

# Contemporary seed and pollen immigration in an altitudinal transect of silver fir (*Abies alba* Mill.) in a fragmented area in Central Apennines

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## BACKGROUND

Silver fir (*Abies alba* Mill.) is one of the Central-Southern European conifers with the greatest ecological and economic value. In Central Apennines, towards the southern edge of the species distribution, silver fir populations are highly fragmented due to post-glacial history and anthropogenic pressure (Piovani *et al.* 2010, Magri *et al.* 2014). Recent studies found evidence of low genetic diversity in this area, possibly due to non-negligible effects of genetic drift (Leonarduzzi 2014).

## AIMS

In this work, we studied the effect of fragmentation on genetic structure and gene flow patterns in two silver fir stands located along an altitudinal transect in Central Apennine, within the National Park of Gran Sasso - Monti della Laga (PNGSML), using nSSRs and cpSSRs.

The main aims were:

- to assess genetic diversity patterns and spatial genetic structure along the altitudinal transect;
- to describe pollen and seed dispersal dynamics in each stand.

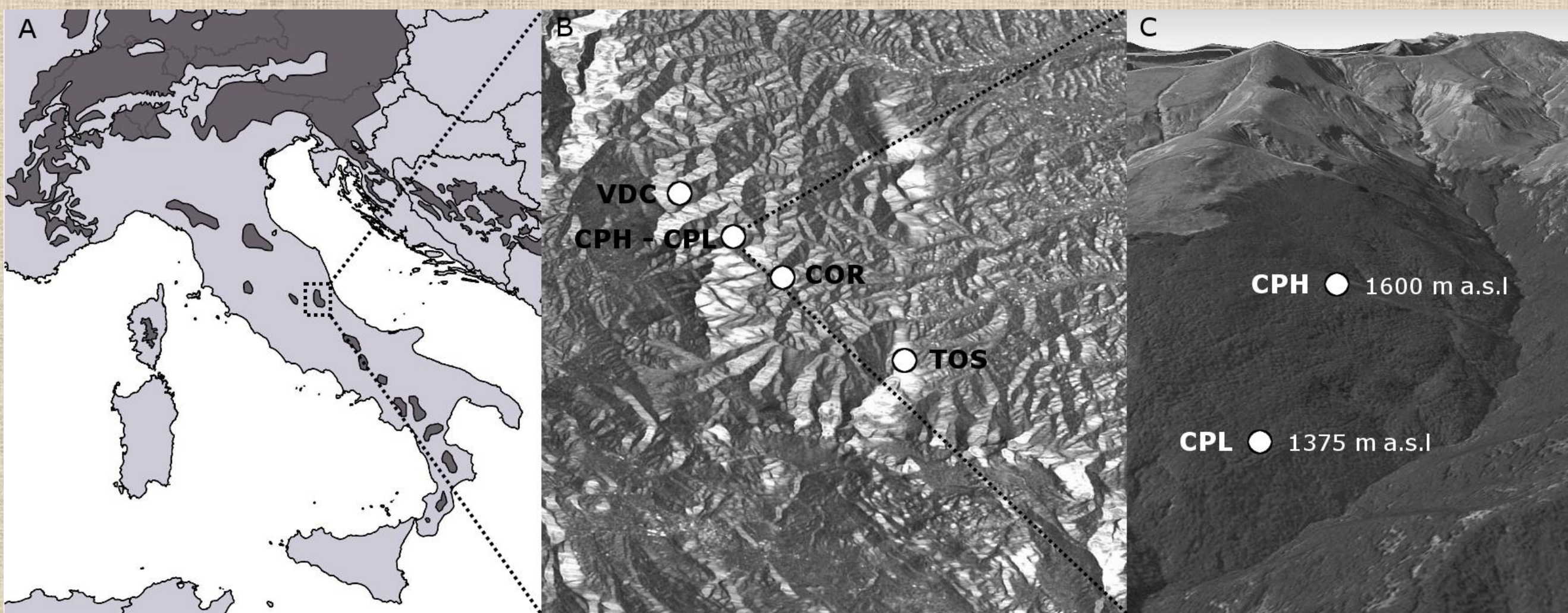


Fig.1 - A: Distribution range of silver fir in South-Eastern Europe; B: location of the sampled stands in PNGSML; C: location of the two stands (CPH and CPL) of the altitudinal transect.

## SAMPLING AND GENOTYPING

The altitudinal transect comprised two of the largest stands with natural regeneration at the maximum altitudinal span (200 m) in the area.

We sampled:

- 100 juveniles and 71 adults in the lower stand (CPL),
- 58 juveniles and 50 adults in the upper stand (CPH) (Fig.1).

All individuals were genotyped at 16 nSSRs (Postolache *et al.* 2014) and 3 cpSSRs (Vendramin *et al.* 1999).

## DATA ANALYSIS

Standard diversity indexes were calculated for each stand and demographic stage (adults and juveniles). Small scale processes were studied by spatial autocorrelation and parentage analysis.

Parentage analysis was carried out in CPH and CPL separately, using 4 different approaches:

- *Cervus*: a maximum-likelihood method with categorical assignment of parentage (Marshall *et al.* 1998);
- *cpCervus*: filtering results from *Cervus* using cpSSR compatibility;
- *NM+*: a full probability method based on a mating model (Chybicki and Burczyk 2010);
- *Colony*: a full-pedigree likelihood analysis (Jones and Wang 2010).



Fig. 2 – Juvenile individual of silver fir

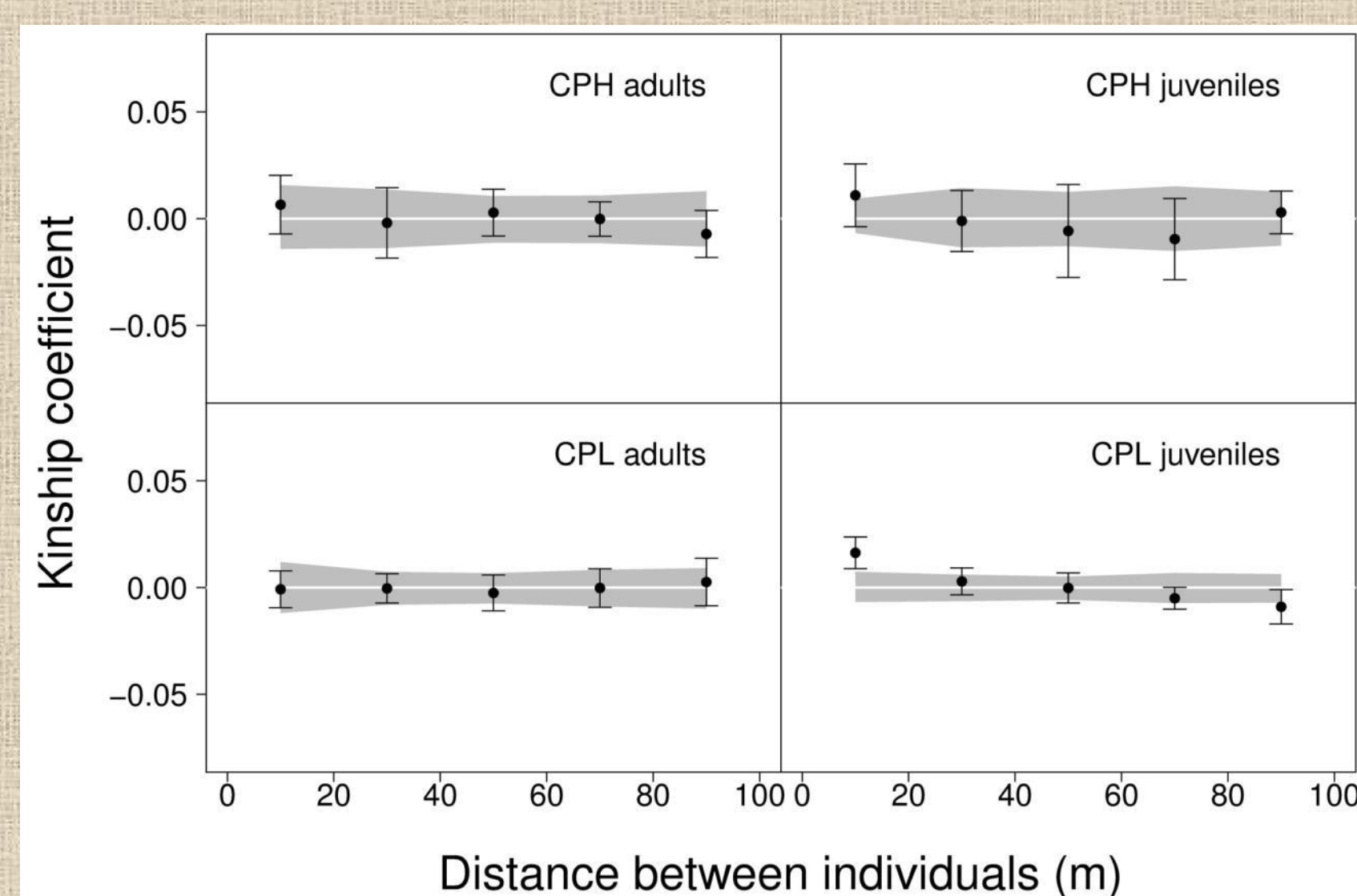


Fig. 3 -Correlograms resulting from spatial autocorrelation analysis.

## RESULTS - Genetic diversity and structure

Levels of genetic diversity were similar in the two stands and across demographic stages ( $A_r$  ranged from 3.83 in CPH juveniles to 4.26 in CPL juveniles and adults).

Pair-wise  $F_{ST}$  were generally low (from 0.003 to 0.016).

The assembly of nSSRs and cpSSRs provided high exclusion probabilities (single parent =0.9943, parent pair =0.9999).

Spatial genetic structure was weak to absent. Spatial autocorrelation was statistically significant only for CPL juveniles in the first distance class (0-20 m) (Fig.3).

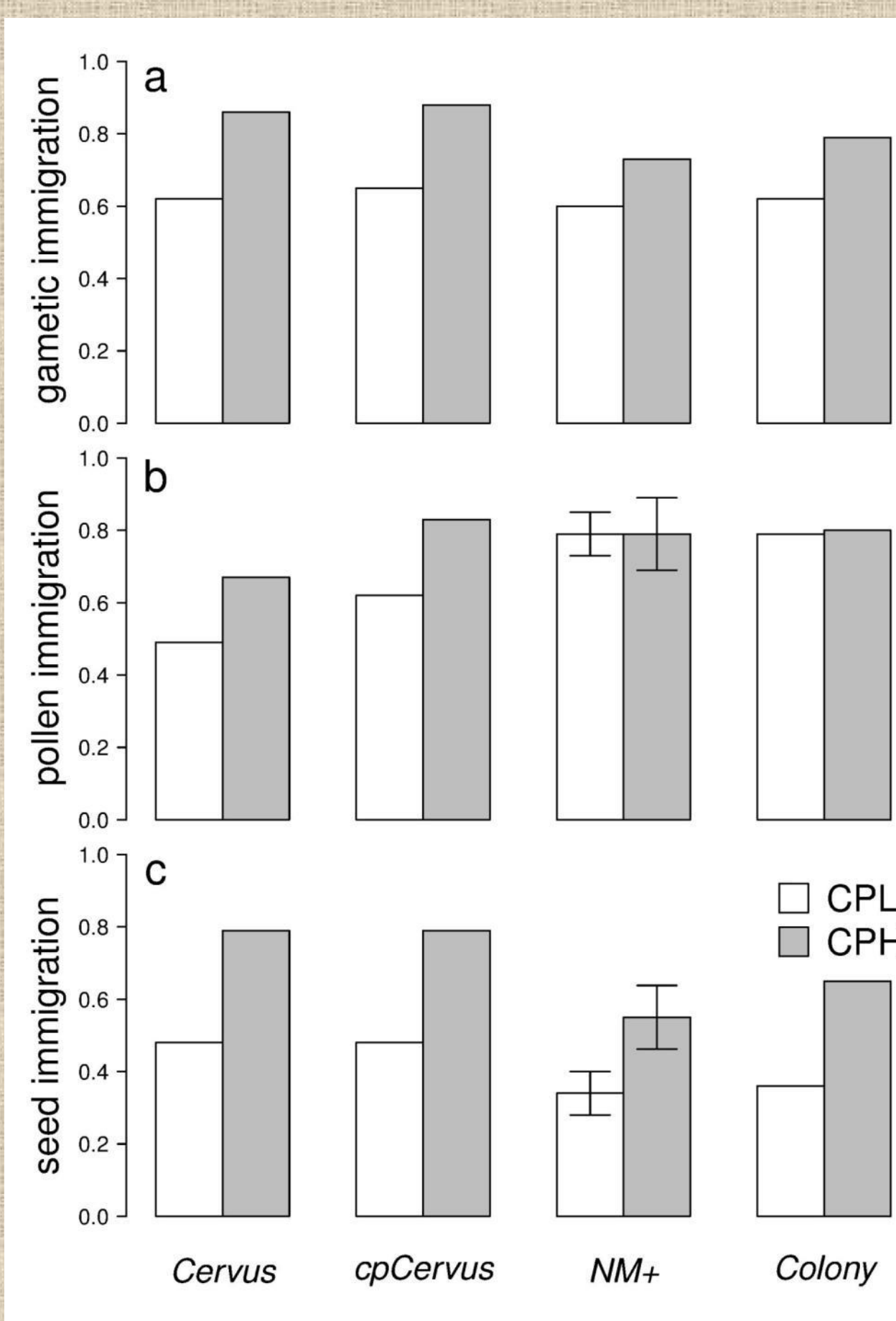


Fig.4 - Gene flow estimates (gametic, pollen and seed immigration) obtained using four different approaches

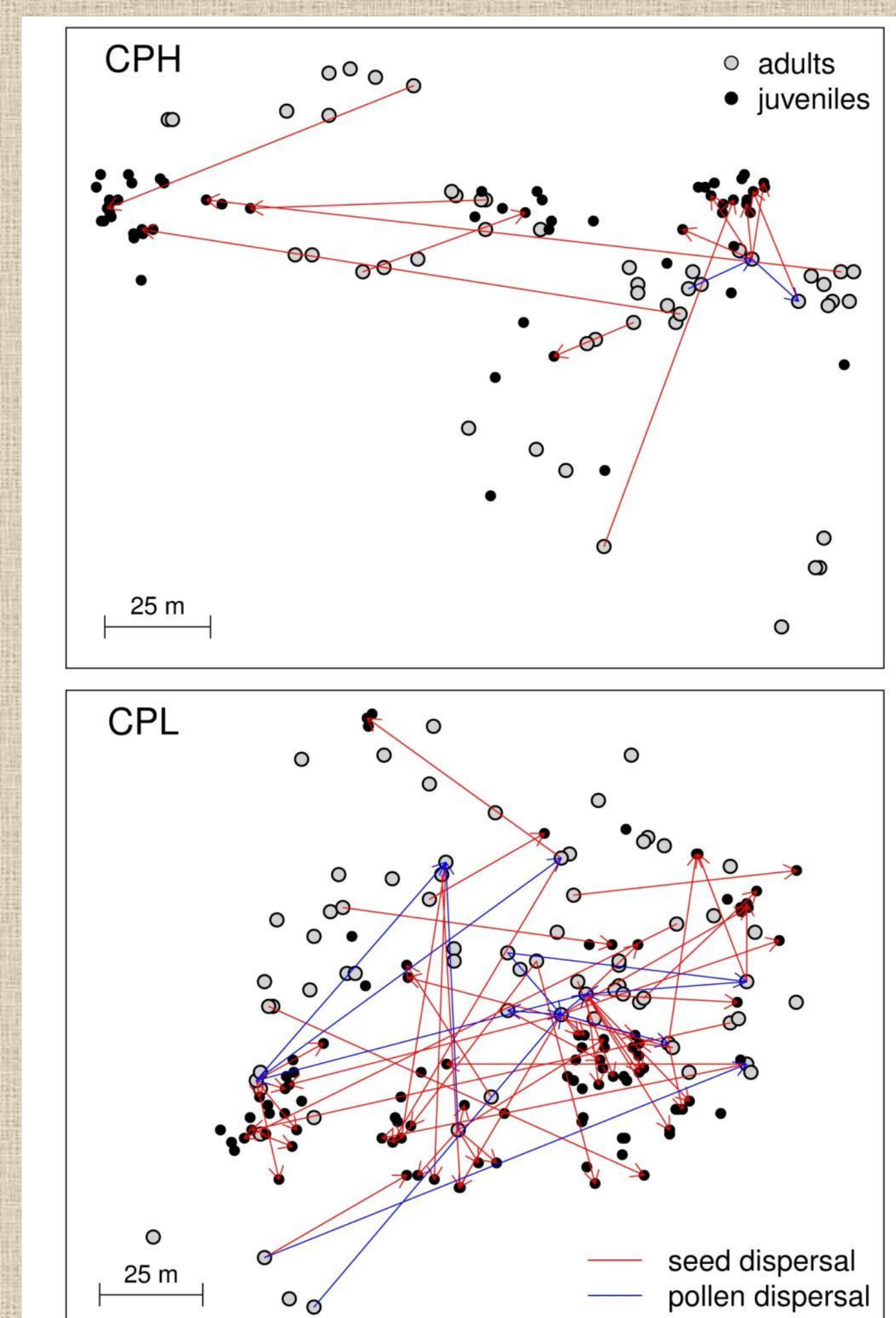


Fig. 5 - Maps of the two stands along the altitudinal transect, and patterns of realized seed and pollen dispersal reconstructed using parentage analysis according to *cpCervus* approach

## RESULTS - Parentage analysis

All four methods provided concordant gene flow estimates (Fig.4).

Estimates of gametic gene flow (*i.e.* the ratio between foreign gametes and the total number of gametes) ranged from 0.60 (*NM+*) to 0.65 (*cpCervus*) in CPL, and from 0.73 (*NM+*) to 0.88 (*cpCervus*) in CPH.

## CONCLUSIONS

This study revealed scarce genetic differentiation and comparable levels of genetic diversity both along the altitudinal gradient and across generations. In addition, evidence of substantial gene flow indicates potentially high genetic connectivity between fragmented populations of the PNGSML area. However, all gene flow estimates were higher in CPH, suggesting differences in reproductive and dispersal patterns along the transect, with CPL being mainly affected by local reproductive events and CPH more influenced by external dynamics.

## ACKNOWLEDGEMENTS

This work was partially funded by PNGSML. We thank Urbinati C., Piermattei A., Gallucci V., Garbarino M. and Leonardi S. for help during field work and data analysis.

## REFERENCES

- Chybicki and Burczyk (2010) *Mol Ecol Res*  
 Jones and Wang (2010) *Mol Ecol Res*  
 Leonarduzzi (2014) *Doctoral dissertation, Università di Parma*  
 Magri *et al.* (2014) *Review Palaeobot Palynol*  
 Marshall *et al.* (1998) *Mol Ecol*  
 Piovani *et al.* (2010) *Plant Biosyst*  
 Postolache *et al.* (2014) *Plant Mol Biol Repr*  
 Vendramin *et al.* (1999) *Mol Ecol*