## S.1-1

# Evidence of gene flow between wild and domestic *Triatoma infestans* populations in the Andes

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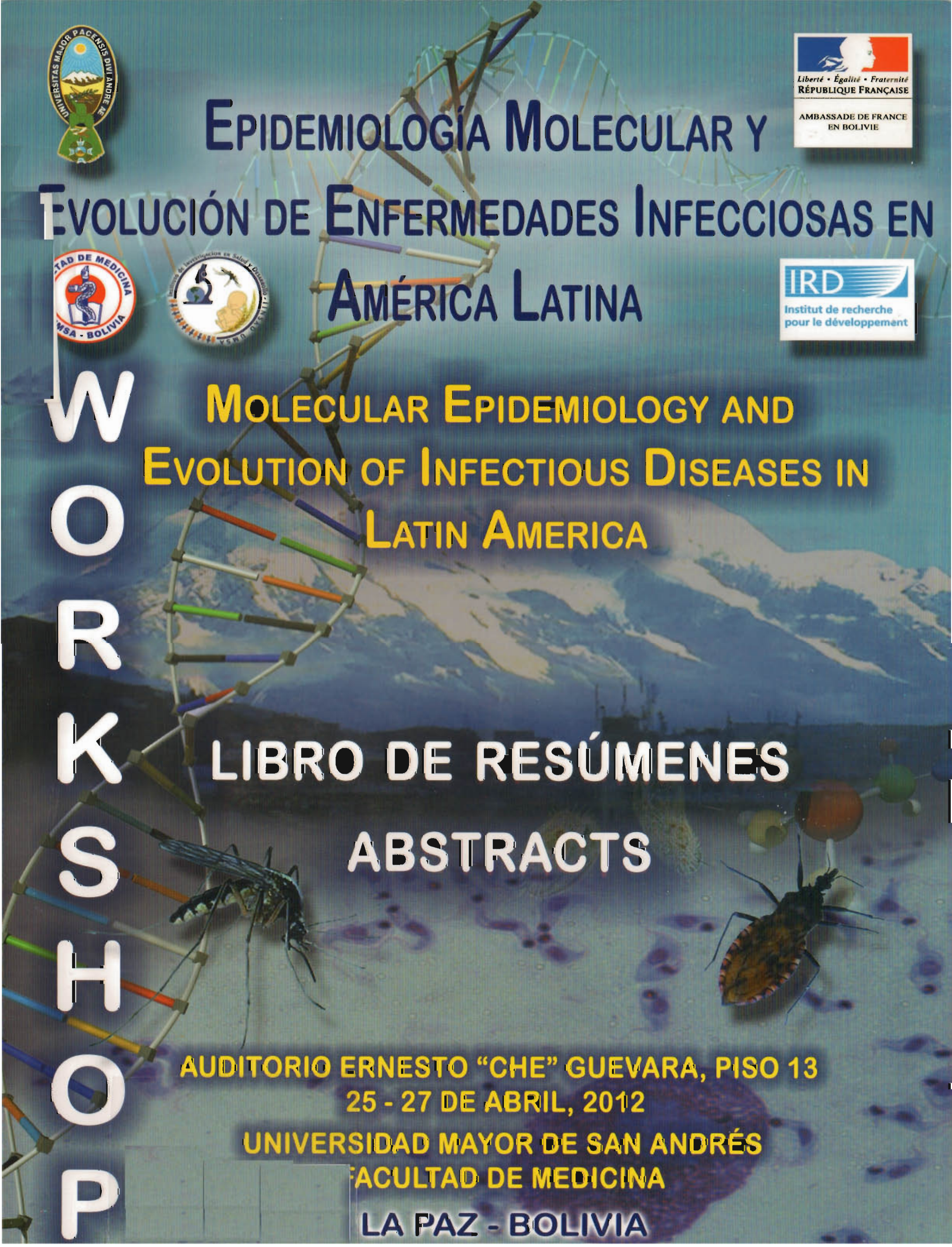
To assess whether wild populations near human dwellings could infest the habitat, gene flow between natural populations of *Triatoma infestans* collected in sylvatic and domestic environments were studied by the method MLMT (Multilocus Microsatellite Typing) for 7 locus. A total of 277 insects distributed in 25 populations (13 domestic and 12 wild), of three localities (Sapini, Thago Thago and Quillacollo) located in the "Inter Andean Dry Forests" ecoregion in Bolivia, where the persistence of the infestation by *T. infestans* was observed, were studied. The inter-localities analysis showed high geographical structure between the three areas. At the intra-population level, Hardy-Weinberg equilibrium was the rule. However positive $F_{IS}$ values, significantly different from zero, were observed for the entire samples from Quillacollo and Thago Thago but not Sapini, a result probably related with sub-structuring within localities. Testing structuring between domestic and wild populations in each locality, no significant test was found showing an absence of structure between the two environments. Moreover, the number of true genetic populations that could be inferred in each locality was assessed with The STRUCTURE software. In Sapini and Quillacollo, 2 populations were inferred but these populations did not correlated with the places of captures of the bugs (peridomestic versus sylvatic). In Thago Thago, 8 populations were inferred, but the majority of individual had an admixed origin. The results reflect in the three localities, gene flow between environments supporting the moving of wild bugs to human habitat that may be linked to persistence of infestation in the localities.



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# EPIDEMIOLOGÍA MOLECULAR Y EVOLUCIÓN DE ENFERMEDADES INFECCIOSAS EN AMÉRICA LATINA

## MOLECULAR EPIDEMIOLOGY AND EVOLUTION OF INFECTIOUS DISEASES IN LATIN AMERICA

## LIBRO DE RESÚMENES

## ABSTRACTS

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