

Movement patterns and genetic analyses reveal different patterns of population structuring of Southwestern Willow Flycatchers

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Movement dynamics

- Localized breeding populations often linked through dispersal
- Dispersal increases gene flow
- Philopatry reduces gene flow
- Two approaches to documenting movement

Using direct observations of **movements** to predict population structure

- May overestimate gene flow
 - “Effective dispersal” (Prugnolle and de Meeus 2002)
- May underestimate gene flow
 - Failure of mark-recapture to detect movements (Schweizer et al. 2007)



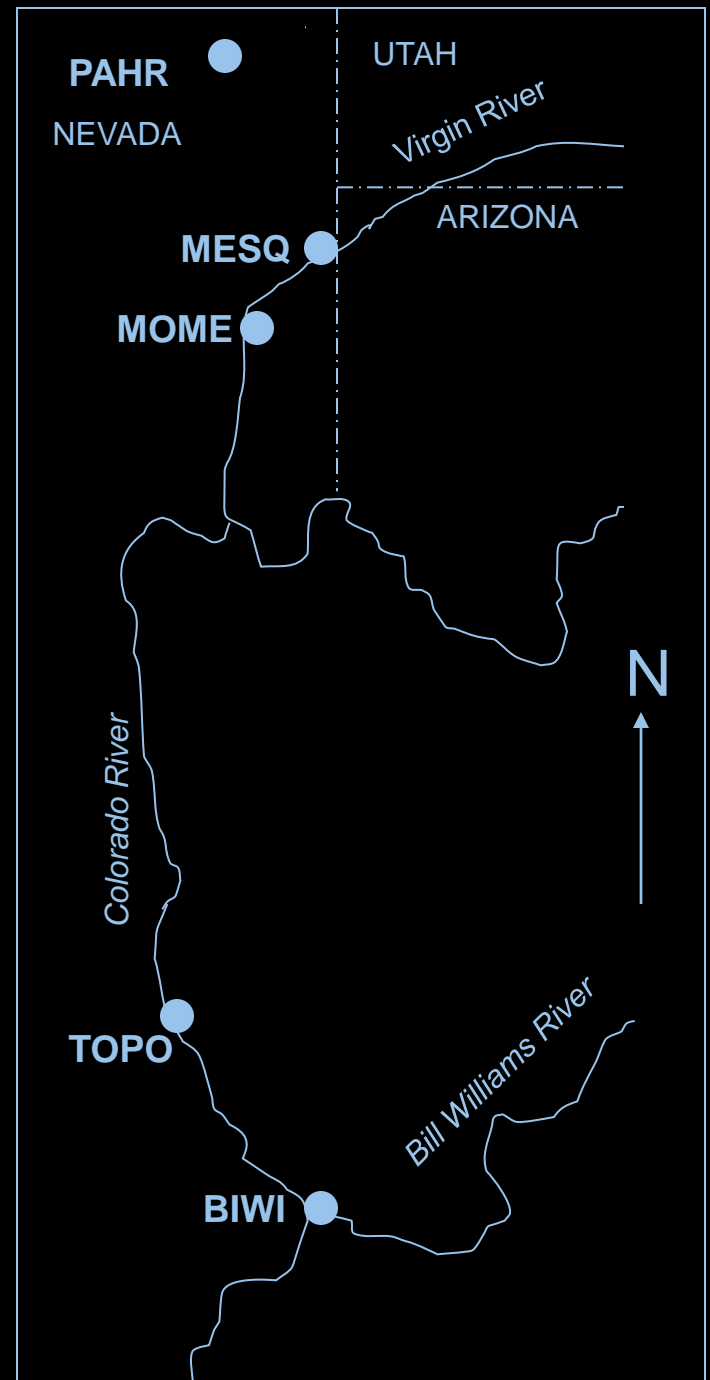
Using **genetics** to predict population structure



- Detect movements traditional analyses would miss
 - Rare and/or long-distance movements
 - Species with low detection probabilities
- May reflect historical patterns of gene flow
 - May not reflect changes in movement patterns caused by recent habitat changes

Southwestern Willow Flycatcher

- Expect low population differentiation
 - Highly mobile, migratory
- Expect high population differentiation
 - High philopatry
 - Short dispersal distances



Do movement patterns and genetic analyses predict same patterns of population structure?

1. Predict population structure based on long-term movement data

Nest monitoring and extensive resighting from 2003 – 2008



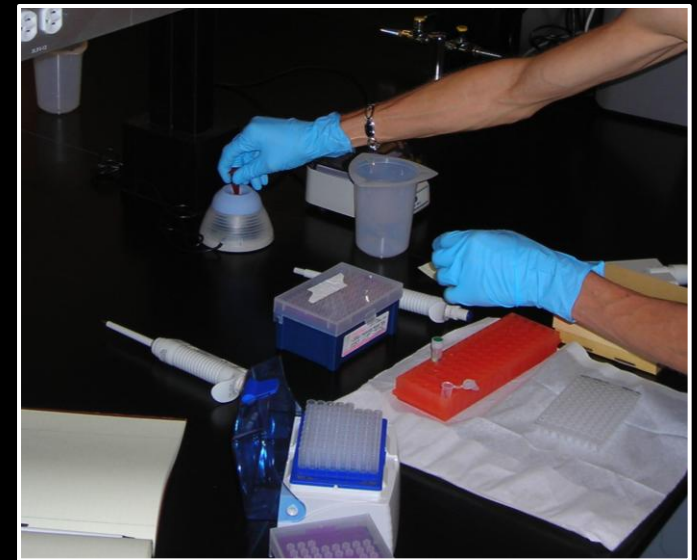
2. Predict population structure using genetics of breeding adults

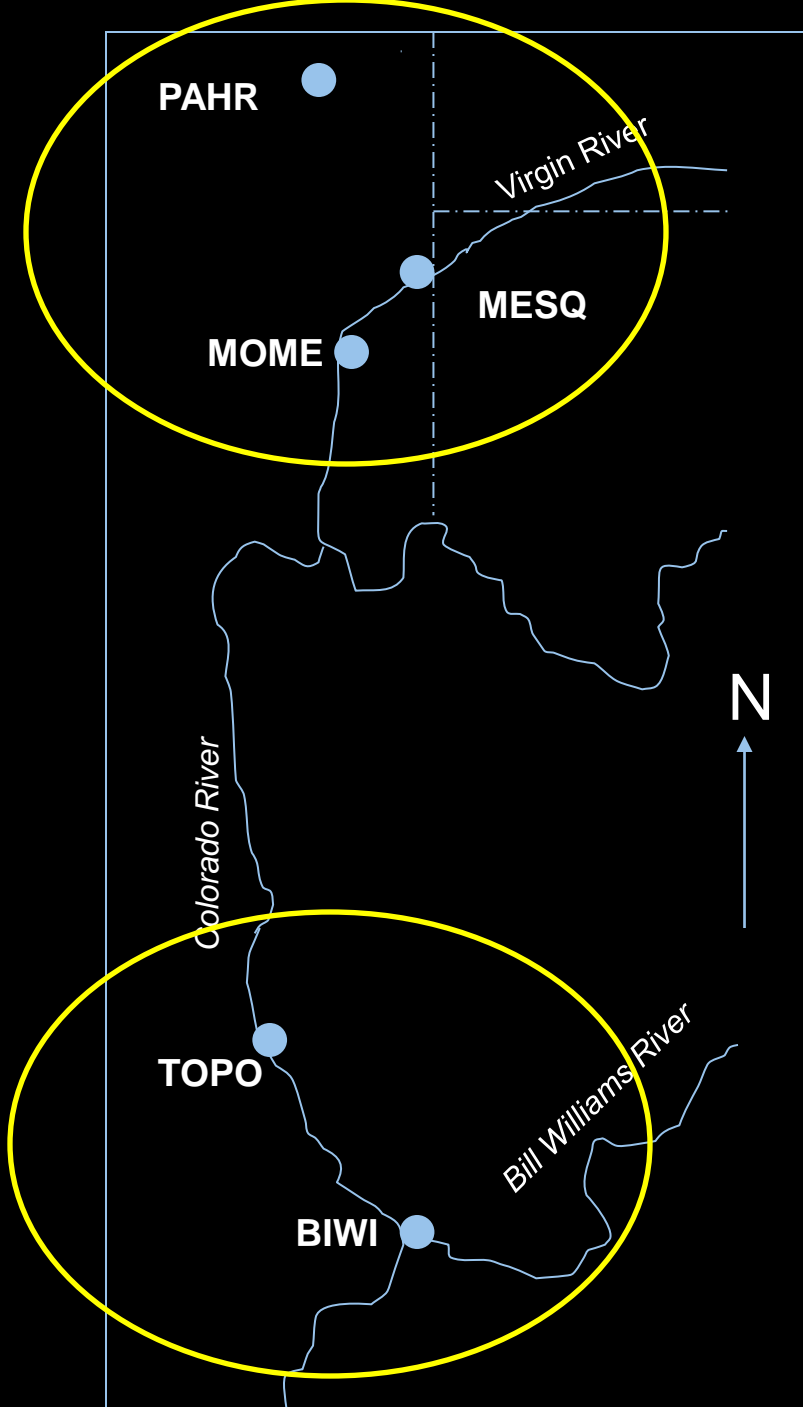
7 microsatellite loci

(Pearson et al. 2006)

2 Bayesian population clustering approaches

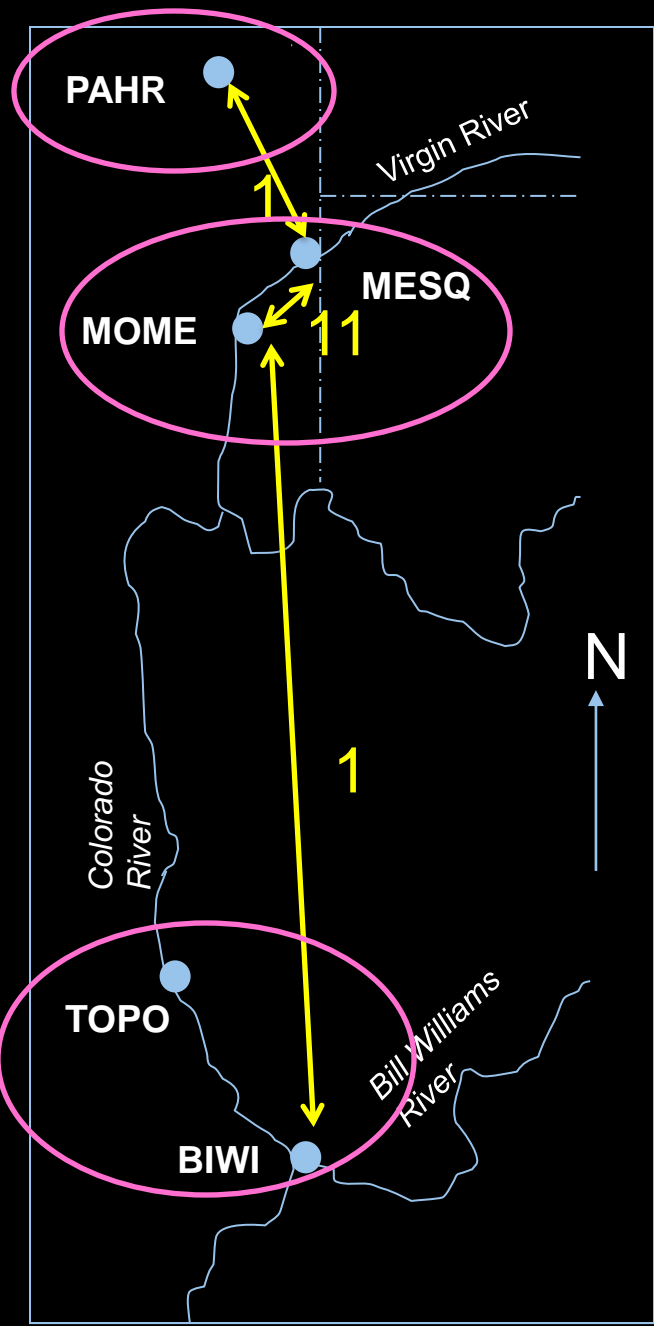
– 1 used spatially explicit data, 1 did not





Hypothesis based
on geographic
distance:

2 distinct
populations

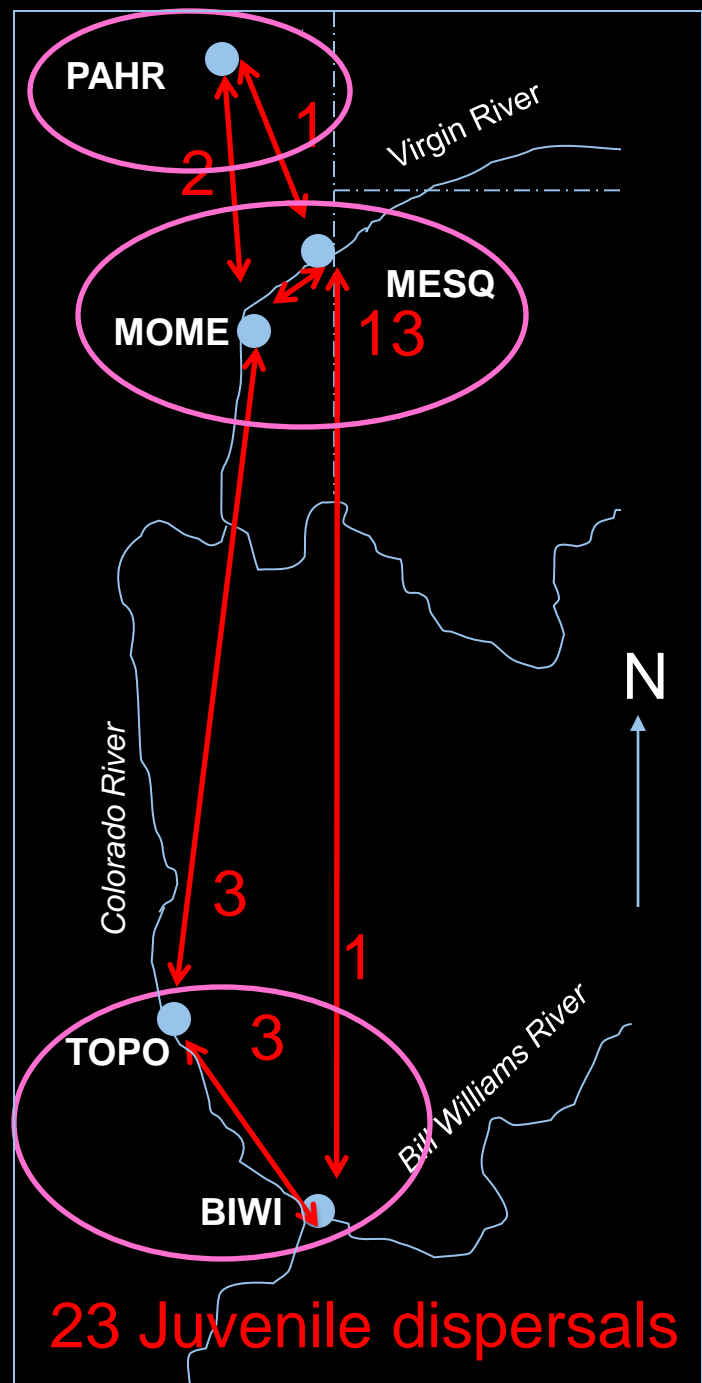


13 Adult movements

Hypothesis based on movements

EITHER
1 panmictic population

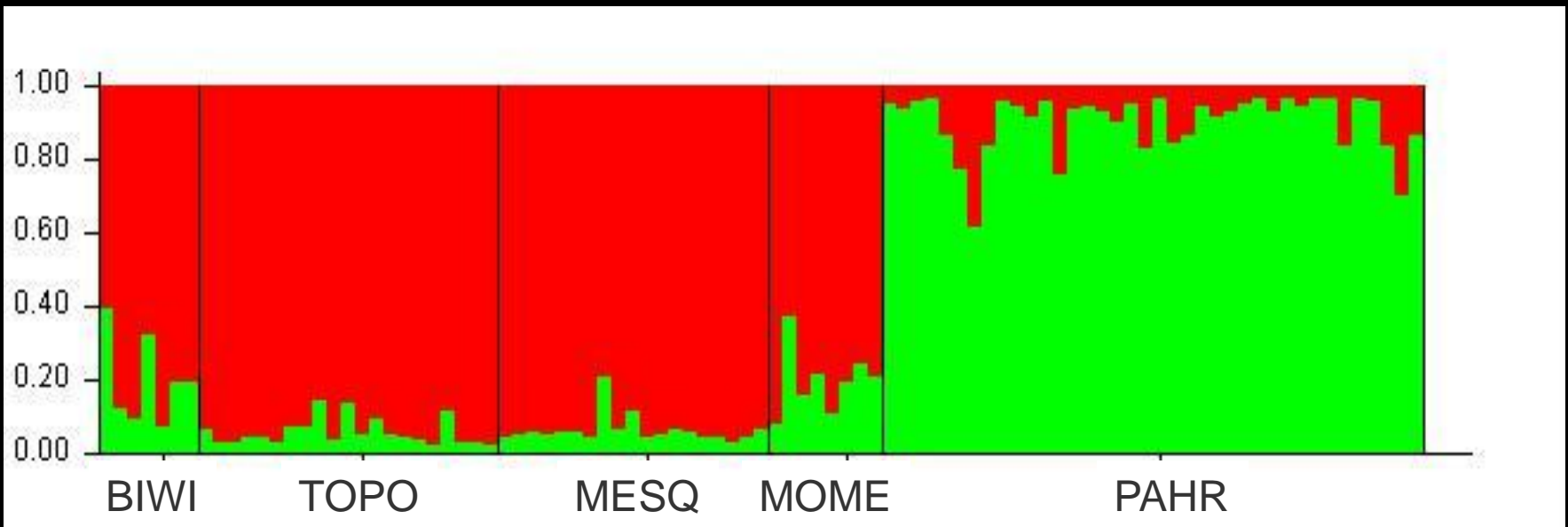
OR
3 distinct populations



23 Juvenile dispersals

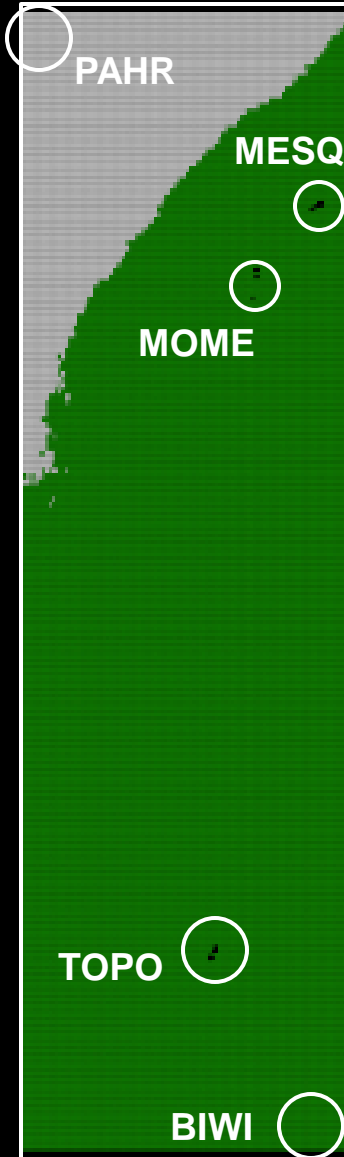
Genetic population structure: STRUCTURE

- 7 loci from 93 individuals
- 2 populations most supported by multiple runs



Genetic population structure:

GENELAND



- Uses spatial location of individuals in analysis
- 2 populations supported in 12/15 runs
 - Each run is a new analysis
 - PAHR always distinct

Why are more distant sites more genetically similar?

- Low individual turnover at PAHR keeps gene flow minimal?
 - May be due to less water and/or habitat variability among years
- Elevation and latitude gradient provide ecological barrier to gene flow (e.g. Paxton et al. 2009)

Why do movement and genetic data suggest different patterns?

1. Incomplete movement data?

- 75% of nestlings banded (McLeod et al. 2009) but still some unbanded birds at start of season

2. Floater males may contribute to gene flow?

- EPP rates for WIFLs high (Pearson et al. 2006)



Why do movement and genetic data suggest different patterns?

1. Incomplete movement data

Unbanded birds, lack of detection

1. Floater males may contribute to gene flow

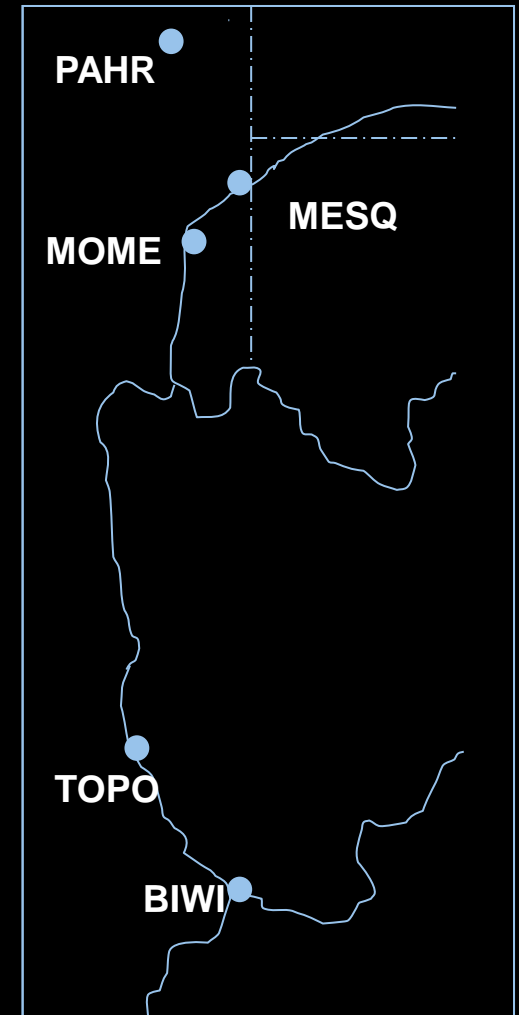
– EPP rates for WIFLs high (Pearson et al. 2006)

Why do movement and genetic data suggest different patterns?

3. Low effective dispersal?

- Migrant individuals may contribute fewer offspring than resident (Parn et al. YEAR)

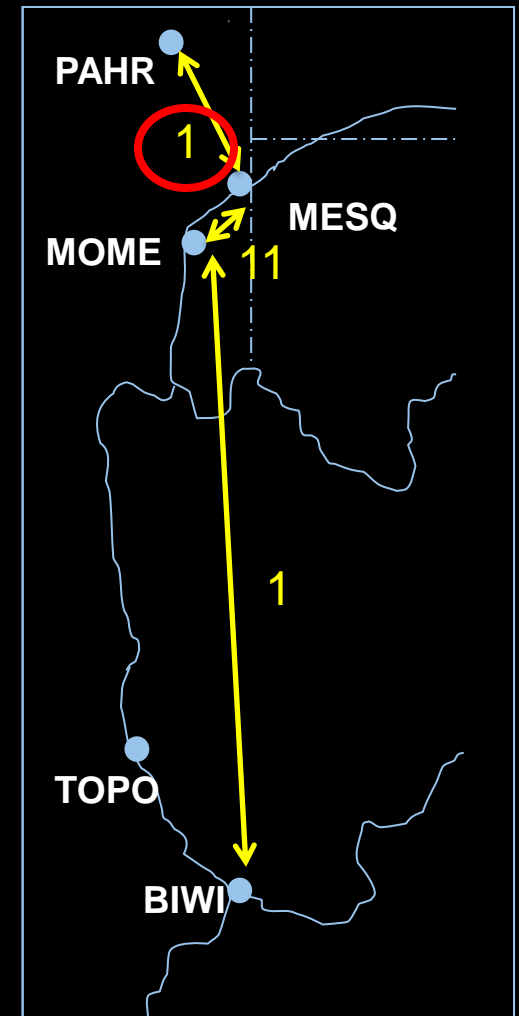
How effective were the dispersals into and out of PAHR?



Why do movement and genetic data suggest different patterns?

3. Low effective dispersal?

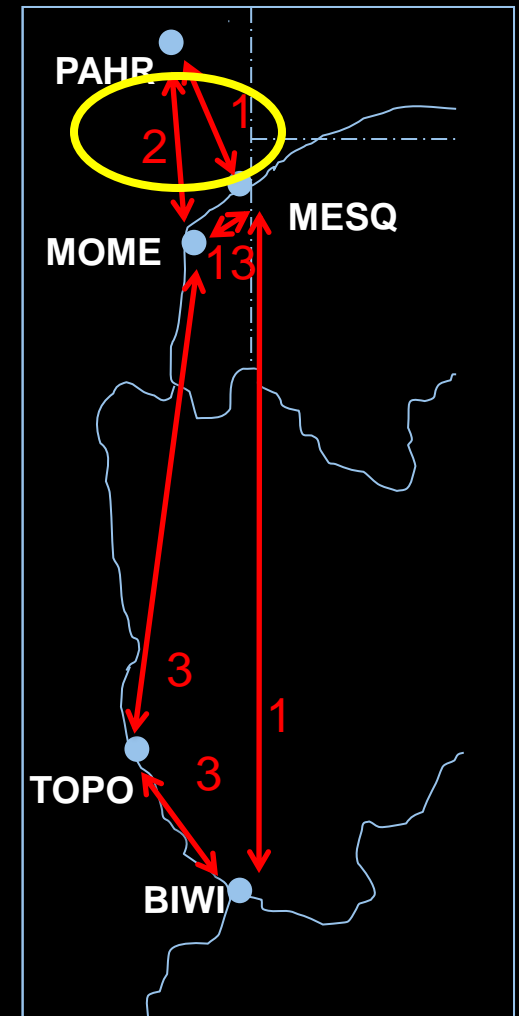
- One adult moved from MESQ to PAHR produced 15 OS, but only 1 female successfully recruited
No successful repro



Why do movement and genetic data suggest different patterns?

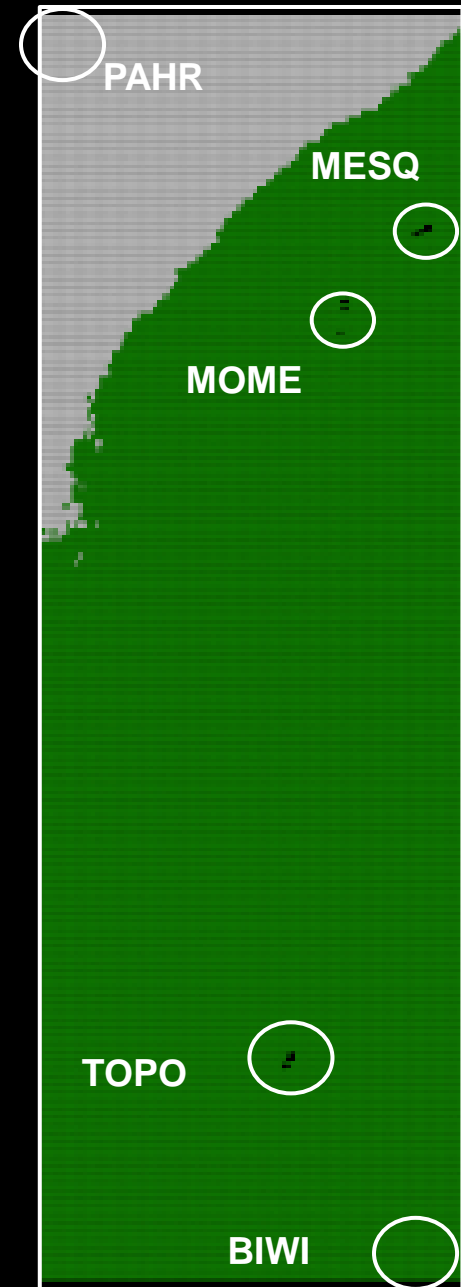
3. Low effective dispersal?

- One adult moved from MESQ to PAHR produced 15 OS, but only 1 female successfully recruited
- **3 juvenile dispersals resulted in 0 recruited offspring**



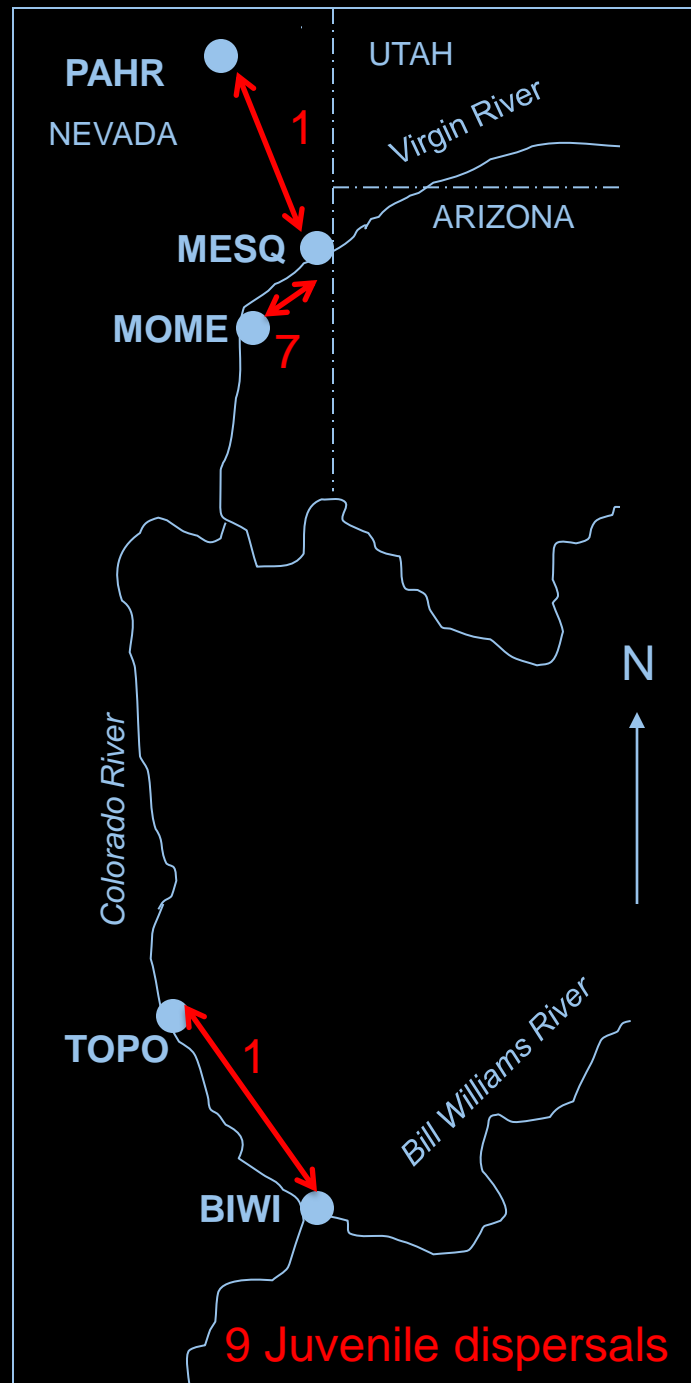
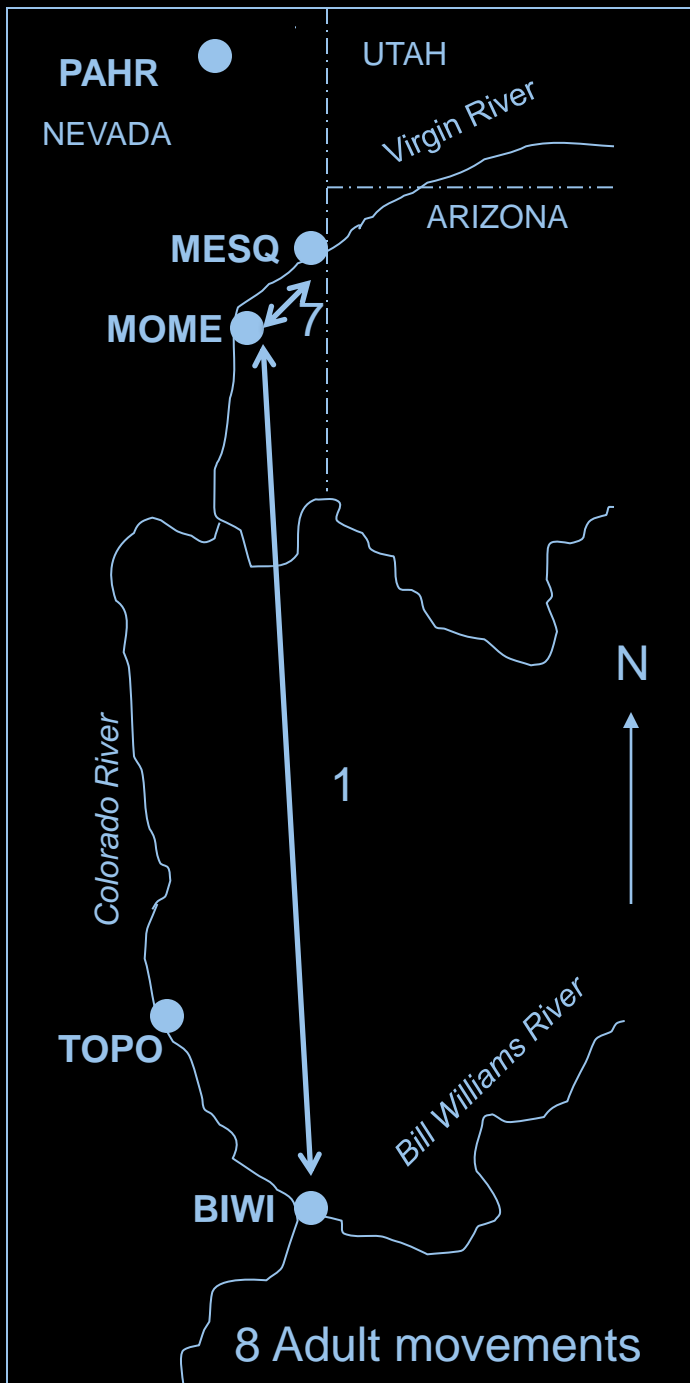
Behavioral difference with
elevation/latitudinal gradation
across subspecies
boundary?

Suggests PAHR less strongly
linked to other sites
demographically



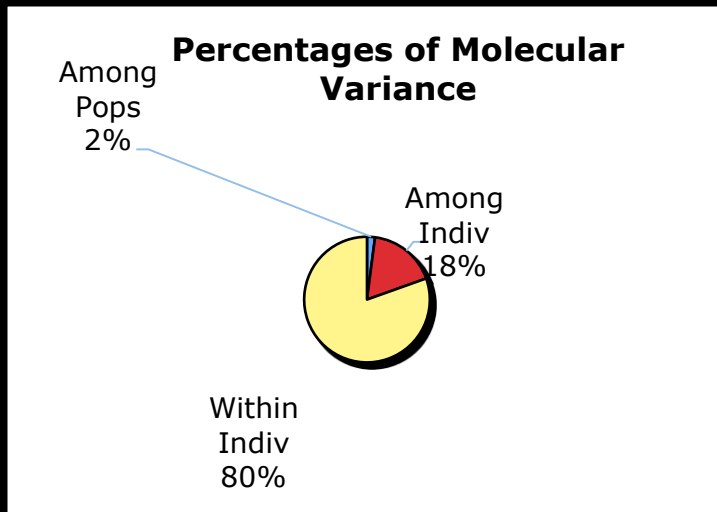
Thanks!





Population genetics

SITE	AVE ALLELES / LOCUS (SE)	# PRIVATE ALLELES	H_o	H_e	F_{IS}
BIWI	5 (0.93)	1	0.55 (0.79)	0.65 (0.67)	0.19(0.08)
MESQ	6.57 (1.11)	3	0.66 (0.05)	0.7 (0.06)	0.015 (0.13)
MOME	5.43 (0.92)	1	0.64 (0.1)	0.66 (0.099)	0.002 (0.078)
PAHR	8.43 (1.325)	8	0.69 (0.06)	0.75 (0.06)	0.06 (0.07)
TOPO	7 (1.31)	0	0.66 (0.08)	0.68 (0.09)	-0.002 (0.056)



Significant isolation by distance