10. INTERNATIONAL ANIMAL SCIENCE CONFERENCE



ZOOTEKNİ
FEDERASYONU 2013

BOOK OF PROCEEDINGS 2018

October 25 - 27, 2018 ANTALYA / TURKEY

CamScanner ile tarandı

Determination of conservation priorities in Bombus terrestris populations in Antalya region by using microsatellite markers

B. Argun Karsli, F. Gürel

Department of Animal Science, Faculty of Agriculture, Akdeniz University, 07070, Antalya, Turkey

Introduction

Bumble bees are among the most recognizable, abundant and ecologically important groups of pollinating insects. In natural plant pollinator communities, bumble bees are often considered keystone species because of their generalist pollination services, whereby they support plant community diversity by visiting both rare and common plant species (Memmot et al., 2004; Goulson et al., 2008; Burkle et al.,2013; Brosi & Briggs, 2013). Bombus terrestris L. is the most common bumble bee species found in Turkey and especially in the natural fauna of Antalya region. In addition, B. terrestris is reared extensively today on a mass scale and is widely spread commercially in many countries including Turkey where it is used as a pollination agent. In recent years, wild B. terrestris populations have been decreasing, likely due to reduced genetic diversity, habitat destruction and subsequent loss of nesting and food resources, inbreeding in fragmented wild populations, introduction of non-native parasites and impacts of pesticides (Goulson et al., 2008; Williams & Osborne 2009; Graystock et al., 2013). That is, wild bumble bee populations with low levels of genetic diversity may suffer from reduced population growth and increased disease susceptibility (Beekman et al., 2000). The ecological and economic importance of B. terrestris, coupled with their recent declines, has led to a growing interest in the investigation of bumble bee genetic diversity conservation. For this reason, the determination of conservation priorities for B. terrestris populations has become very important. In summary, the aim of this study was to analyze genetic diversity, genetic relationships and in the wild B. terrestris populations conservation priorities using microsatellite markers.

Materials and methods

Microsatellite-based genetic characterization has the potential to provide useful information for conservation of bumble bee genetic resources.

CamScanner ile tarandı

Based upon sites in which the same short sequence is repeated multiple times, they present a high mutation rate and codominant nature, making them appropriate for the study of both within- and between-breed genetic diversity (Sunnucks 2000). In this study, a total of 192 worker bee samples were collected from seven wild B. terrestris populations (AK, KM, DM, GB, TM, BB and FS). Total DNA was extracted from one leg of each of the sampled workers following a modified Chelex extraction protocol as described by Walsh et al (1991). All individuals were genotyped at twenty polymorphic microsatellite markers ((BT06, BT09, BT20, B100, B116, B118, B119, B121, B124 and B126). (B100, B118, B119, B124, B126, B132, B96, B11, BT06, BT09, BT20, BT28, BT26, BT10, BTMS0033, BTMS0119, BTMS0131, BTMS0082, BTMS0124 and BTMS0045) to quantify genetic differentiation and assess conservation priorities (Estoup et al., 1995, 1996; Funk et al., 2006; Stolle et al., 2009). And then 96 automated capillary electrophoresis was used for detect the sizes of the PCR products. Determination of conservation priorities in the B. terrestris populations, were made according to the methods described by Petit et al (1998) and Caballero and Toro (2002) by using MolKin program (Gutirrez et al. 2005).

Results

We applied different methods to assess conservation priorities for the wild B. terrestris populations. There were slight differences in results of the two methods. This may be attributable to their methodological differences [i.e., these methods quantify the importance of each subpopulation (line) in terms of maximization of gene diversity (Caballero and Toro, 2002) or allelic richness (Petit et al., 1998)].The contribution to genetic diversity of each populastion is shown in Table 1. According to the methods described by Cabellaro and Toro (2002) the highest contribution to genetic diversity was made by FS (-0.278), while the lowest contribution was made by the BB population (0.032). According to Petit et al. (1998), FS population (1.070) made highest and GB population (-0554) made lowest contribution to genetic diversity. This result indicates that the lowest contribution to total genetic diversity was obtained from BB according to the method of Caballero and Toro (2002), whereas the lowest contribution was obtained from GB according to the method of Petit et al. (1998).

CamScanner ile tarandı

Conclusion

The importance of preserving B. terrestris populations biodiversity has received increasing attention in recent years. The commercial populations gene pool lacks the considerable genetic diversity found in wild bumble bee populations, given that the commercial population gene pool has its root in a limited number of queen samples. Conservation of diverse wild B. terrestris populations genetic resources is accordingly considered to be important for sustainable natural ecosystem and commercial rearing production.

In conservation genetics, main objective is to preserve the genetic variability within populations, assuming there is a positive correlation between genetic variation and population viability. In conclusion, according to the results of this study, the FS population showed the highest genetic diversity in both methods of analysis. Therefore, conservation studies should be started from FS population.

Table 1. Contribution to genetic diversity in seven wild B. terrestris populations.

	According to Cabellaro and Toro			According to Petit et al.		
	Total (%)	Within pop. (%)	Between pop. (%)	Total (%)	Within pop. (%)	Between pop (%)
AK	-0.107	0.014	-0.122	0.449	0.071	0.378
KM	-0.074	0.079	-0.153	0.065	-0.362	0.428
DM	-0.109	0.018	-0.126	0.456	-0.175	0.631
GB	-0.021	0.173	-0.194	-0.554	-0.756	0.202
TM	-0.145	-0.175	0.029	0.109	0.486	-0.377
BB	0.032	0.084	-0.053	0.612	0.442	0.170
FS	-0.278	-0.208	-0.070	1.070	0.294	0.776

Acknowledgements

We thanks to the Akdeniz University Scientific Research Projects Coordination Unit (Turkey).

CamScanner ile tarandı

References

Beekman, M., Stratum, P., Lingeman, R. (2000). Artificial rearing of bumble bees (Bombus terrestris) selects against heavy queens. Journal of Apicultural Research, 39: 61-65.

Brosi, B.J., Briggs, H.M. (2013). Single pollinator species losses reduce floral fidelity and plant reproductive function. Proceedings of the National Academy of Sciences, USA, 110: 13044-13048.

Burkle, L.A., Marlin, J.C., Knight, T.M. (2013). Plant-poolinator interactions over 120 years: loss of species, co-occurence, and function. Science, 339: 1611-1615.

Estoup, A., Scholl, A., Pouvreu, A. and Solignac, M. (1995). Monoandry and polyandry in bumble bees (Hymenoptera; Bombinae) as evidenced by highly variable microsatellites. Molecular Ecology, 4: 89-93.

Estoup, A., Solignac, M., Cournet, J.M., Goudet, J. and Scholl, A. (1996). Genetic differentiation of continental and island populations of Bombus terrestris (Hymenoptera: Apidae) in Europe. Molecular Ecology, 5(1): 19-31.

Funk, C.B., Schmid-Hempel, R. and Schmid-Hempel, P. (2006). Microsatellite loci for Bombus spp. Molecular Ecology Notes, 6: 83-86.

Goulson, D., Lye G.C., Darvill, B. (2008). Decline and conservation of bumble bees. Annual Review of Entomology, 53: 191–208.

Graystock, P., Yates, K., Evison, S.E.F., Darvill, B., Goulson, D., Hughes, W.O.H. (2013). The Trojan hives: pollinator pathogens, imported and distributed in bumblebee colonies. Journal of Applied Ecology, 50: 1207-1215.

Gutierrez, J. P., L. J. Royo, I. Alvarez, and F. Goyache. (2005). MolKin v2.0: A computer program for genetic analysis of populations using molecular coancestry information. Journal of Heredity, 96:718-721.

Memmott, J., Waser, N.M., Price, M.V. (2004). Tolerance of pollination Networks to species extinctions. Proceedings of the Royal Society of London. Series B: Biological Sciences, 271: 2605-2611.

Petit, R.J., El Mousadik, A., Pons, O. (1998). Identifying populations for conservation on the basis of genetic markers, Conservation Genetics, 12: 844–855.

Stolle, E., Rohde, M., Vautrin, D., Solignac, M., Schmid-Hempel, P., Schmid-Hempel, R. and Moritz, R.A.F. (2009). Novel microsatellite DNA loci for Bombus terrestris (Linnaeus, 1758). Molecular Ecology Resources, 9(5): 1345-1352.

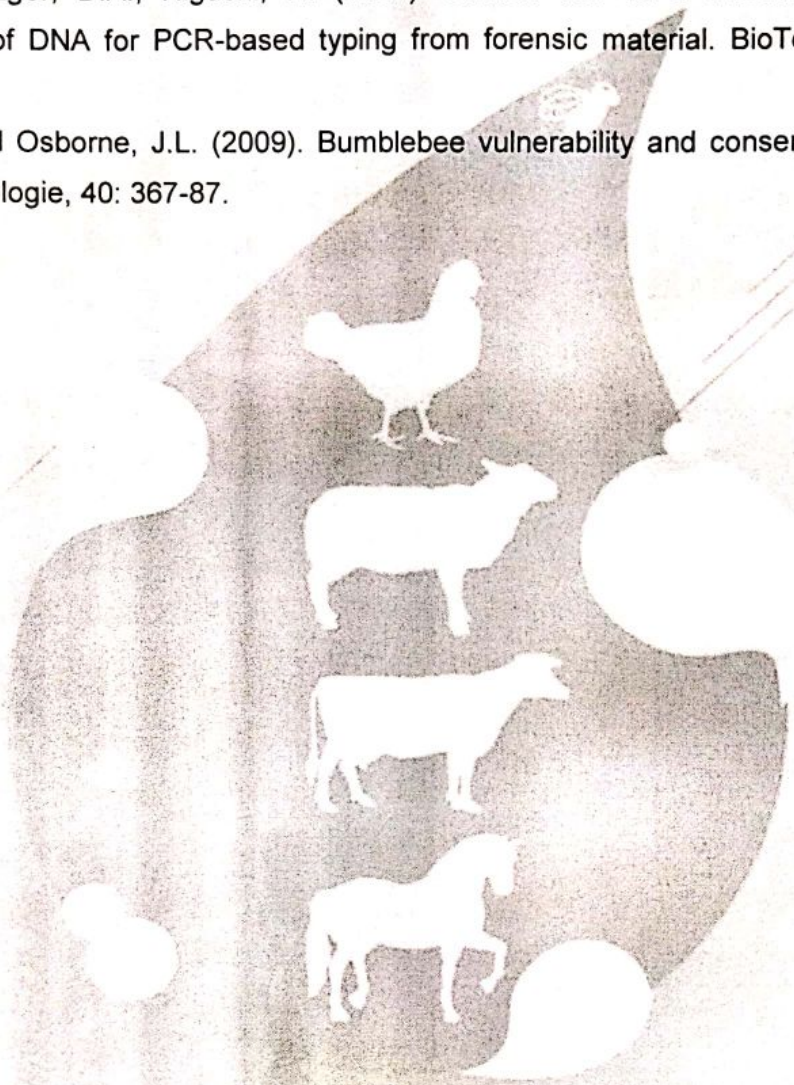
Sunnucks, P. (2000). Efficient genetic markers for population biology. Trends Ecology Evolution, 15(5): 199-203.

CamScanner ile tarandı

Tadano, R., Nagasaka, N., Goto, N., Rikimaru, K. and Tsudzukı, M. (2013). Genetic characterization and conservation priorities of chicken lines. Poultry Science, 92: 2860-2865.

Walsh, P.S., Metzger, D.A., Higuchi, R. (1991). Chelex 100 as a medium for simple extraction of DNA for PCR-based typing from forensic material. BioTechniques, 7: 506-513.

Williams, P.H. and Osborne, J.L. (2009). Bumblebee vulnerability and conservation world-wide. Apidologie, 40: 367-87.



CamScanner ile tarandı