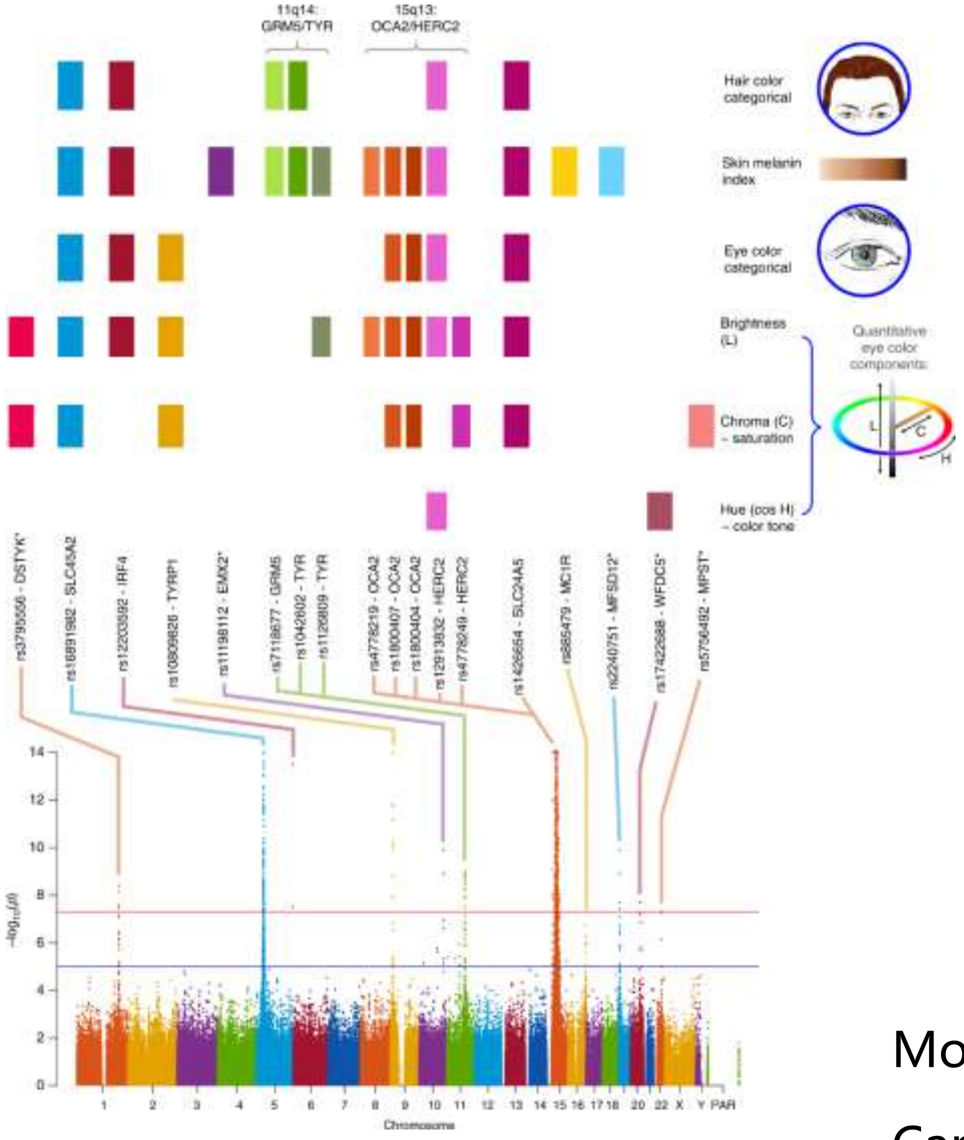
A mosaic of modular variation at a single gene underpins convergent plumage coloration

Na Kang

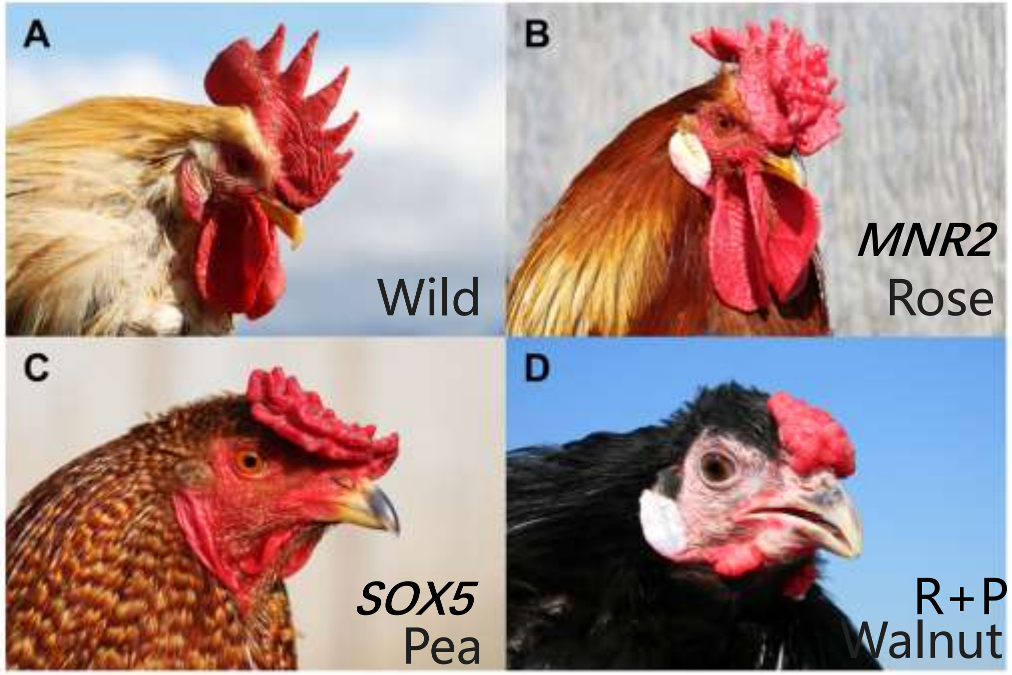
2025.12.26

PART 01

How do complex phenotypes evolve?



(Kaustubh Adhikari., et al 2019)



Four comb phenotypes in chickens

(Freyja Imsland., et al 2012)

Most phenotypic traits are thought to be **polygenic.**

Can a single gene drive phenotypic diversity?

PART 01 Introduction

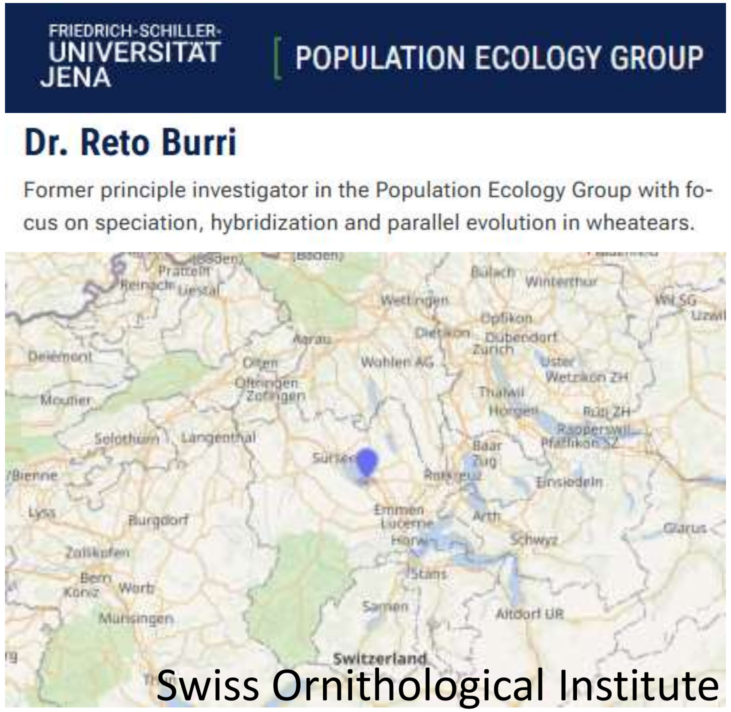
RESEARCH ARTICLE SUMMARY

PIGMENTATION

A mosaic of modular variation at a single gene underpins convergent plumage coloration

Dave Lutgen *et al.*

Reto Burri



FRIEDRICH-SCHILLER-UNIVERSITÄT JENA | POPULATION ECOLOGY GROUP

Dr. Reto Burri

Former principle investigator in the Population Ecology Group with focus on speciation, hybridization and parallel evolution in wheatears.

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Dave Lutgen

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Dave Lutgen

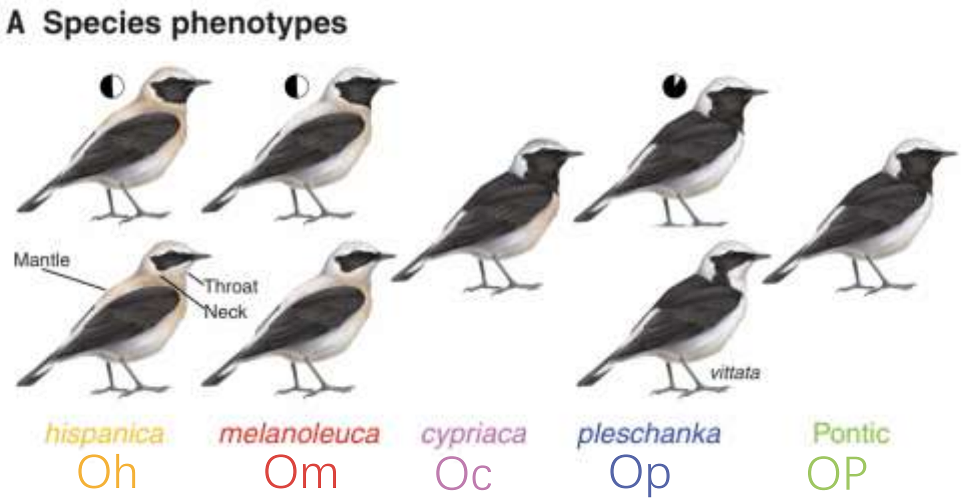
Former PhD student in the Population Ecology Group with a focus on speciation and hybridization in wheatears.

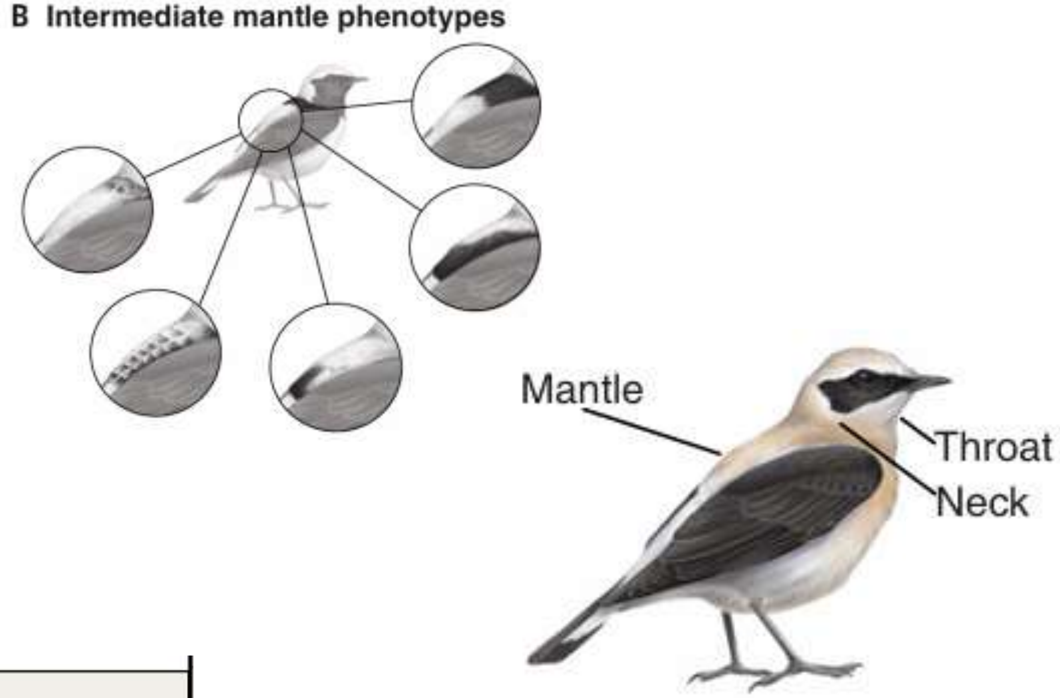
PhD Student 2021-2025

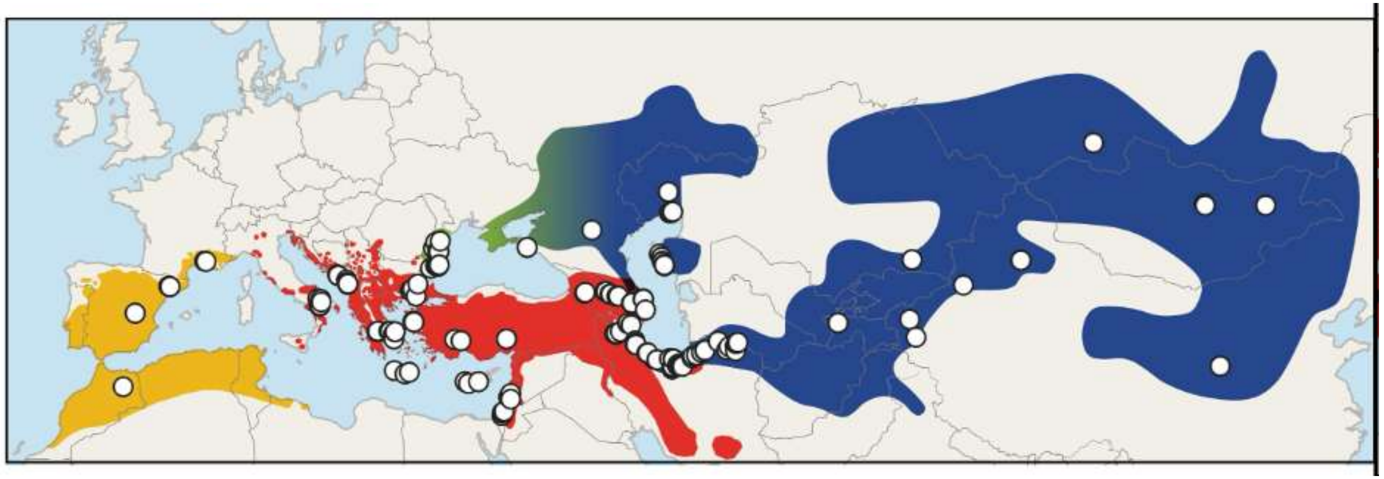
PART 01

Introduction

Wheatears (genus *Oenanthe* 鵖屬)





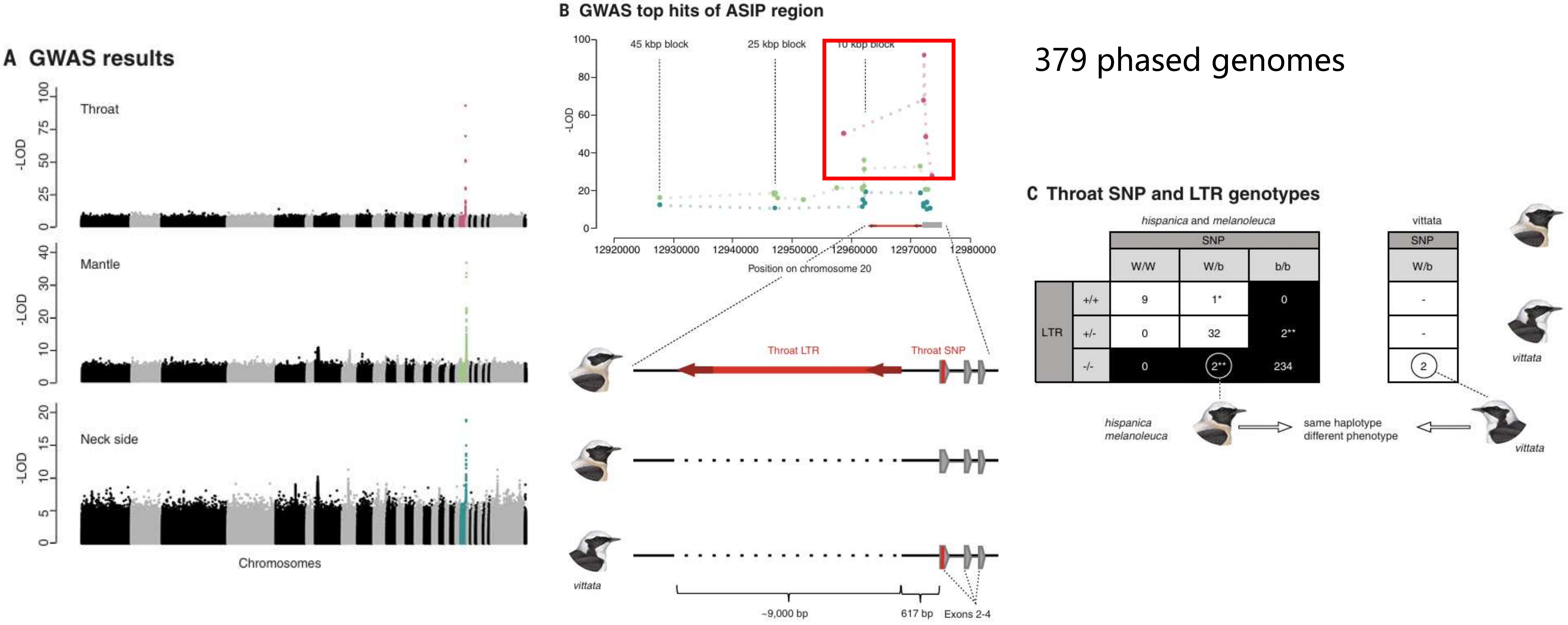


- How did these color traits evolve?
- What is the genetic basis of plumage coloration in wheatears?
- Which single gene can generate complex, modular phenotypes?

PART 02

A single gene controls all three color traits

Throat coloration: TE insertion + coding mutation



hispanica and *melanoleuca*

		SNP W/W	SNP W/b	SNP b/b
LTR	+/+	9	1*	0
	+/-	0	32	2**
	-/-	0	2**	234

vittata

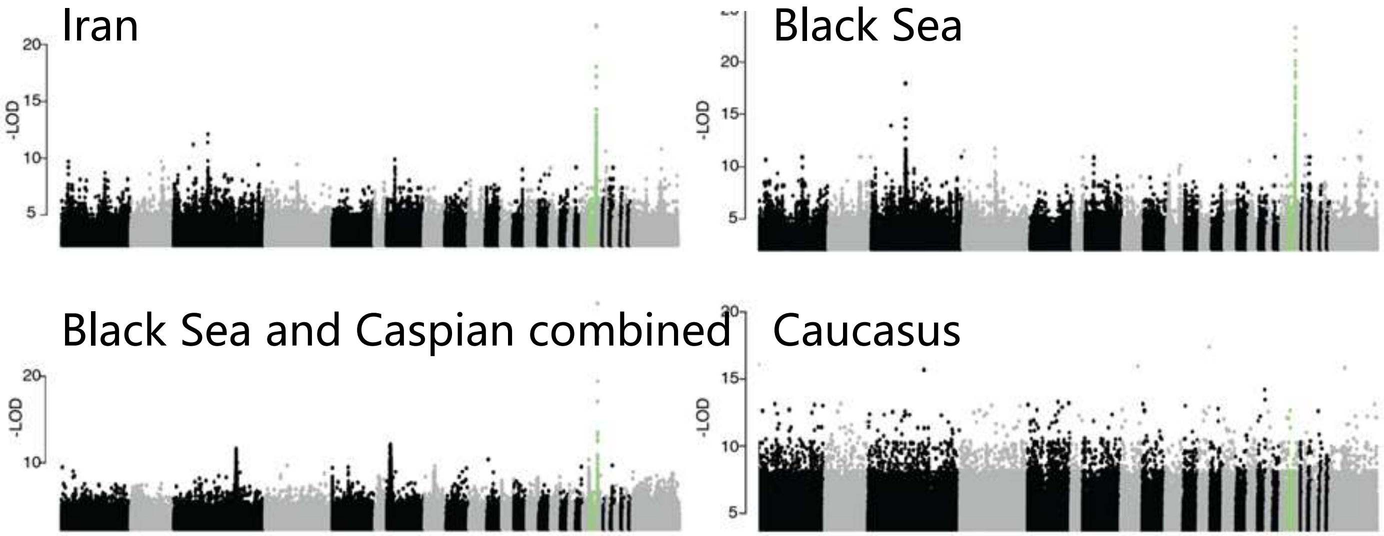
SNP W/b
-
-
2

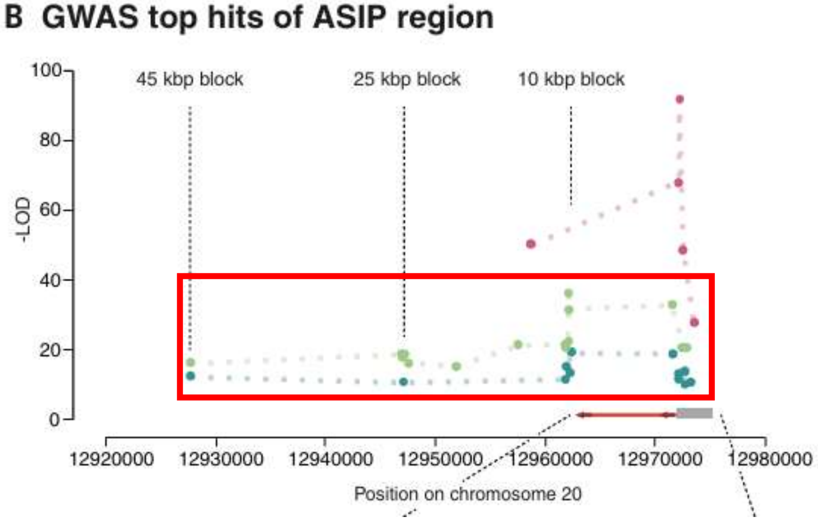
379 phased genomes

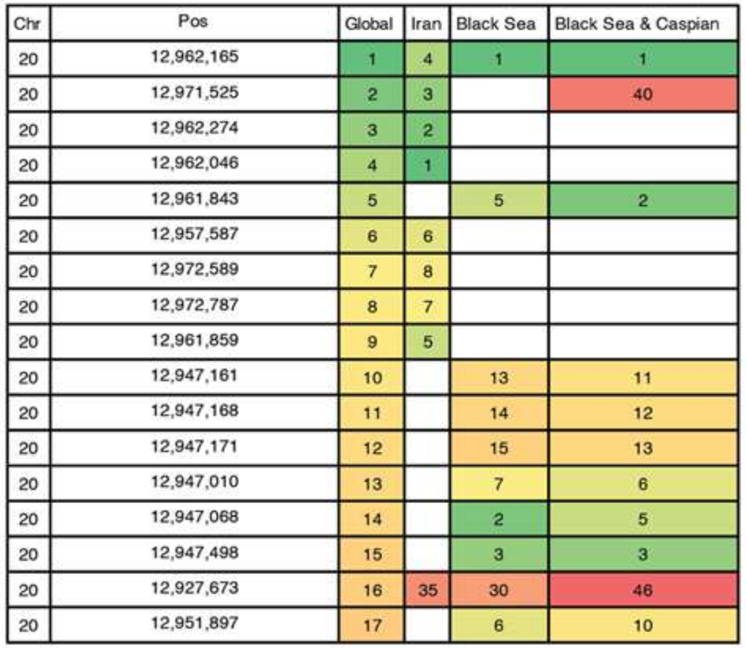
ASIP gene (Agouti Signaling Protein): well-known regulator of melanin synthesis (黑色素合成)

PART 03

Mantle and neck coloration





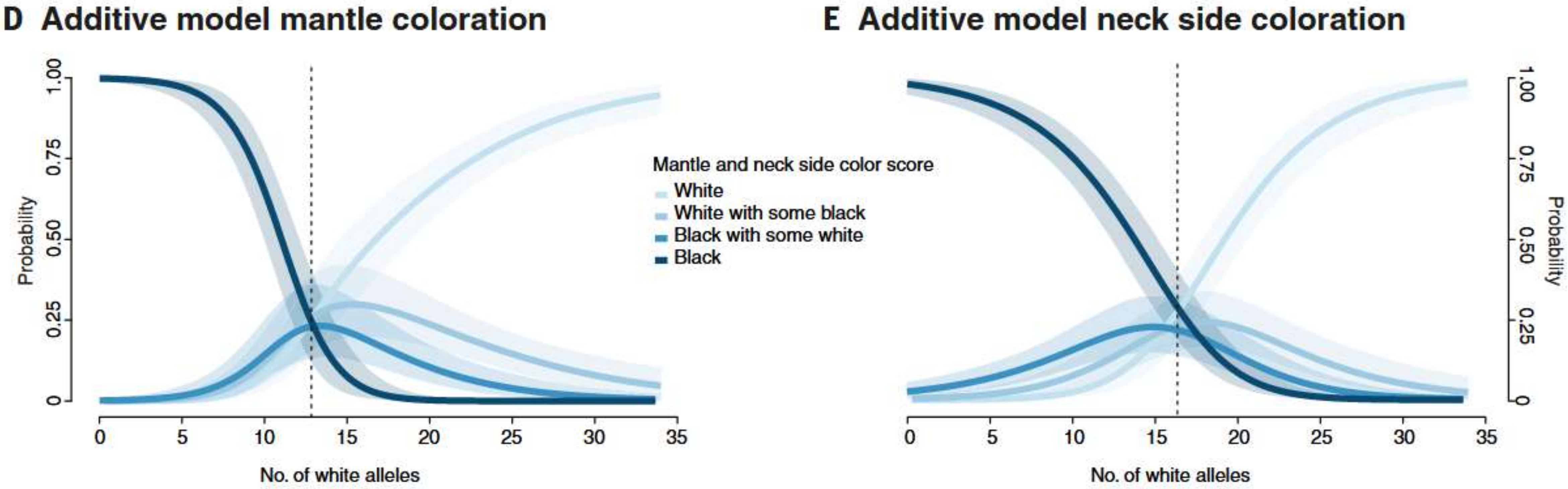


Chr	Pos	Global	Iran	Black Sea	Black Sea & Caspian
20	12,962,165	1	4	1	1
20	12,971,525	2	3		40
20	12,962,274	3	2		
20	12,962,046	4	1		
20	12,961,843	5		5	2
20	12,957,587	6	6		
20	12,972,589	7	8		
20	12,972,787	8	7		
20	12,961,859	9	5		
20	12,947,161	10		13	11
20	12,947,168	11		14	12
20	12,947,171	12		15	13
20	12,947,010	13		7	6
20	12,947,068	14		2	5
20	12,947,498	15		3	3
20	12,927,673	16	35	30	46
20	12,951,897	17		6	10

Mantle coloration is controlled by:
17 variants near ASIP;
Located up to 50kb upstream of exon 2;
Mostly noncoding SNPs and small indels.

PART 03

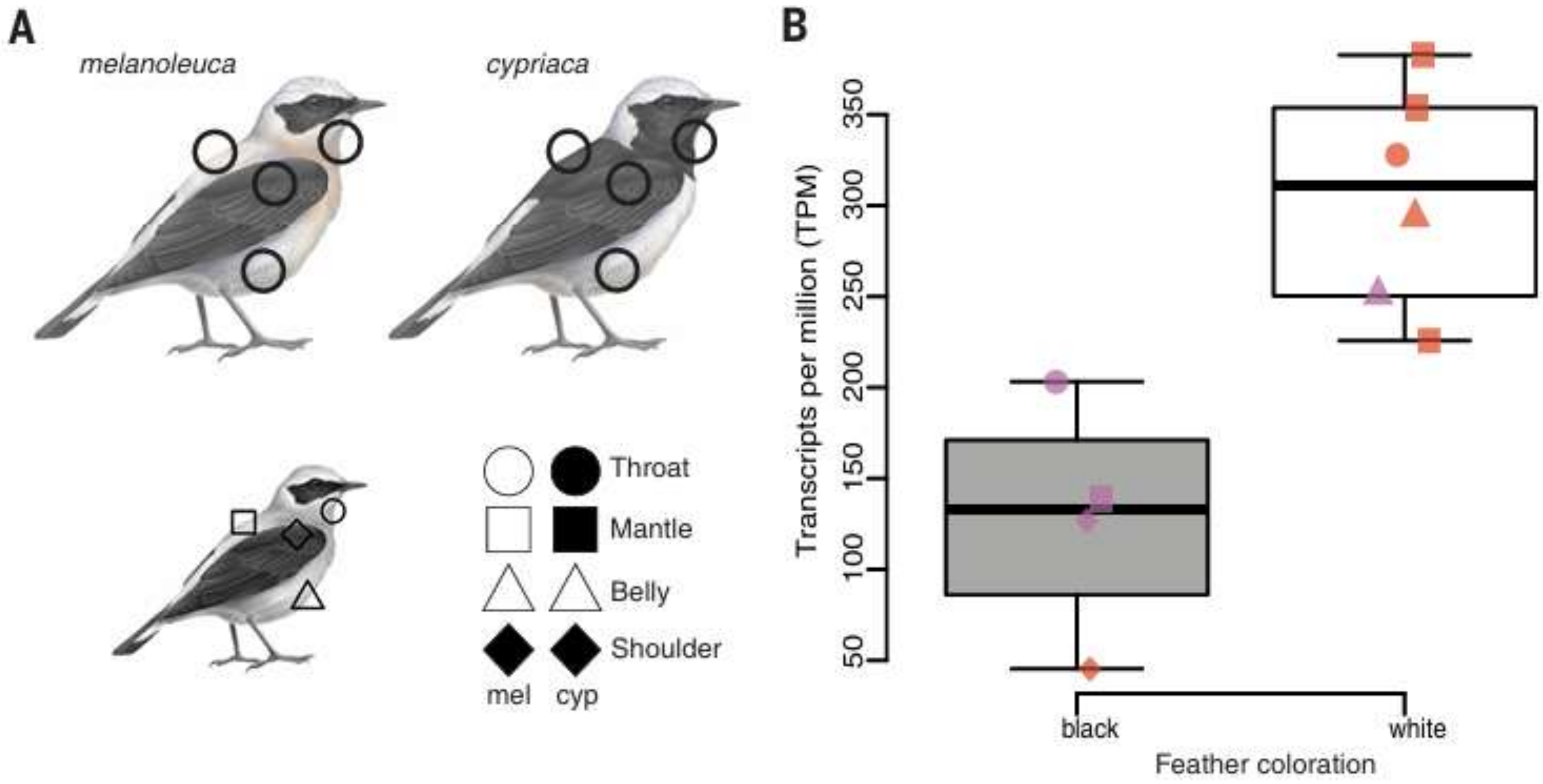
Additive ASIP-based architecture of mantle and neck coloration



Birds with more white variants – white mantles
Neck color requires more “white” ASIP alleles to express white.

PART 04

Association of ASIP expression with feather coloration

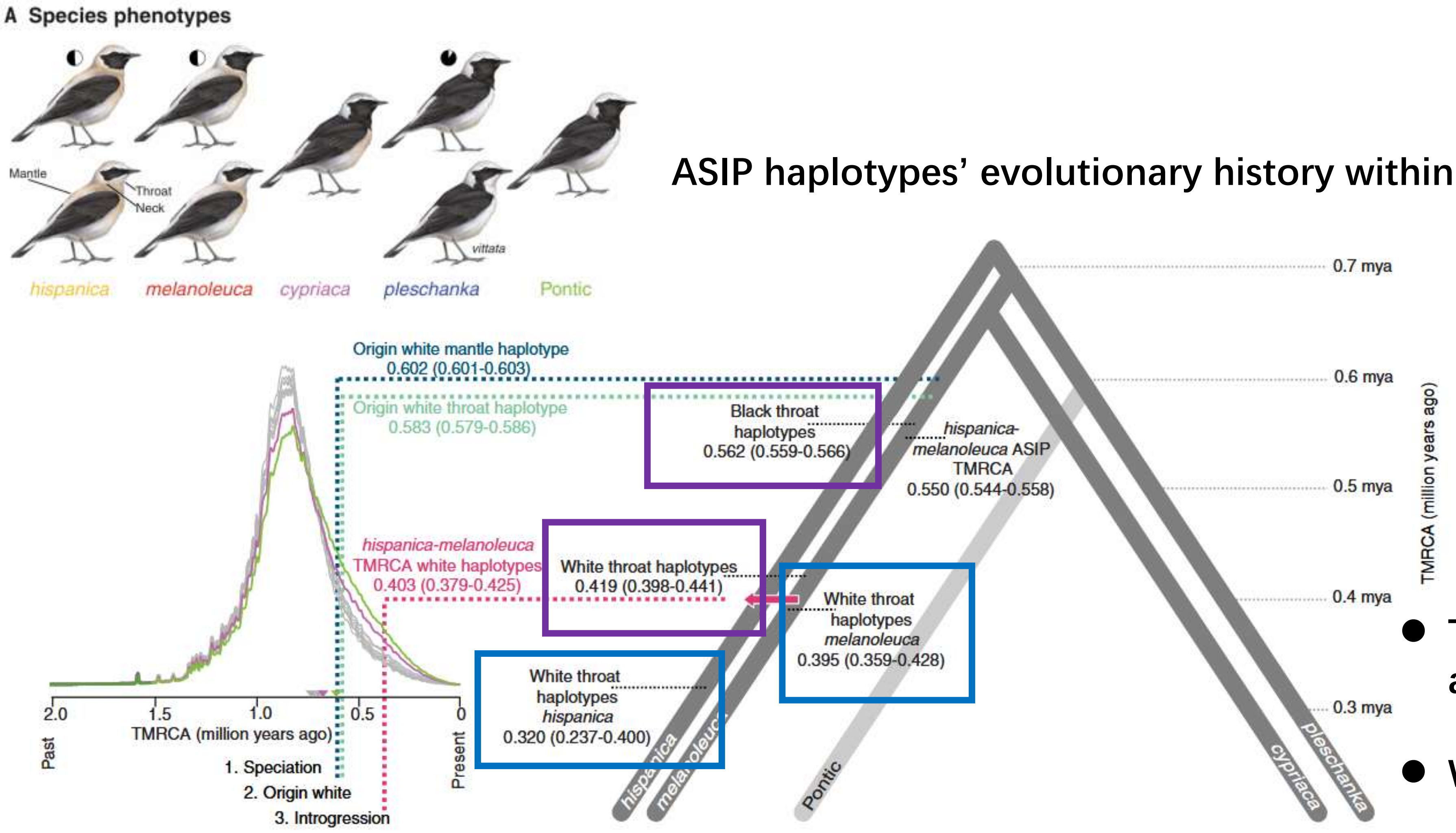


ASIP expression is ~4x higher in white feathers than black ones

PART 05

Introgressed origins of ASIP variation.

ASIP haplotypes' evolutionary history within the species tree



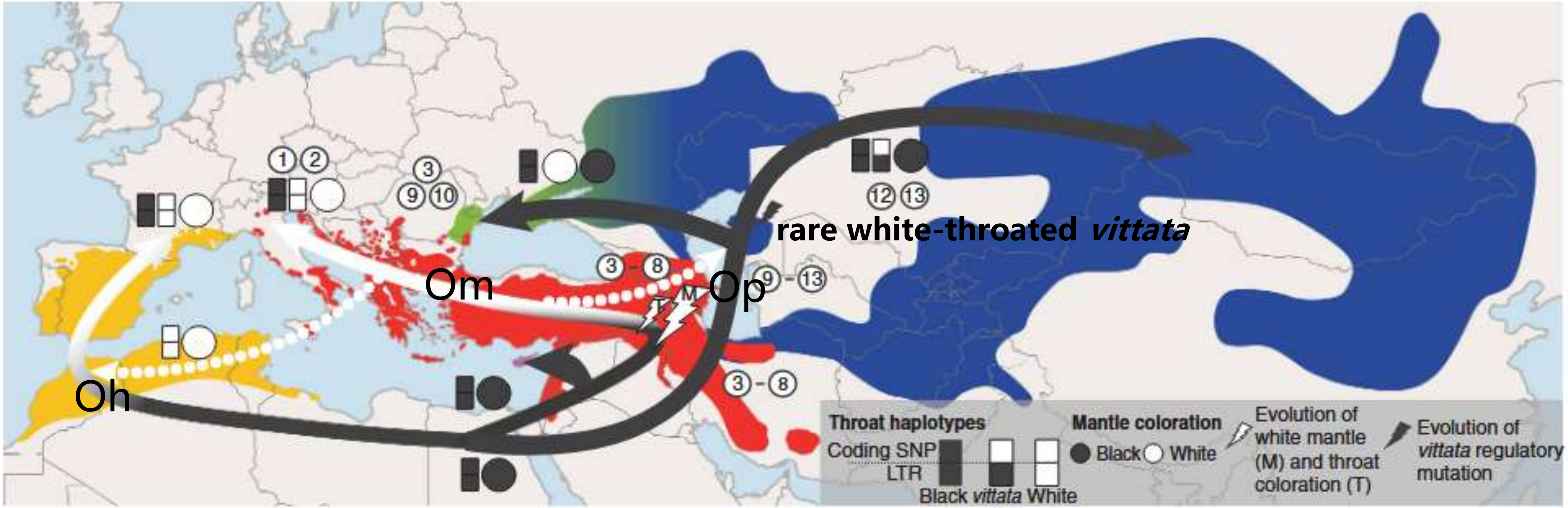
- The white haplotypes evolved after the speciation
- White plumage is a derived trait

Distributions of interspecific TMRCAs
TMRCA: Time to Most Recent Common Ancestor 最近共同祖先时间

PART 06

Multistage introgression underpins color convergence and polymorphism

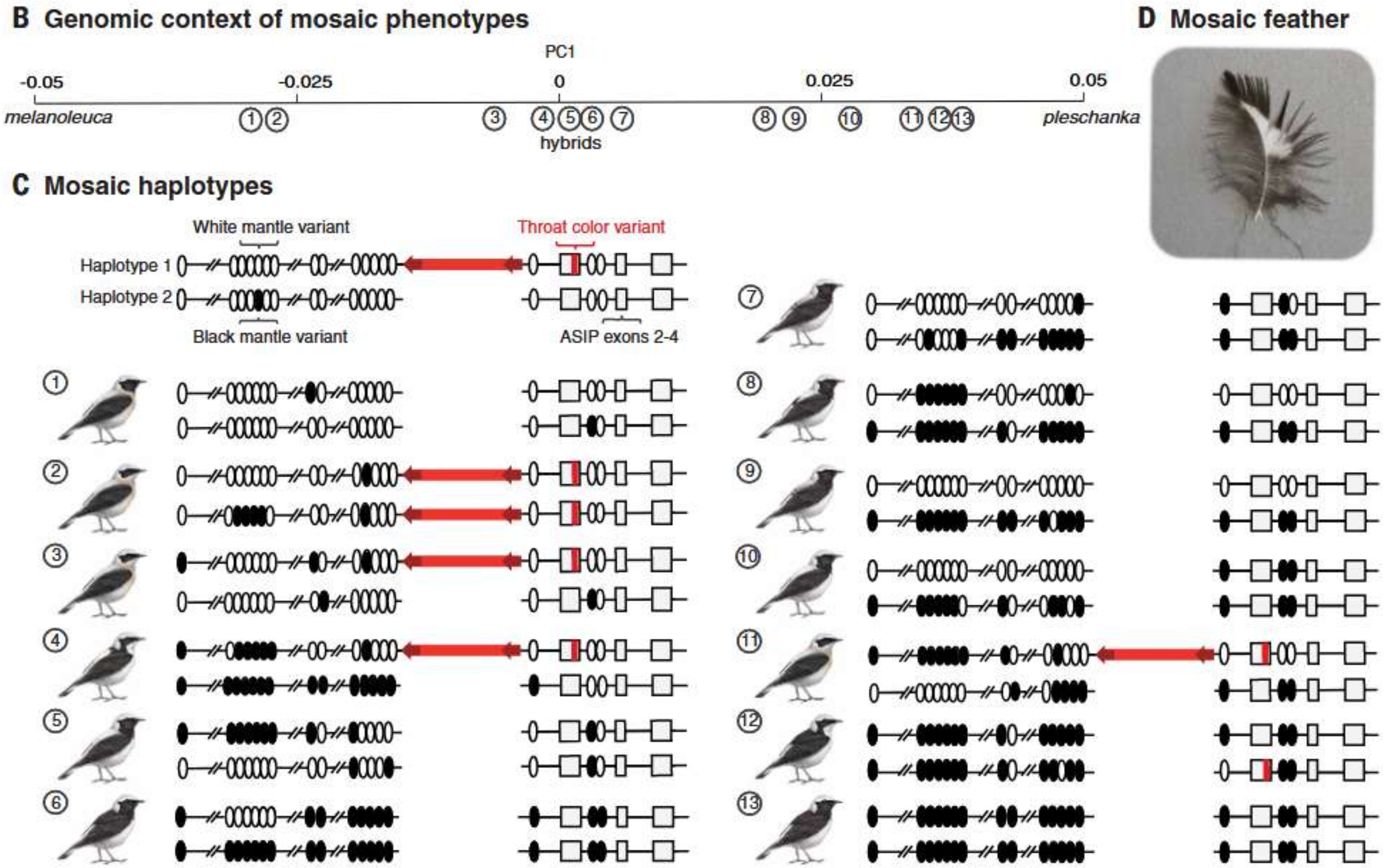
A Evolutionary history of plumage coloration



Ancestral wheatears were black-throated and black-mantled.

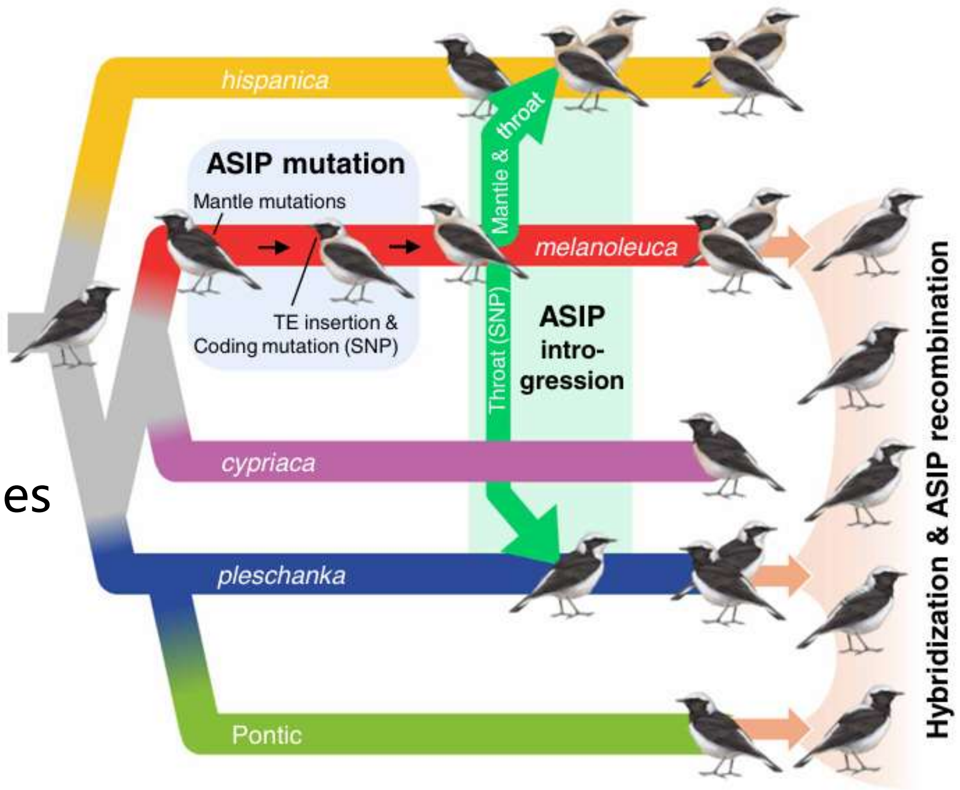
PART 06

Multistage introgression underpins color convergence and polymorphism



PART 07 Conclusion

1. A single gene can produce modular variation
2. Introgression acts as evolutionary “raw material”
3. New mutations and introgressed variation interact
4. Fine-scale recombination within a gene can build new phenotypes
5. Hybrid zones serve as evolutionary “melting pots”



Complex phenotypes do not always require many genes. They can arise from modular regulatory and coding mutation within a single gene, reshuffled over evolutionary time through hybridization and recombination.

PART 08 Limitation

1. Limited taxonomic and phenotypic sampling.

2. Functional validation is limited and requires additional experiments (e.g., CRISPR).

Thanks!

Na Kang

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