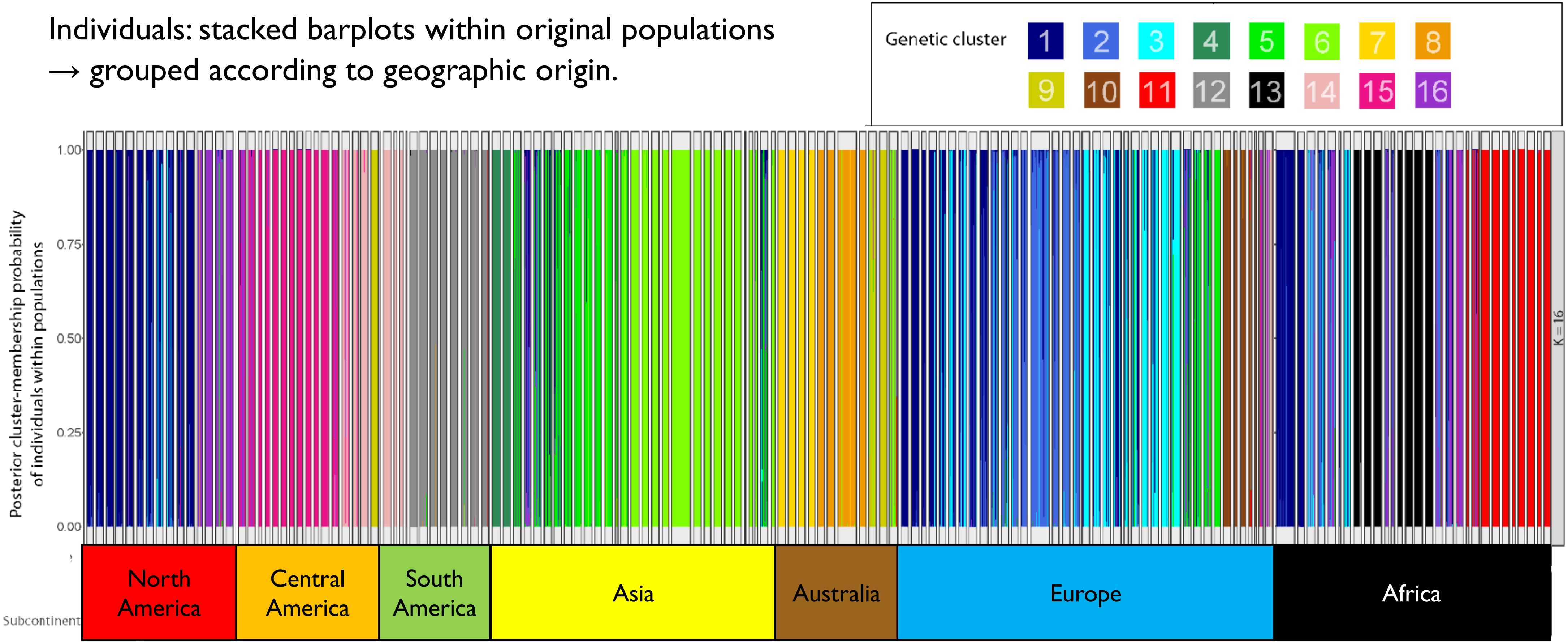
Highest genetic diversity

Cluster pairwise F_{ST}: 0.05 – 0.38

BSF global population genetic structure

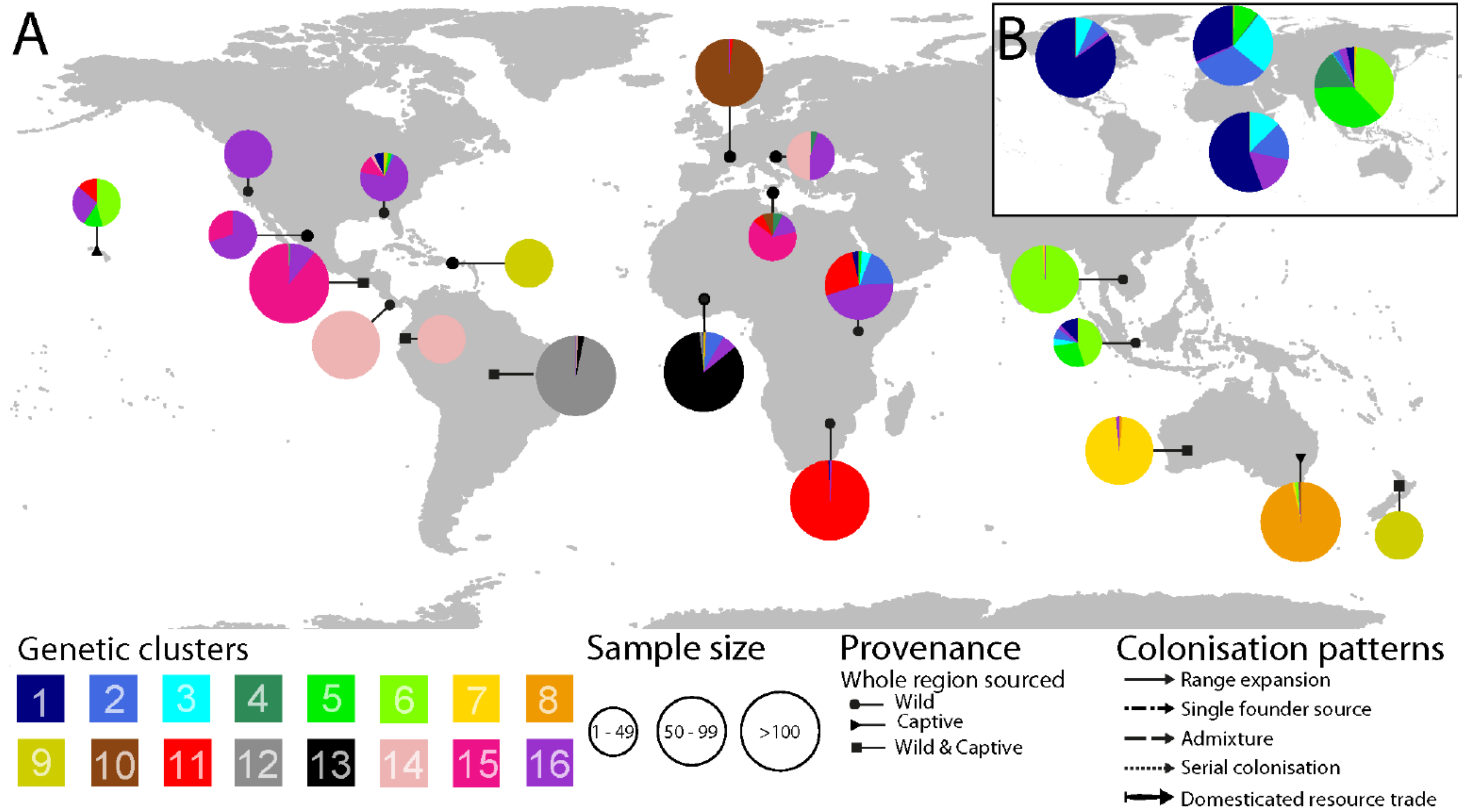
Genetic cluster analysis: individuals' posterior assignment probabilities (including admixture)

Individuals: stacked barplots within original populations
→ grouped according to geographic origin.

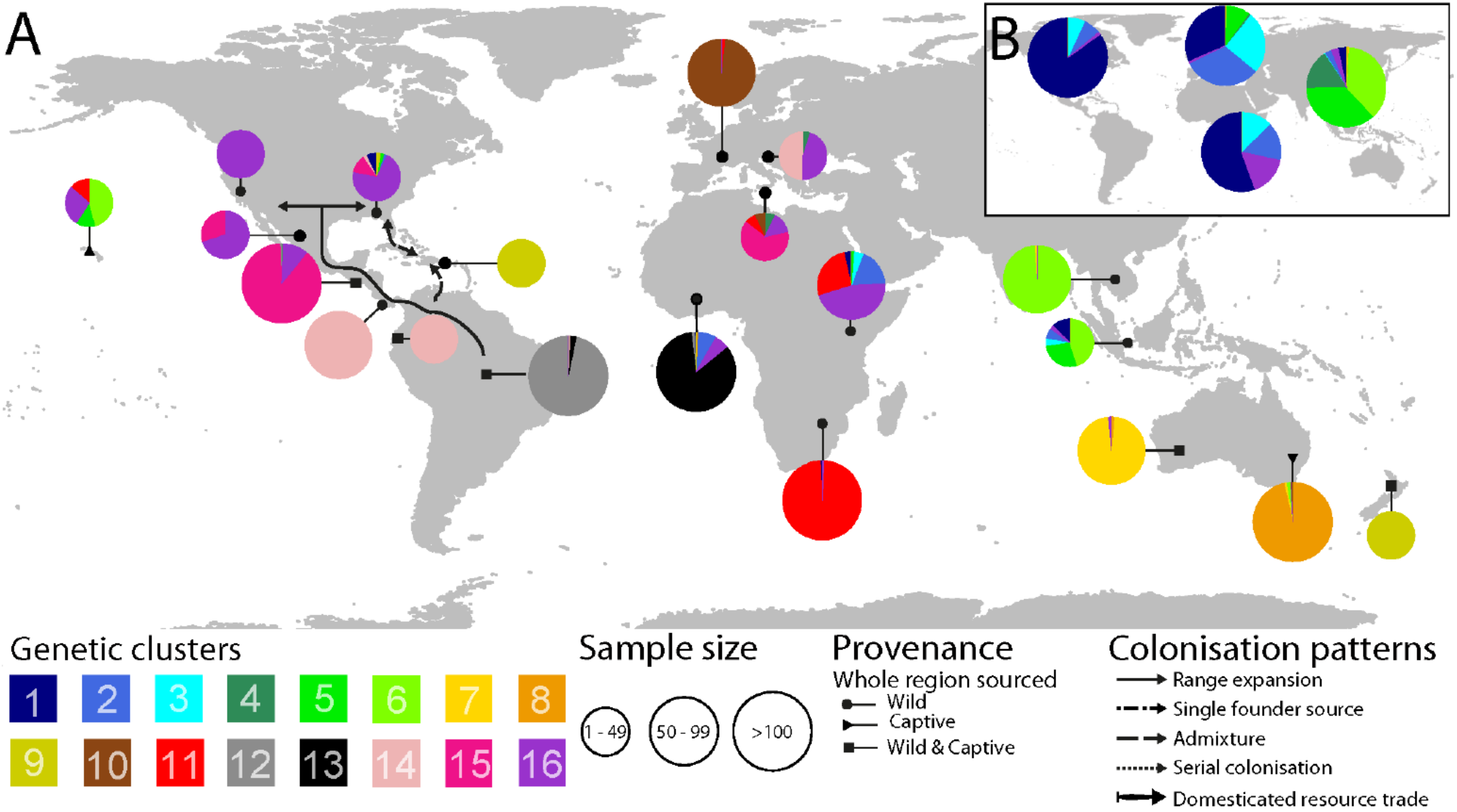


BSF global population genetic structure & demographic trajectories

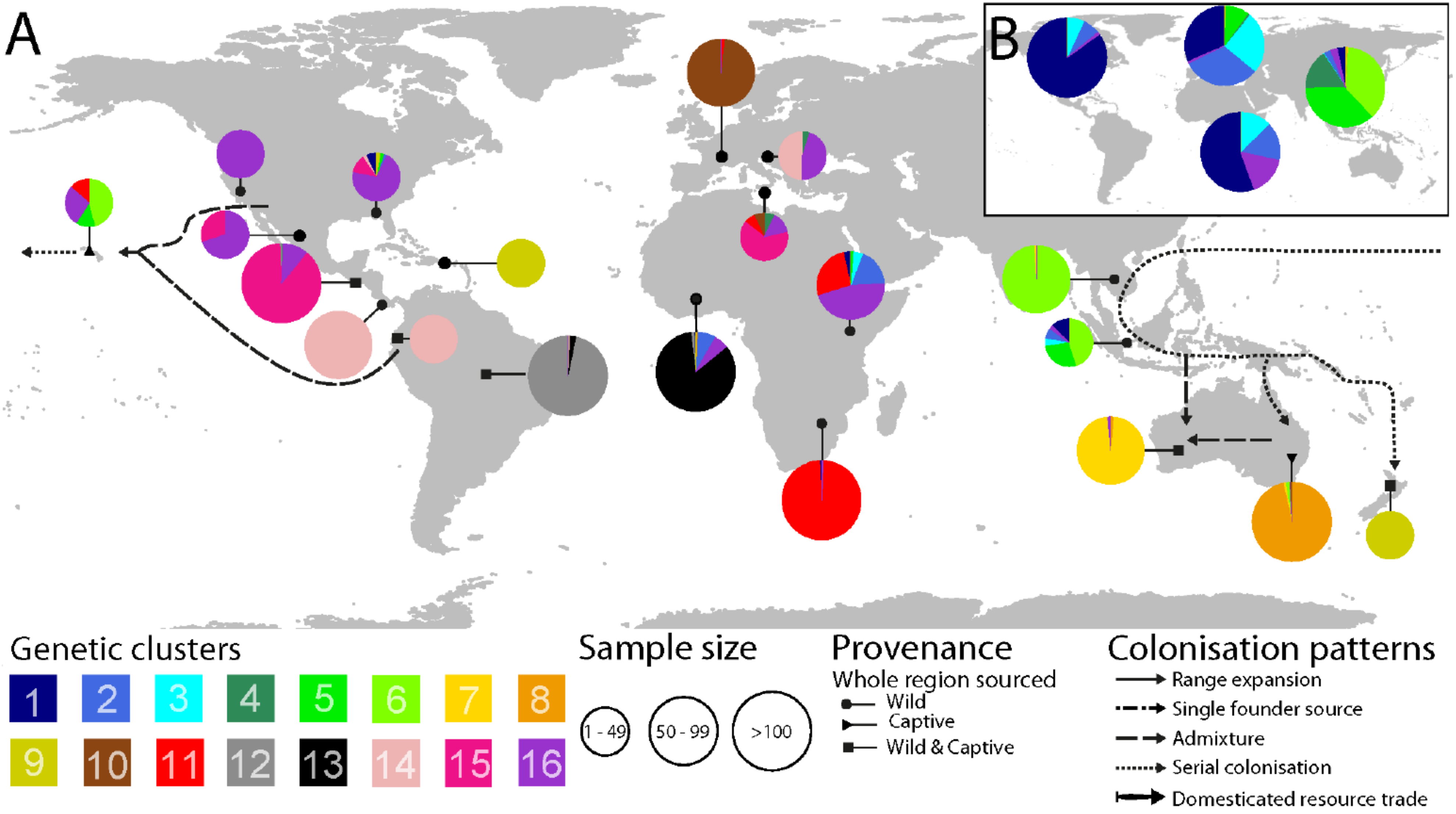
Coalescence-based simulations for demographic inference with Approximate Bayesian Computation



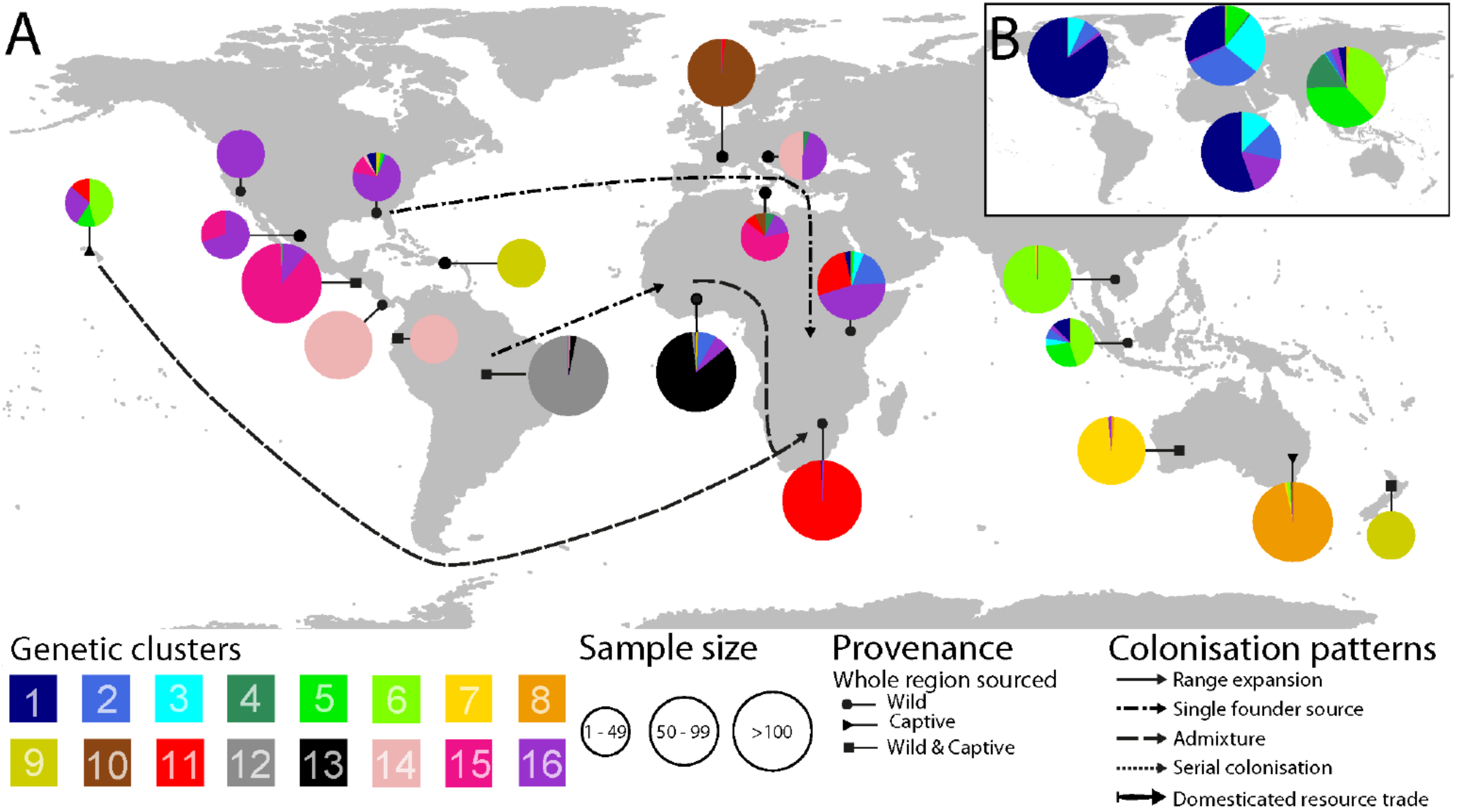
Inferred BSF demographic trajectories – *the Americas*



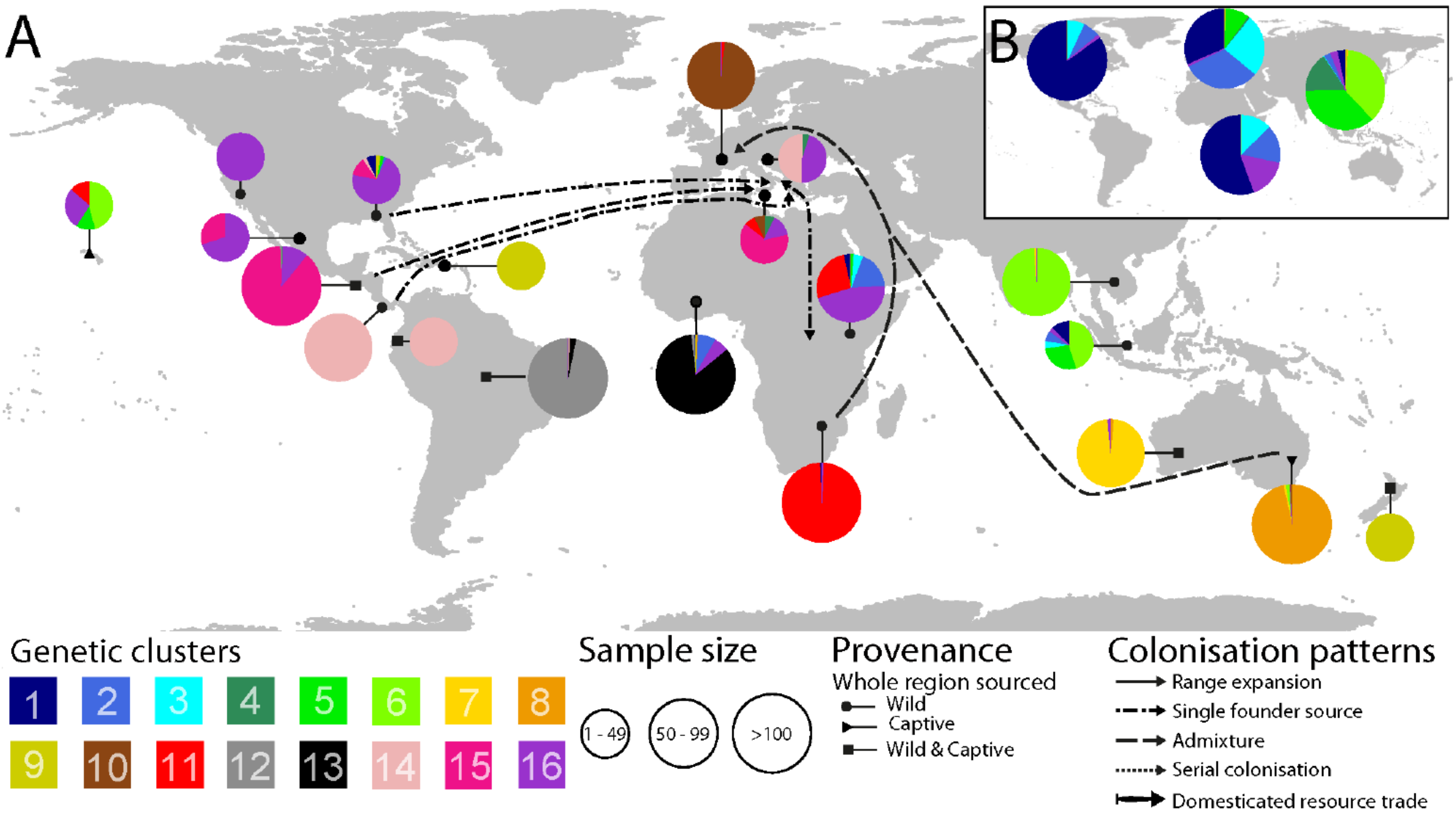
Inferred BSF demographic trajectories – *Australasia*



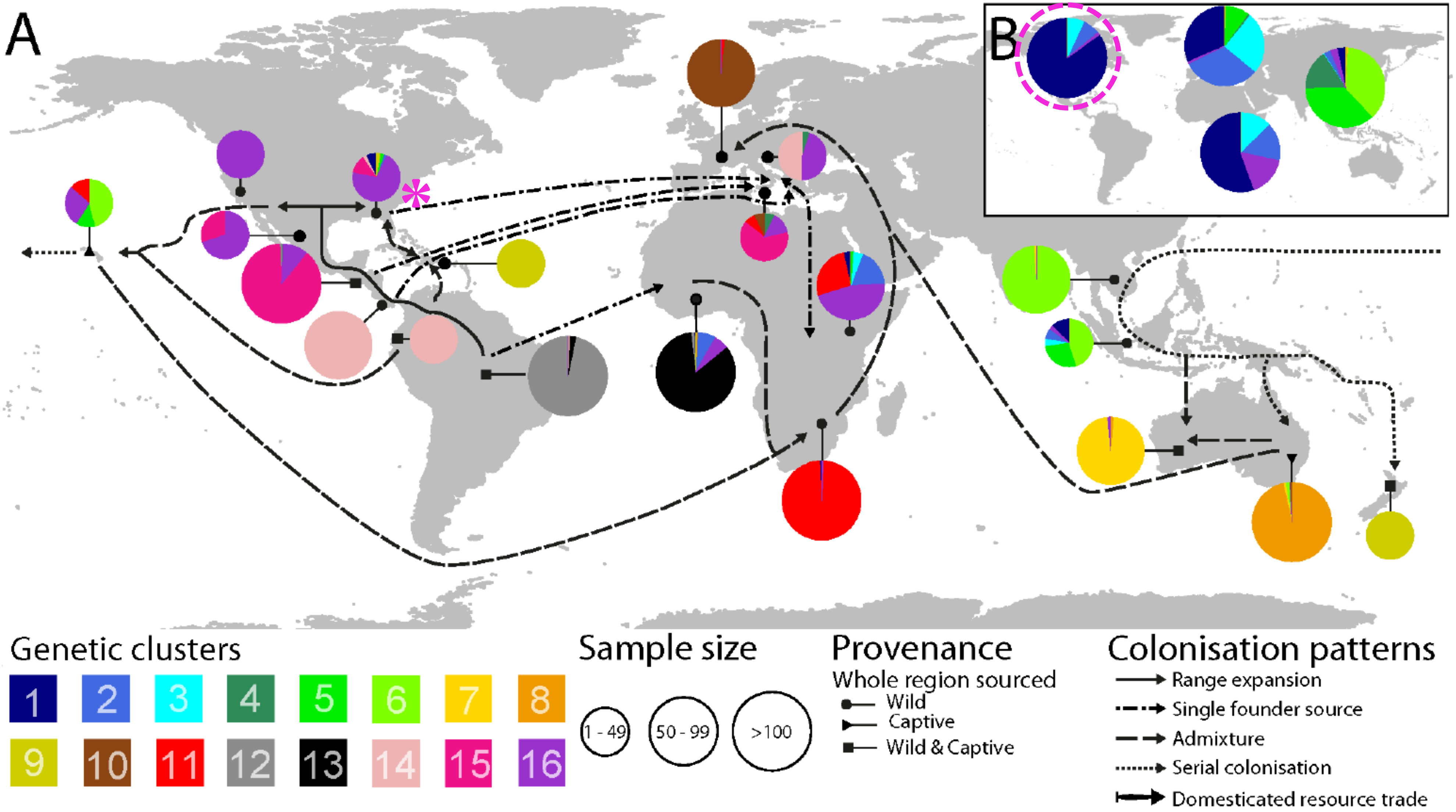
Inferred BSF demographic trajectories – *Africa*



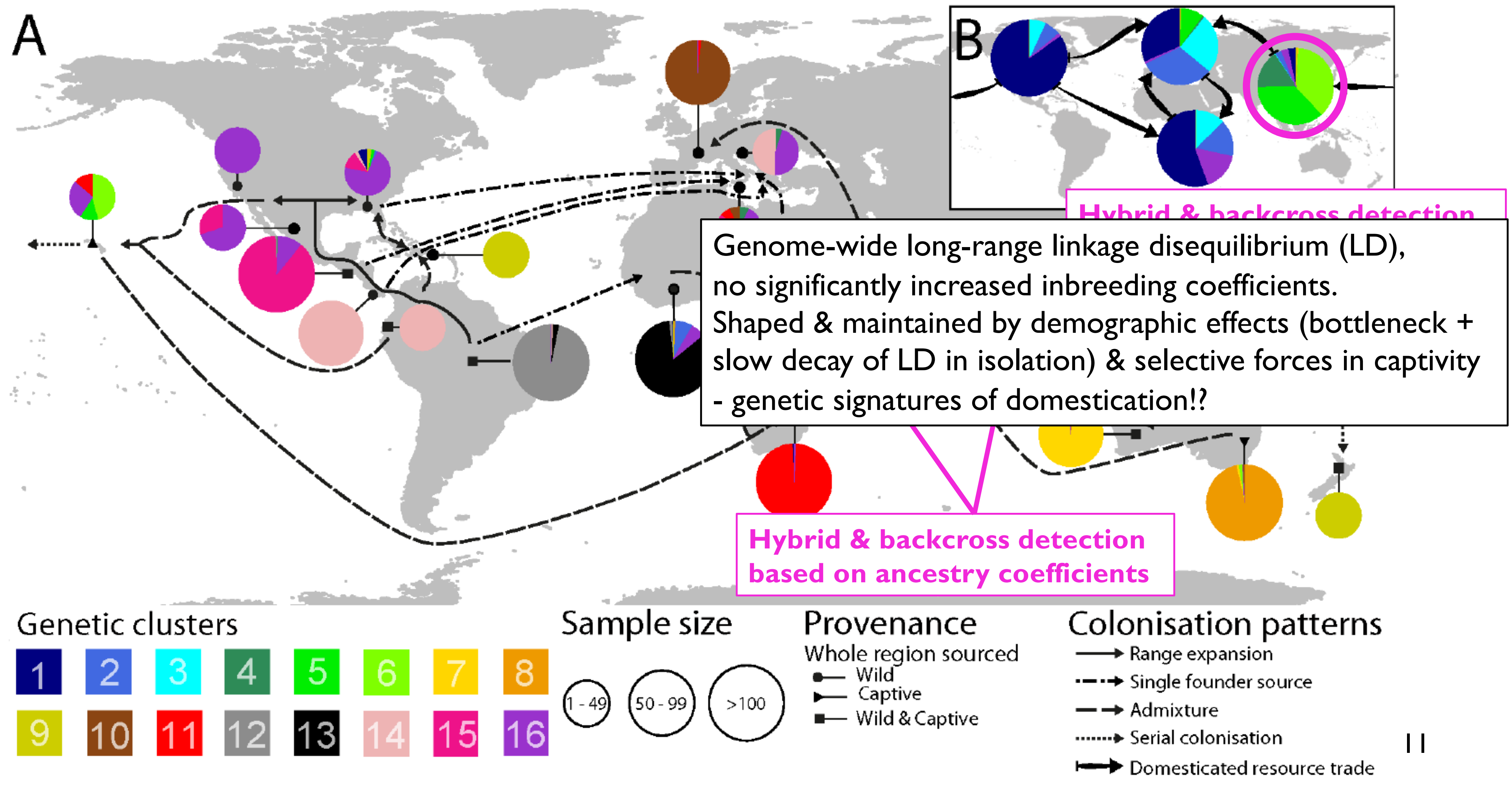
Inferred BSF demographic trajectories – *Europe*



Inferred BSF demographic trajectories – *predominant captive strains*



Inferred BSF demographic trajectories – *predominant captive strains*



Hybrid & backcross detection

Genome-wide long-range linkage disequilibrium (LD), no significantly increased inbreeding coefficients. Shaped & maintained by demographic effects (bottleneck + slow decay of LD in isolation) & selective forces in captivity - genetic signatures of domestication!?

Hybrid & backcross detection based on ancestry coefficients

Conclusions

Complex global population genetic structure:
→ native & non-native diversification in space, likely shaped by environmental adaptation,
→ different evolutionary time scales & relative anthropogenic impact,
→ genetic consequences of management & domestication.

Reconstructing demographic trajectories:
→ ancient American range expansion: likely no anthropogenic drivers.
→ last centuries' global naturalisation: admixture-based bridgehead-mediated colonisation-pulses
→ present production era: widespread, continuous & geneticially uniform introgression.

Implications for long-term breeding strategies?
→ broadly supported monitoring of the global population genetic inventory,
→ mitigate challenges to genetic integrity of unique (wild) resources.

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