

Species ^a	Eastern plot		Western plot		Northern plot	
	Marked/ recaptured (% recapt.)	Focal plants ^b	Marked/ recaptured (% recapt.)	Focal plants ^b	Marked/ recaptured (% recapt.)	Focal plants ^b
<i>Anthophora dispar</i>	0/ 0 (0)	-	0/ 0 (0)	-	2/ 1 (50)	-
<i>Anthophora plumipes</i>	0/ 0 (0)	-	0/ 0 (0)	-	6/ 2 (33.33)	AU,PM
<i>Anthophora rubricrus</i>	42/ 28 (66.66)	AT,AU	17/9 (53)	AT,LB	9/ 0 (0)	AU,PM
<i>Cubitalia parvicornis</i>	7/ 1 (14.28)	AU,VH	0/ 0 (0)	-	3/ 0 (0)	AU
<i>Eucera aeaqata</i>	4/ 2 (50)	AU	0/ 0 (0)	-	2/ 0 (0)	AU
<i>Eucera cypria</i>	21 /0 (0)	AU,VH	1/0 (0)	VH	51/ 6 (11.76)	AU,VH
<i>Eucera graeca</i>	59/ 18 (30.5)	AT,AU,VH	1/0 (0)	AU	24/ 6 (25)	AU,VH
<i>Eucera g. sp. nova</i>	15/ 4 (26.66)	AU,VH	0/ 0 (0)	-	16/ 4 (25)	AU,VH
<i>Eucera m. sp. nova</i>	99/ 30 (30.3)	AT,AU,VH	0/ 0 (0)	-	104/ 40 (38.46)	AU,VH
<i>Eucera nigrilabris</i>	0/ 0 (0)	-	0/ 0 (0)	-	1/ 0 (0)	AU
<i>Eucera parnassia</i>	1/0 (0)	-	0/ 0 (0)	-	0/ 0 (0)	-
<i>Eucera w. sp. nova</i>	0/ 0 (0)	-	0/ 0 (0)	-	2/ 0 (0)	AU
<i>Megachile sicula</i>	3/ 1 (33.33)	AT,AU,VH	1/0 (0)	AU	0/ 0 (0)	-
<i>Synhalonia spectabilis</i>	5/ 1 (20)	AT,AU	2/0 (0)	AT	2/ 0 (0)	AU
<i>Xylocopa iris</i>	15/ 3 (20)	AT,AU,SH,VH	0/ 0 (0)	-	23/ 5 (21.74)	AU,VH
Total bees	271/88	-	22/9 (40.9)	-	245/ 64 (26.1)	-

^a *sp. nova*, undescribed species (Risch personal communication)

^b *Alakanna tinctoria* (AT), *Anchusa undulata* (AU), *Prassium majus* (PM), *Leopoldia bicolor* (LB), *Scilla hyacinthoides* (SH), *Vicia hybrida* (VH)

Appendix 2. Large, long-tongue bee species recorded in three mark-recapture experiments in four sampling plots, representing natural habitat fragments in Sha'ar-Poleg nature reserve and in Yaqum, Israel

Abundant species	Sha'ar-Poleg, plot A		Sha'ar-Poleg, plot B		Yaqum, plot C		Yaqum, plot D	
	Marked/ recaptured (% recapt.)	Focal plants	Marked/ recaptured (% recapt.)	Focal plants	Marked/ recaptured (% recapt.)	Focal plants	Marked/ recaptured (% recapt.)	Focal plants
<i>Anthophora agama</i>	11/ 10 (90.9)	AF,AU,PM,TP	14 (0)	PM	12/ 1 (8.3)	BB,PM,TD	20/ 7 (35)	BB,EA,PM,TD
<i>Anthophora plumipes</i>	81/ 16 (19.75)	AF,AU,PM,VH	94/ 21 (22.3)	AF,AR,PM	12 (0)	AF,CV,VH	41/ 19 (46.3)	AT,PM
<i>Anthophora rubricrus</i>	4/ 2 (50)	AR,VH	8/ 0 (0)	AR	1/ 1 (100)	BB	35/ 21 (60)	AT
<i>Eucera cypria</i>	32/ 5 (15.6)	LO,VH	9/ 0 (0)	VH	44/ 3 (6.8)	VH	1/ 1 (100)	-
<i>Eucera kilikiae</i>	89/ 13 (14.6)	VH	24/ 3 (12.5)	VH	0	-	9/ 1 (11.1)	AT
<i>Eucera nigrilabris</i>	54/ 0 (0)	AF	3/ 0 (0)	AF	1/ 0 (0)	OP	15/ 1 (6.6)	AT
<i>Eucera w. sp. nova^a</i>	5/ 0 (0)	TP	1/ 0 (0)	VH	38/ 7 (18.4)	BB,TD	28/ 2 (7.1)	BB,TD
<i>Megachile sicula</i>	0	-	0	-	23/ 5 (21.7)	RR,BB	1/ 0 (0)	AT
<i>Synhalonia spectabilis</i>	0	-	0	-	46/ 3 (6.5)	BB,TD	107/ 20 18.7	BB,PM,TD
<i>Xylocopa iris</i>	15/ 0 (0)	AF,AU,NS,PM	2/ 0 (0)	-	8/ 1 (12.5)	RR,SM,VH,BB	1/ 0 (0)	PM
All bees (14 species)	295/ 45 (15.25)	-	157/ 24 (15.3)	-	199/ 20 (10)	-	272/ 71 (26.1)	-

^a undescribed species (Risch, personal communication)

^b *Anagryris foetida* (AF), *Asphodelus ramosus* (AR), *Alakanna tinctoria* (AT), *Anchusa undulata* (AU), *Bituminaria bituminosa* (BB), *Calicotome villosa* (CV), *Lathyrus ochrus* (LO), *Echium angustifolium* (EA), *Notobasis syriaca* (NS), *Oxalis pes-caprae* (OP), *Prassium majus* (PM), *Retama raetam* (RR), *Silybum marianum* (SM), *Trifolium dichroanthum* (TD), *Trifolium purpureum* (TP), *Vicia hybrida* (VH)

Appendix 3. Description of the maximum likelihood statistical model:

In the following, Φ represents the cumulative distribution function of the standard univariate (one-dimensional) normal distribution, with mean 0 and variance 1.

The total log-likelihood, L , is a function of the three parameters we want to estimate, f , q and V (as defined in the main text), given the observed data,

$$L(f,q,V | data) = \sum_i L_i,$$

where summation is over all marked individuals, and L_i is the contribution of marked individual i to the total log-likelihood function. This individual-specific contribution is dependent upon whether the individual has been recaptured within its plot of origin, recaptured in a different plot, or not recaptured at all.

For example, given plot j (j being an index over the different experimental plots) the probability to remain in plot j is $f + (1-f)[\Phi(w_j / 2V^{1/2}) - \Phi(-w_j / 2V^{1/2})][\Phi(l_j / 2V^{1/2}) - \Phi(-l_j / 2V^{1/2})]$, where w_j and l_j are the width and length, respectively, of plot j . This last expression is the sum of the probability to display site fidelity and the probability to still be within the plot of origin, given that the individual does not display site fidelity, after being randomly distributed according to a normal distribution with variance parameter, V . The probability of actually being recaptured in the plot of origin requires a final step of multiplying by q , the success probability of recapture within a sampled area. This finally gives us a probability to be recaptured in plot of origin $p_{jj} = qf + q(1-f)[\Phi(w_j / 2V^{1/2}) - \Phi(-w_j / 2V^{1/2})][\Phi(l_j / 2V^{1/2}) - \Phi(-l_j / 2V^{1/2})]$. Therefore, the contribution, to log-likelihood function, of an individual i that was marked in plot j

and recaptured in plot j is $L_i = \log p_{jj} = \log q + \log \{ f + (1-f) [\Phi(wj / 2V^{1/2}) - \Phi(-wj / 2V^{1/2})] [\Phi(lj / 2V^{1/2}) - \Phi(-lj / 2V^{1/2})] \}$.

Similar calculations are done for p_{jk} , the probability of being marked in plot j but recaptured in plot k ($k \neq j$; taking into account the area of the different plot and its distance from the plot of origin), and for the probability of not being recaptured at all ($1 - p_{jj} - \sum_{k \neq j} p_{jk}$; which includes the majority of individuals in our case). The contribution L_i of individual i to the total log-likelihood function is $\log p_{jj}$, if recaptured in plot of origin, $\log p_{jk}$, if recaptured in a different plot, or $\log(1 - p_{jj} - \sum_{k \neq j} p_{jk})$, if not recaptured at all.

The total log-likelihood function is then

$$L = \sum_j \left[n_{jj} \log p_{jj} + \left(n_j - n_{jj} - \sum_{k \neq j} n_{jk} \right) \log \left(1 - p_{jj} - \sum_{k \neq j} p_{jk} \right) \right] + \sum_{k \neq j} n_{jk} \log p_{jk},$$

where n_j is the total number of marked individuals in plot j , n_{jj} is the total number of marked individuals from plot j recaptured in plot j , and n_{jk} is the total number of individuals marked in plot j and recaptured in plot k . Note that the summation here is over all plots (indices j and k), and not over individuals. The estimated values of the parameters are obtained by finding the combination f , q , and V that maximizes the likelihood function, L .

Finally, the gradient (i.e., the score) and the hessian (i.e., the Fisher information matrix) of the log-likelihood, L , were obtained by calculating first- and second-order derivatives, with respect to f , q , and V . In particular, the hessian, evaluated at the

maximum-likelihood estimate of f , q , and V , was used in obtaining standard errors and confidence intervals, following standard maximum likelihood asymptotic results. The likelihood-ratio test was done by comparing the full model (with three parameters, f , q , and V) to a reduced model where f is constrained to be 0.

Maximization of the likelihood function and all other numerical work was done in R v.2.14.1 (R Development Core Team 2011). Maximization used the R-library optimx (Nash and Varadhan 2011). For numerical reasons, we used $\log V$, rather than V , as the variance parameter.

References:

John C. Nash, Ravi Varadhan (2011). Unifying Optimization Algorithms to Aid Software System Users: optimx for R. Journal of Statistical Software, 43(9), 1-14.

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