

Introduction

Natural hybridization can be easily detected between closely relative species, either in geographically defined hybrid zones or after human induced faunal or vegetable introductions (Highton *et al.* 1989; Barton & Hewitt 1989; Avise 1994; Sites *et al.* 1996; Arnold 1997; Goodman *et al.* 1999; Highton and Peabody 2000; Alfred *et al.* 2005; Weisrock *et al.* 2005). A hybrid zone is an area where individuals from genetically distinct populations or species interbreed and produce genetically mixed offspring. This phenomenon of hybridization has been recognized as fertile grounds for evolutionary studies (Hewitt 1988), which concern models of speciation (David *et al.* 1974; Bock 1984; Solignac and Monnerot 1986; Aubert and Solignac 1990), selection (Butlin 1989; Butlin and Ritchie 1991; Butlin *et al.* 1991; Dowling and DeMarais 1993), the recombination (Shaw 1976, 1990; Ferris *et al.* 1993), the maintenance of species boundaries (Robertson 1983; Neems and Butlin, 1994; Underwood, 1994), and the evolution of host-parasite interactions (Boecklen and Spellenberg 1990).

Hybridization between species is taken for maladaptive due to fewer and/or less fertile offspring (Darwin 1872; Dobzhansky 1937, 1940; Mayr 1942, 1963; Paterson 1985; Arnold 1997), and even lead to species extinction (Rhymer and Simberloff 1996; Allendorf *et al.* 2001). Hybrid load may lead to gamete deficiency in the parental species, and influence stability of pure species (Ditte *et al.* 2005). In the case of parapatric species, intermediate morphotypes can occasionally be found in the contact zone. The mechanisms in which animal hybrids become

reproductively and ecologically isolated are poorly understood, and there are only a few examples of speciation in animals by introgressive hybridization recorded in the literature (DeMarais *et al.* 1992; Salzburger *et al.* 2002; Smith *et al.* 2003; Dietmar Schwavz 2004). More specifically, hybridization is poorly understood in the order Squamata. Interspecific hybridization of the parthenogenetic lizard *Cnemidophorus tigris spp.* (Dessauer *et al.* 2000) shows out no inferior genetic fitness. The multiple chromosome races of the lizard *Sceloporus grammicus* complex show random mating within different chromosome races, forming a hybrid zone with mix chromosomal genotypes (Arevalo 1993, Reed 1995, Sites 1996, Jonathon 2001). However, it seems that intraspecific hybridization is uncommon in Squamata.

East Asian grass lizards (Lacertidae: *Takydromus spp.*) are distributed in the Oriental and Palearctic regions with a total of 16-17 known species (Arnold 1997). With five species, including four endemics on a single island (Arnold 1997; Lue *et al.* 1999), Taiwan has the highest diversity of this group. Recently, two more undescribed, cryptic species were identified within *Takydromus formosanus* Boulenger 1894 on Taiwan through mitochondrial DNA sequences (Lin 2003) and morphological analyses (Lin unpublished data).

Takydromus formosanus is widely distributed in Taiwan at low altitudes. Morphological and genetic data showed that *T. formosanus* is comprised of three paraphyletic Evolutionarily Significant Units (ESUs), including two unpublished cryptic species, which tentatively named *Takydromus viridipunctatus* and *Takydromus luyeanus*. *Takydromus viridipunctatus* is distributed in northern Taiwan including Taipei,

Keelung, and Yilan, and its southern boundary is around the northern bank of the Liwu River. The second new species, *T. luyeanus*, is distributed in eastern Taiwan and the southern area of the Liwu River. *Takydromus viridipunctatus* and *T. luyeanus* come into close proximity at the Liwu River and a few individuals of intermediate morphotypes can be found in adjacent areas (personal observation). Detecting the existence of hybrids and the distributional boundary between *T. viridipunctatus* and *T. luyeanus* is important in clarifying the systematics of this genus. This model of distribution with such closely related species being so close geographically, might serve as an ideal model to study the evolutionary consequence of natural hybridization between sister species.

In this study, we will check the patterns of natural hybridization and introgression between *T. viridipunctatus* and *T. luyeanus* in the adjacent area of the Liwu River. Accurate detection of hybrids of distinct populations has been applied in conservation and population genetics (Pritchard *et al.* 2000). Statistical techniques which utilize the information of highly polymorphic molecular markers such as microsatellite were developed to detect hybridization and hybrid individuals in contact zones of populations or species (Pritchard *et al.* 2000; Anderson and Thompson 2002). Detecting hybridization of closely related species and delineating species boundaries can be used to study speciation and selection. Thus, it is necessary to clarify the hybridization of *T. viridipunctatus* and *T. luyeanus* at their potential contact zone.