

# Impact of landscape and trade on population genetics of solitary bees



Asia Piovesan<sup>a,\*</sup>, Peter Neumann<sup>a</sup>, Alexis Beaurepaire<sup>a,b</sup>

<sup>a</sup> Institut für Bienengesundheit, Vetsuisse Fakultät, Universität Bern

<sup>b</sup> Zentrum für Bienenforschung, Agroscope Liebefeld, Switzerland



## Introduction

Human land use is a major driver of biodiversity loss globally and wild bees are certainly no exception<sup>1</sup>. Moreover, release of managed bees may disrupt local adaptations of con-specific wild ones<sup>2</sup>. However, population genetics data on the actual impact of these factors remain scarce for wild bees<sup>3</sup>. Here we study population genetics of *Osmia cornuta*, a common, solitary bee in Europe, which is also managed, to investigate consequences of land use and trade on local wild populations.



Fig.1: Map of Switzerland with the urban (blue) and rural (green) sampling areas. Trap nests are shown in the landscapes.

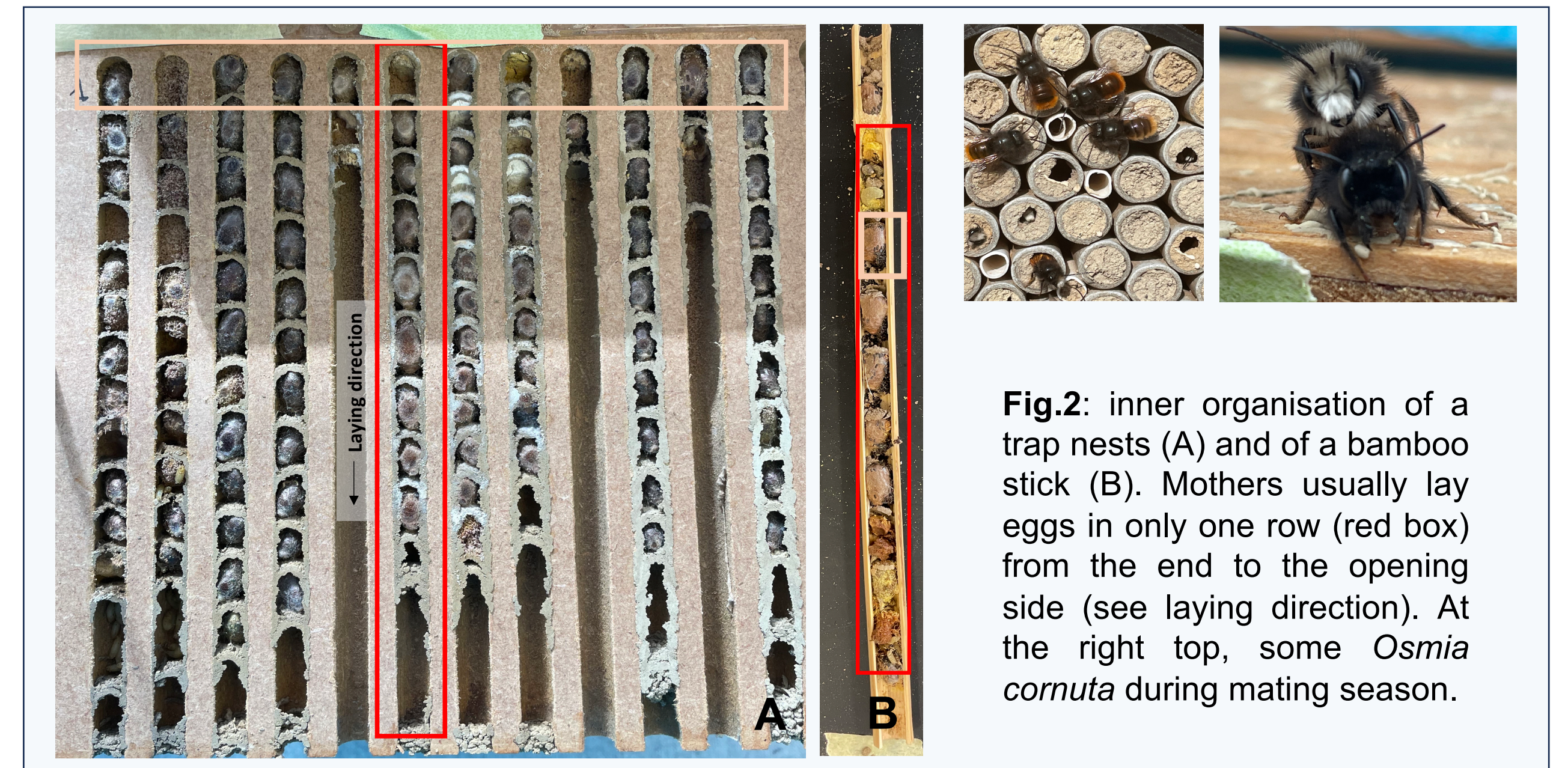


Fig.2: inner organisation of a trap nests (A) and of a bamboo stick (B). Mothers usually lay eggs in only one row (red box) from the end to the opening side (see laying direction). At the right top, some *Osmia cornuta* during mating season.

## Materials and Methods

In two regions with different landscapes (Fig.1), trap nests were placed before the mating season of *Osmia cornuta* (early March) and left until early fall. The first cocoon of each row (N=190 rural area, N=47 urban area) (orange box in Fig.2) and cocoons from the two companies were used for DNA analysis (N=56 Company 1, N=39 Company 2). DNA was extracted using Chelex<sup>TM</sup> 4 and genotyped at 11 polymorphic microsatellite loci<sup>5</sup>. The results were visualized with Peak Scanner software and analysed with GenAlEx 6.5 software<sup>6</sup> and *adeigenet* package from R (version 4.2.3)<sup>7</sup>. Genetic Distance index (Fst), Inbreeding index (Fis), number of private alleles, allelic richness (NA) and observed heterozygosity (H obs) were calculated with GenAlEx. PCA was performed with *adeigenet* package. A Kruskal-Wallis test was performed on observed heterozygosity and allelic richness.

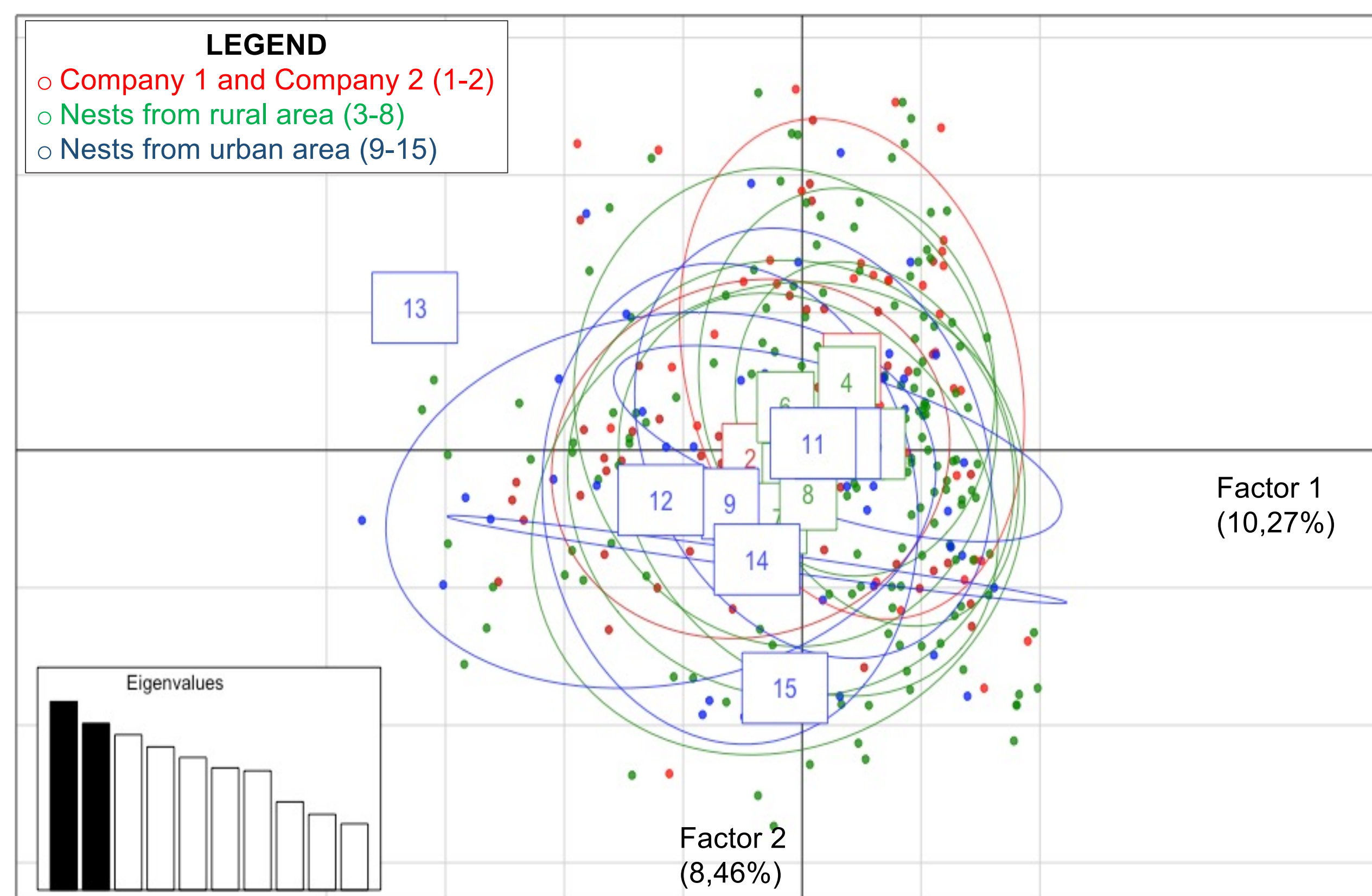


Fig.4: Principal Component Analysis of *Osmia cornuta* populations from all the nests of urban and rural areas and from the two companies.

Fst	COMPANY 2	RURAL AREA	COMPANY 1	URBAN AREA
URBAN AREA	0,024 ***	0,01 **	0,015 **	0
COMPANY 1	0,022 ***	0,007 *	0	
RURAL AREA	0,019 ***	0		
COMPANY 2	0			

Table 1: Pairwise total Genetic Distance index (Fst) of *Osmia cornuta* populations. \*\*\* p-value = 0,01, \*\* p-value = 0,02, \* p-value = 0,09. Probability value is based on 99 permutations.

	Fis	N. PRIVATE ALLELES
COMPANY 1	0,215	2
COMPANY 2	0,222	0
RURAL AREA	0,424	9
URBAN AREA	0,339	17

Table 2: Inbreeding index (Fis) and number of private alleles of *Osmia cornuta* populations.

## Results

The Principal Component Analysis (Fig.4) shows that the populations analysed are mixed. Fst values (Table 1) confirm that genetic distances between populations are small, but significant. Both rural and urban populations are closer to the population from Company 1 than to the population from Company 2, even if for the rural population both distance values are smaller than for the urban population. Populations from the two sampling areas are genetically not far from each other.

According to Kruskal-Wallis test, there are no significant differences between populations in the observed heterozygosity and in the allelic richness (Fig.5). Fis values (Table 2) show a low level of inbreeding in all four populations, but rural populations present twice the level of inbreeding of the two companies. The urban population presents the highest number of private alleles.

## Discussion

The observed low levels of genetic differentiation suggest that the *Osmia cornuta* populations are interconnected. The Fst values and the higher number of private alleles in the urban population, combined with a lower request of pollination services in the city, may suggest that trade could be responsible for this admixture. However, the higher level of inbreeding in rural area despite more trade contrasts to that. The number of private alleles in urban population suggests also the potential presence of local genotypes.

More analyses and sampling are required to better understand the impact of landscape and trade on *Osmia cornuta* populations.

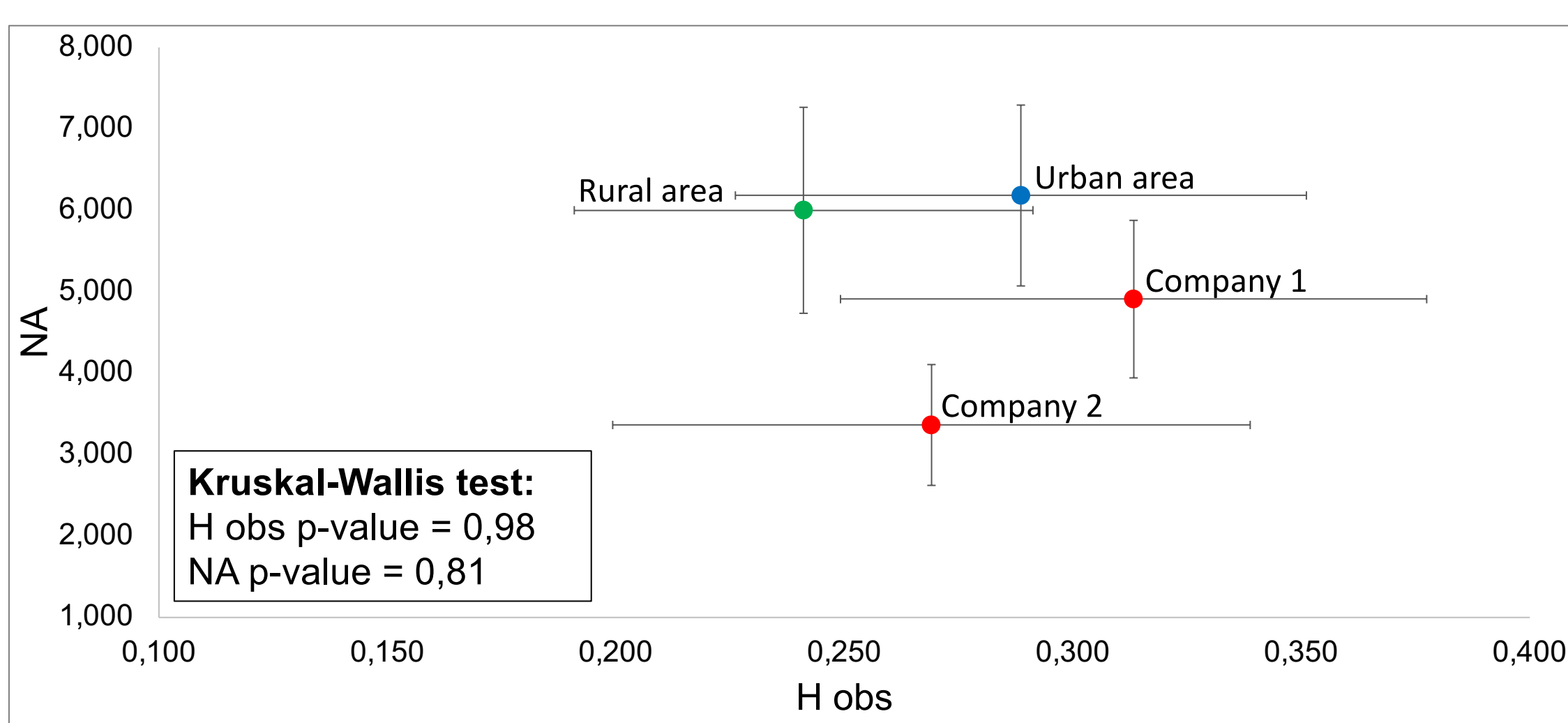


Fig.5: Average (±S.D) allelic richness (NA) vs observed heterozygosity (H obs) in *Osmia cornuta* populations from urban and rural areas and the two companies.

## References

- Brown M.J.F. & Paxton, R.J. (2009). The conservation of bees: a global perspective. *Apidologie* 40:410-416.
- Bartomeus I., Molina F.P., Hidalgo-Galiana A., Ortego J. (2020). Safeguarding the genetic integrity of native pollinators requires stronger regulations on commercial lines. *Ecological Solutions and Evidence* 1:e12012.
- Webster M.T., Beaurepaire A., Neumann P., Stolle E. (2023). Population Genomics for Insect Conservation. *Annual Review of Animal Biosciences* 11:115-140.
- Strange J.P., Knoblett J., Griswold T. (2009). DNA amplification from pin-mounted bumble bees (*Bombus*) in a museum collection: effects of fragment size and specimen age on successful PCR. *Apidologie* 40:134-139.
- Van Eeckhoven J., Horsburgh G.J., Dawson D.A., Mayer K., Bretman A., Duncan, E.J. (2022). Development of a multiplex microsatellite marker set for the study of the solitary red mason bee, *Osmia bicornis* (Megachilidae). *Molecular Biology Reports* 49:783-788.
- Peakall R. & Smouse (2012). GenAlEx 6.5 genetic analysis in Excel. Population genetic software for teaching and research—an update. *Bioinformatics* 28(19):2537-2539.
- Jombart T. (2008). *Adegenet*: a R package for the multivariate analysis of genetic markers. *Bioinformatics* 24(11):1403-1405.