

Surrogates of spider diversity, leveraging the conservation of a poorly known group in the Savanna Biome of South Africa (Arachnida: Araneae)

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Abstract

The inclusion of spiders in conservation planning initiatives is confounded by several factors. Surrogates might provide a viable alternative for their inclusion. In this paper we investigate the performance of a number of surrogate measures, such as higher taxa (genus, family), cross-taxon surrogates that are subsets of the spider assemblages (certain spider families) or non-overlapping groups (woody vegetation and birds), and the use of morphospecies. Birds and woody vegetation were included because they often form the focus of conservation planning initiatives. We assessed the surrogate measures based on their predictive power for species richness and extent to which conservation planning that maximizes representation of the surrogate is effective in representing spider diversity. A measure for the latter is the species accumulation index (SAI). Generic richness as a higher taxon surrogate and the combined richness of the families Thomisidae and Salticidae were the best estimators of total species richness. Based on the surrogacy efficiency criterion, genera and the family Salticidae had species accumulation indices (SAI) that were significantly larger than 95 % confidence intervals of a random curve, while woody vegetation and birds turned out to be poor surrogates for spider diversity. The use of morphospecies as estimators is cautiously supported (adjusted R² = 0.85, for species richness, SAI = 0.73). The surrogates identified here provide a viable alternative to whole assemblage analysis but should be used with caution. The use of genera is confounded by unstable taxonomy and the difficulty of identifying specimens up to genus level. Geographic location and varying sampling effort between surveys did not have an effect on the surrogate performance of the two spider families, *viz.* Salticidae and Thomisidae. The former family has seen a flood of recent systematic work, whereas the latter's taxonomy is fairly well developed. These two families comprise ca. 20% of spider species observed in the Savanna Biome of South Africa and could provide a viable handle on spider diversity in this region.

Key words – rapid assessments

Introduction

Signatories of the Convention of Biological Diversity (UNEP 1992) are obliged to develop a strategic plan for the conservation and sustainable use of biodiversity. However, before we can take steps to conserve biodiversity, inventories are necessary. The inclusion of invertebrates in these biodiversity inventories is clearly desirable (Samways et al. 2010). However, the demand on time and resources is immense. Determining invertebrate diversity is particularly challenging because: (1) there is a high proportion of undescribed species; (2) a large percentage of specimens are juveniles (ca. 50%); (3) no revisions or keys are available making species-level identification time consuming and, in taxa whose taxonomy is poorly known, impossible; (4) species determinations are costly and identifying all species, even in a limited area, is thus a very expensive task; (5) species distributions are poorly known; (6) professional taxonomists are few; and, (7) comparative sampling methods are not standardized (Cardoso et al. 2011).

The potential use of biodiversity surrogates could provide a cost effective alternative that might aid in the inclusion of invertebrates in conservation assessments (Cardoso et al. 2011). Surrogates are small subsets, indicator taxa or quantities that are more easily determined and which correlate strongly with biodiversity as a whole (Gaston and Blackburn 1995). Criteria for the selection of a surrogate are that they must represent the conservation goals, be cost effective, be logistically suitable and have good biological efficacy (Lovell et al. 2007; McGeoch 1998) .

There are many kinds of surrogates but Hirst (2008) lists three types that are typically mentioned in the literature: indicator groups, habitat surrogates and higher taxa. The measured richness of indicator groups is used to represent the richness of one or more target taxa (Lewandowski et al. 2010) and it is implicit in the use of better known taxa such as birds (Larsen et al. 2012) and plants (Axmacher et al. 2011) as surrogates. The higher taxon approach involves reducing the level of identification of samples to taxa above species (e.g. genus or

family) (Balmford et al. 2000; Kallimanis et al. 2012; Mandelik et al. 2007; Rosser and Eggleton 2012; Vieira et al. 2012). Higher taxa are markedly fewer than species, and their spatial distributions tend to be proportionately better known that is a requirement for conservation planning (Gaston and Williams 1993). This approach has become one of the more popular surrogates for predicting biodiversity. Habitat surrogates focus on environmental variability as a measure of species richness (Faith 2003).

Richness and complementarity are two approaches used to determine the conservation status of habitats (Lewandowski et al. 2010). Complementarity approaches maximize the inclusion of species, phylogenetic coverage and communities across habitats of a surrogate. This approach will benefit target taxa if there is a strong correlation with the distribution of surrogate taxa (Lewandowski et al. 2010). Richness approaches focus on the conservation of surrogate hotspots. If surrogate richness is correlated with target taxa richness, conservation efforts focusing on surrogates will also benefit the target taxa. This principle is commonly used when selecting areas but neglect higher taxon diversity and diversity at broader scales (Hirst 2008).

A further approach to improve cost efficiency, particularly for invertebrates, is through the use of non-specialists, also known as biodiversity technicians in Australia (Nipperess et al. 2008; Oliver and Beattie 1993) or parataxonomists in Costa Rica (Abadie et al. 2008; Goldstein 1997, 2004) to assign invertebrate specimens to morphospecies (Obrist and Duelli 2010; Oliver and Beattie 1996), i.e. distinguishing a group of specimens that differ in some morphological character from all other groups. These non-specialists receive little training and are used to divide species into recognizable taxonomic units (RTU's). Morphospecies-level identifications are frequently used for the following reasons: (1) no taxonomic expertise is required since organisms are grouped on a like-with-like basis and (2)

it is relatively quick and cost effective (Krell 2004; New 1999; Obrist and Duelli 2010; Oliver and Beattie 1993; Roy and Foote 1997).

Oliver and Beattie (1996) have shown that morphospecies identified by non-specialists can provide estimates of richness and turnover consistent with those generated using species identified by taxonomic specialists. However, since species determinations of invertebrates are rarely based on characteristic features apparent to the inexperienced eye, the estimates of morphospecies are likely to be either an under- or over-estimate of the true level of diversity. Furthermore, juvenile, female and male spiders often look like different species to non-specialists, leading to overestimation of diversity for some groups (Slotow and Hamer 2000). Irrespective of these shortcomings it is a technique that is widely used in many groups (McGeoch 1998; Obrist and Duelli 2010; Oliver and Beattie 1996; Pryke and Samways 2010).

When the conservation goal is to conserve all-species biodiversity, the surrogate must be congruent with all-species biodiversity. An underlying assumption of surrogacy is that across higher taxa diversity is determined by the same mechanisms. Most studies have not found support for this assumption, particularly not at finer scales (Grenyer et al. 2006; Lawton et al. 1998; Lovell et al. 2007; Prendergast et al. 1993; Van Jaarsveld et al. 1998; Wolters et al. 2006). However, these studies either correlated species richness between taxa over grid cells or assessed the overlap of areas selected by a complementarity algorithm for the different taxa. The problem with the latter approach is that complementarity algorithms often yield multiple solutions which have identical representation of biodiversity features, but which can be very different spatially (Rodrigues and Brooks 2007; Rodrigues and Gaston 2002). It is possible then that based on spatial overlap a taxon can be a poor surrogate of itself. One should therefore not measure spatial overlap between selected areas, but rather how much area selected using the surrogate taxon contribute to the protection of target

organisms (Balmford 1998; Faith et al. 2001). The Species Accumulation Index (SAI) provides a measure of such efficiency by comparing the species accumulation curves of the target taxon when a surrogate taxon is used for the area selection with the curve constructed by the random selection of sites and the optimal curve that indicate the maximum representation of the target taxon in a set of sites (Rodrigues and Brooks 2007). When the optimal and surrogate curve are identical the index equals 1, when the surrogate curve is no different from the curve created by random selection of areas it equals 0, with values less than 0 suggesting performances that are worse than random. The efficiency of a surrogate is therefore higher the closer its SAI is to unity (Ferrier and Watson 1997; Rodrigues and Brooks 2007).

Using this approach, Rodrigues and Brooks (2007) reviewed 27 studies which contained 575 surrogacy tests. Their conclusions are somewhat more optimistic than those in other cited studies (Grenyer et al. 2006; Lawton et al. 1998; Lovell et al. 2007; Prendergast et al. 1993; Van Jaarsveld et al. 1998; Wolters et al. 2006), although most positive SAI values were low (Rodrigues and Brooks 2007).

A considerable amount of attention has focused on the development of indicators of biodiversity, particularly in relation to estimates of species richness in highly diverse groups, such as invertebrates, where comprehensive species-level surveys are usually not possible (Rodriguez et al. 1998). Coddington (1996) and New (1999) propose that spiders are a group that show potential as biodiversity indicators as they show the characteristics required of efficient indicators (i.e. they are diverse, easily sampled, functionally important and reflect changes in the environment). Spiders are among the most speciose orders of animals with more than 40 000 species described worldwide (Platnick 2013). Although the spider diversity for each of the Afrotropical countries is known through the African Arachnida Database (AFRAD), their distribution patterns in each country are still largely unknown (Dippenaar-

Schoeman et al. 2012). The South African National Survey of Arachnida (SANSA) (Dippenaar-Schoeman and Haddad 2006) attempts to address this lack of information for South Africa in particular by producing the first Spider Atlas for the country (Dippenaar-Schoeman et al. 2010). However, large gaps still exist even for this relatively well-sampled region of the continent (Foord et al. 2011a; Foord et al. 2011b).

Savanna is the largest biome in South Africa and also hosts the largest diversity of spiders based on current information (Foord et al. 2011b). This manuscript reviews the result of three studies carried out by the authors (Dippenaar et al. 2008; Foord et al. 2008; Mueelwa et al. 2010) over a period of two years in the Limpopo province of South Africa. It investigates the efficiency of three surrogates of spider diversity in the Savanna biome of South Africa. These included: (1) indicator taxa in the form of cross-taxon surrogates where a subset of species (specific spider family) or a non-overlapping group (woody plants and birds) is used (Cameron and Leather 2012; Churchill 1997; Faith and Walker 1996; McGeoch 1998; Noss 1990; Sebek et al. 2012; Van Wynsberge et al. 2012); (2) the use of the higher taxon approach, which involves reducing the level of identification of samples to groups above species (e.g. genus or family) (Balmford et al. 1996a; Biaggini et al. 2007; Cardoso et al. 2004a; Lin et al. 2012; Lovell et al. 2007), and (3) species composition or the allocation to morphospecies by non-specialists (Abadie et al. 2008; Balmford et al. 1996a; McGeoch 1998; Obrist and Duelli 2010; Oliver and Beattie 1996). The surrogate estimators were evaluated within the context of two measures of surrogacy efficiency, namely the degree to which the surrogates can estimate species richness and their performance in selecting complementary sets of areas for the target taxon.

Methods

Study sites

More than 95% of the Limpopo province of South Africa is Savanna (Fig. 1) . The three surveys used for this meta-analysis were done over a period of two years, May 2004 – March 2006, focusing largely on the growing season (November – March) in the region. An ideal situation would be to sample all sites in this study during the same year, but the distance between the sites and the sampling effort involved precluded this.

The first study (Foord et al. 2008) was done at the Lajuma Research Station (LRS, 23°1.5'S 29°25.7'E, Fig. 1). The station is situated on the Soutpansberg mountain, a quartzitic inselberg in the northern parts of the Limpopo province (Hahn 2011). The Soutpansberg are characterized by extreme variation in climate and topography resulting in a strong north-south climatic dichotomy (Mostert et al. 2008). The southern aspect of the mountain includes mesic savanna, thickets and forests with twice as much rainfall as the northern aspect and rainfall variation that is ameliorated by mist precipitation (Munyai and Foord 2012). The northern aspect is characterized by arid savanna and large variations in annual rainfall. Five sites representative of habitats on the southern aspect of the mountain were set out at LRS over an elevational range of 1200 – 1400 m a.s.l. The survey consisted of three sampling events between May 2004 and May 2005 (Table 1).

The second study consisted of two sites on the arid northern slopes and foothills of the Soutpansberg and Blouberg mountains (Muelelwa et al. 2010). The Blouberg is a smaller inselberg to the west of the Soutpansberg. The first site was in the Blouberg Nature Reserve

(BNR, 23°1'S 29°6'E, 1084 – 1128 m a.s.l.) and the second in the Mashovela Nature Reserve (MNR, 22°50'S 29°47'E, 864 – 904 m a.s.l.). Four habitats representative of habitat diversity in the reserves were sampled in each of the two areas (Fig. 1), eight sites in total. Spiders were sampled in spring (November, 2005) and summer (March, 2006) following a modified Coddington protocol as outlined by Muelelwa et al. (2010), where samples are time-based (Table 1).

The third survey was approximately 150 km to the south of the previous two surveys, in the Polokwane Nature Reserve (PNR, 23°58'S 29°28'E) at 1200 – 1500 m a.s.l. (Fig. 1). Six representative habitats were sampled on a monthly basis between April 2005 and March 2006 at this site (Dippenaar et al. 2008) which makes this survey the most intensively sampled of the three.

A suite of sampling methods was used at all of the habitats which together targeted spiders in all the strata of a habitat. This included sweepnetting, aerial collecting, ground collecting, branch beating, pitfall trapping and leaf litter sifting, targeting different, but overlapping sections of the spider communities (Table 1). Spiders from all three the studies were identified up to species level by the second author. An MSc student (University of Venda), with no prior experience in identifying spiders and limited prior knowledge of arachnology, identified spiders from BNR and MNR up to morphospecies level. Morphospecies are defined as the separation into distinct recognizable groups based on morphology, with the aid of a dissecting microscope and an identification manual that enables family level determinations (Dippenaar-Schoeman and Jocqué 1997). Juvenile spiders were included in determinations except for the MNR and BNR surveys.

Although this review includes three different studies, using with somewhat varying methodologies, all the surveys were semi-quantitative, generating relative abundances that were used to determine completeness indices for each of the habitats sampled based on the ratio between observed species and the Chao1 richness estimator in EstimateS 8.2 package (Colwell 2009) , which were all larger than 50% (Dippenaar et al. 2008; Foord et al. 2008; Muelelwa et al. 2010). The Chao 1 estimator was highly correlated with observed species richness, Pearson's $r = 0.91$, $P\text{-value} < 0.01$. The observed species richness was therefore used in subsequent analyses. The study also resemble other reserve selection studies that rely on biodiversity data from various sources.

We evaluated the effectiveness of woody plants and birds as estimator surrogates of spider diversity by recording all the species of woody vegetation at a site, while bird species at each of the sites were recorded by point counts over a period of one day, 06h00 – 18h00. All birds were recorded either through observation or sound. Due to the varying methodologies of the three studies, data for birds were only available for the BNR/MNR study, whereas data for woody plants was available for the BNR/MNR as well as LRS study.

Statistical Analysis

The ability of the surrogates to predict spider species richness was tested with simple least squares linear regression. The predictive power of each estimator was quantified with R^2 , and also by visual inspection of the scatterplots. Model residuals were examined to test for linearity, normal distribution and homogeneity of variance. Ideally predictive models should also be independent of space. Independence of model residuals, spatial autocorrelation in particular, was evaluated with the Durbin-Watson test. The effect of the geographic location and sampling effort on the performance of indicator and higher taxa was visually

inspected by comparing difference between the slopes of fitted regressions for the three surveys. Spearman's rank correlation statistic was used to test the reliability of surrogates in ranking sites and scatterplots were used to inspect reliability visually.

The extent to which areas selected for surrogates represent total spider diversity was evaluated with Ferrier & Watson's Species Accumulation Index (SAI). The analysis was done at three spatial scales. For the first and smallest scale, the eight sites of the Blouberg/Mashovela study were used because of the number of sites and the availability of data on morphospecies, birds and woody vegetation.. At an intermediate scale, the four sites from Lajuma Research Station were added to the data set and birds and morphospecies had to be omitted as surrogates. The largest scale included an additional six sites of the Polokwane study and excluded birds, morphospecies and woody vegetation. The accumulation curve of each surrogate was compared to two reference curves, the optimal curve (best surrogacy value) representing what is the maximum representation of spiders in sets of sites of a particular area, and the random curve, that is the representation of spiders if sites were selected at random (Rodrigues and Brooks 2007). Surrogate value was visually inspected by inspection of the curves and quantitatively by calculating $SAI = (S - R) / (O - R)$ where S is the area under the surrogate curve, R is the area under the random curve and O is the area under the optimal curve (Ferrier 2002). As there is not only one random solution, the random curve is represented by a random band representing 95 % confidence intervals. If the surrogate curve falls within this band it is not significantly different from random (Rodrigues and Brooks 2007). All calculations were done in R (R Development Core Team 2011).

Results

The three surveys, Dippenaar et al. (2008), Foord et al. (2008) and Muelelwa et al. (2010), yielded a total of 745 species. This represents ca. 60 % of all the species recorded in the Savanna Biome in South Africa (Foord et al. 2011b).

Species richness

Genus richness explained a considerable amount of variation in species richness ($F_{1,17} = 432$, $p = 0.006$, $R^2 = 0.95$), and varied in the same direction (Fig. 2a). Comparisons of genus vs. species ratios suggest that genera contain low numbers of species in almost all surveys, including other studies (Haddad et al. 2006) with ratios varying within a narrow range between 1.76 and 1.81 (Table 2). The relationship between spider family richness and species richness was still positive, but much weaker (Fig. 2b), and not significant ($F_{1,17} = 15.6$, $p = 0.311$, $R^2 = 0.45$) which would be expected with an average family to species ratios larger than 6.8. Predicted values of species richness based on family richness, as a covariate, was not independent and was spatially autocorrelated (D-W statistic = 0.91, $p = 0.045$) whereas the residuals of generic richness were independent of the geographic locality (D-W statistic = 2.1, $p = 0.94$).

Table 2. Accumulation of families in the simple linear regression according to the family that raises the regression coefficient the most at each step.

Families	Family added at each step	Percentage cumulative number of species	Regression coefficient (r^2)
1	Thomisidae	10	0.78
2	Salticidae	20	0.85
3	Theridiidae	28	0.9
4	Araneidae	38	0.95

Table 3. Performance of surrogates based on SAI of surrogates for three spatial scales.

	Small	Intermediate	Large
Random band	(-0.83,0.79)	(-0.93,0.83)	(-0.91, 0.7)
(Confidence intervals 95%)			
Genera	0.89*	0.94*	0.93*
Families	0.45	0.66	0.65
Salticidae	0.87*	0.76	0.83*
Thomisidae	0.06	0.47	0.44
Gnaphosidae	0.51	0.51	0.49
Araneidae	0.34	0.4	0.53
Theridiidae	0.39	0.065	0.59
Oxyopidae	0.35	0.52	-0.03
Morphospecies	0.73	NA	NA
Woody Vegetation	-0.43	-0.53	NA
Aves	0.41	NA	NA

*, <0.05

The family Thomisidae was the best indicator taxon of total species richness, explaining 73% of the variation (Table 3). This relationship was also highly significant ($F_{1,17} = 48.53$, $p < 0.001$, $R^2 = 0.73$). However, there were several sites where the predictive capacity of thomisid diversity either overestimated or underestimated overall richness (Cardoso et al. 2004b). Families were then added according to how much they contributed to the regression coefficient. This was done three times, until a group of four families was formed (Table 3) culminating in an R^2 of 0.95. Salticidae was the family that increased the predictive ability of Thomisidae most, and with no large incongruencies (Table 3 and Fig. 2d). These two families, both free-living mainly plant dwellers, are often the most species rich families in surveys of savannas, sampled from grass, trees and pit traps and collectively they represented 20% of all the species collected in the current study. Gnaphosidae and

Salticidae were the only families whose richness was spatially autocorrelated. The relationship between woody vegetation and spider species richness was non-linear, with the highest species richness observed for sites with intermediate plant species richness (Fig. 2f).

The geographical location of a survey and the survey intensity seems to effect on the relationships between Thomisidae (Fig.3b) and total species richness, whereas there were limited impacts on the performance of the two-indicator group (Thomisidae and Salticidae) with slopes for the three areas almost similar. Regression slopes (Fig. 3) based on family richness were also affected by survey intensity and location, while the performance of generic richness seems to be unaffected.

Ranking of sites based on generic richness was congruent with ranks based on species (Spearman's $\rho = 0.95$, $p < 0.001$). There was also a significant relationship between the ranks based on number of families and species, but the predictive power was weak (Figure 4). Although number of Thomisidae species richness had more predictive power it also had considerable residual variance. Addition of salticid species resulted in a considerable increase in correspondence with rankings based on all the species ($\rho = 0.94$).

In the regression between morphospecies richness and total species richness the R^2 was 0.8 (Fig. 4a). In the sites ranking comparison, morphospecies also performed relatively well ($\rho = 0.88$, Fig 4b).

Complementarity The most effective surrogate was genus, with SAI values larger than 0.9 across almost all of the spatial scales (Table 4). In fact, most surrogates performed consistently over all three spatial scales except for Thomisidae and Theridiidae. Salticidae was the most effective indicator taxon and although it did not perform as well as genera its surrogate curve approached that of the genera (Fig. 6) and outperformed all the other families by a considerable margin (Table 4). Cross-taxon congruency was very weak for woody

vegetation; birds performed better than woody vegetation (SAI = 0.41). As birds were unfortunately not sampled at larger scales, only limited inferences can be drawn from this result. Morphospecies performed better with a SAI of 0.75 (Table 4).

Table 4. Taxon richness of selected surveys summarizing the number of undescribed species and the average number of species within a genus

	Species	Genera	Families	Undescribed (%)	Genus:Species
Lajuma	293	148	43	43	1:1.81
Conservancy					
Blouberg	284	160	44	32	1:1.78
NR					
Ndumo	429	229	46	36	1:1.79
Game Park					
Polokwane	284	150	37	37	1:1.76
NR					

Discussion

Lovell et al. (2007) pointed to the importance of incorporating a multi-taxon approach to invertebrate conservation. Their evaluation of spiders was limited to Thomisidae, Oxyopidae and Araneidae in a Savanna Biome. Except for Thomisidae, our study suggests that Oxyopidae and Araneidae are weak estimators of spider diversity. Although Araneidae performed better as a predictor of total spider species richness (Table 2) it performed worse than Oxyopidae based on SAI (Table 3). Lovell et al. (2007) also found weak cross-taxon congruency for these three families.

Birds and trees, the non-overlapping cross-taxon surrogates in this study, which are often the focus of conservation planning initiatives, were weak surrogate estimators of spider

diversity. Birds have been shown to be relatively poor surrogates (Larsen et al. 2012; Williams et al. 2006) and woody plants were a particularly weak surrogate with large negative SAI scores (Table 3) pointing to the caution that should be taken when considering phyto-diversity as a surrogate for spider conservation (Axmacher et al. 2011)

The combination of Thomisidae and Salticidae proved to be a good predictor of total species richness and the ranking of sites also showed satisfactory correlation with that of total spider species richness. Thomisidae on its own was affected by survey intensity and geographic location, while there was no such effect on the two-family indicator combination of Salticidae and Thomisidae. The surrogacy efficiency of Salticidae as measured by SAI (0.76 – 0.87) is remarkably high, considering that Rodrigues and Brooks (2007) recorded a median SAI of 0.51 for surrogates that are subsets of targets, while the performance of Thomisidae was rather variable. The combination of Thomisidae and Salticidae could be an effective biodiversity surrogate for spiders as a whole in the Savanna Biome and there is considerable scope for their use in other biomes as this study included sites in forests with tall and short trees, thicker and grasslands, habitats that occur together in Savanna mosaics. Both families are wandering spiders and while Thomisidae is largely foliage dwelling, Salticidae are found in a variety of habitats (Dippenaar-Schoeman and Jocqué 1997) and well represented in other biomes in Africa.

Salticidae are also characterized by high levels of endemism in the Savanna Biome of South Africa, more than twice as much as the next family (Foord et al. 2011b), pointing to a considerable degree of habitat specialization across over broad environmental gradients, characteristics of a good surrogate (Lewandowski et al. 2010). There has also been a recent increase in interest in both the taxonomy and ecology of African salticids (Wesołowska 2008; Wesołowska and Haddad 2009). Wesołowska's work on salticids has been the largest contributor to contemporary discoveries of new species (Foord et al. 2011b). There is also

renewed interest in African thomisids with several recent revisions completed or underway (Lewis and Dippenaar-Schoeman 2011; Van Niekerk and Dippenaar-Schoeman 2010). The family Theridiidae could also be considered as a potential indicator taxon but its inclusion is unfortunately confounded by the poor taxonomic treatment the family has received in Africa but its use could be included within the context of morphospecies.

There was a significant correlation between the numbers of species and families and the number of species and genera. This relationship is stronger at the level of genus than family. It follows then that if higher taxon surveys are to be used for biodiversity assessment then estimates at the level of genus should be used. There are several advantages to using a higher taxonomic level identification, making their use extremely tempting to many scientists. These include: (1) this method provides a way of overcoming the insurmountable resource demands (i.e. time and expertise) in obtaining equivalent data on species numbers thus making surveys more cost effective ((Balmford et al. 1996a; Balmford et al. 1996b; Biaggini et al. 2007; Gaston and Blackburn 1995; Williams et al. 1994); (2) the rapid results could facilitate the identification of areas for conservation (Prance 1994); (3) juveniles can often be associated with adults at generic levels and higher levels and incorporated into analysis (New 1999); (4) some source of error, such as incidences of misidentification, can be reduced (5) by reducing the number of species within major taxa requiring taxonomic treatment, a greater range of major taxa can be incorporated into surveys (May 1994).

In several studies this method has been both useful and accurate (Biaggini et al. 2007; Cardoso et al. 2004a; Oliver and Beattie 1996). Studies have shown that even family level interpretation of spiders can be effective (Churchill 1997; Lin et al. 2012) although in this study only genera were a viable surrogate. The use of this surrogate is however constrained by the continual change in spider taxonomy (Platnick 2013), the difficulty of even identifying specimens up to genus level and the fact that all specimens will have to be investigated to get

an estimate of biodiversity (Cardoso et al. 2004b). Advantages includes the fact that there is no loss of information, specimens are readily available for taxonomic work and in many cases even juveniles can be identified up to the genus level.

Our results therefore supports Lovell et al.'s (2007) proposed use of higher taxa for certain groups, and spiders in this instance. The use of genera as a surrogate for spider diversity is strongly supported by our analysis. Cardoso et al. (2004b) did however find that a two family indicator group, Gnaphosidae and Theridiidae, performed well in the Mediterranean region of Portugal as predictors of richness and indicators of complementarity. They did caution though that interpretations of patterns should be tempered by differences in vegetation cover and sampling effort. Their reference to vegetation cover must however be seen within the context of their study where no arboreal spiders were sampled and could therefore be particularly relevant to grassland biomes, but not savanna biomes where arboreal sampling is an essential protocol component (Muelelwa et al. 2010). When using an iterative approach in choosing priority sites for conservation, our results conform with those of Cardoso et al. (2004a) in that genera are more efficient than indicator groups as estimator surrogates.

As different taxa respond to different processes at varying scales several authors have advocated the use of a shopping basket of taxa (Lovell et al. 2007) and although there has been some support for a significant but weak predictive power of cross-taxon surrogacy, several taxa will only show similar diversity patterns if there is a strong environmental process driving patterns. Whatever surrogates used will then not be indicators of biodiversity but environmental indicators (McGeoch 1998).

Melbourne (1999) indicates that rapid assessment of species assemblages may not be possible because new records are discovered with each new sampling period and 75% of the species present were only obtained after 3 to 5 sampling periods. A similar pattern was

observed in this study where none of the species accumulation curves reached an asymptote (Foord et al. 2008; Mueelwa et al. 2010) and new species were added with each new sampling session. It is important to note, that although complete inventories may be required for long-term studies, it may be unnecessary in most instances. Depending on the research question, a limited set of rapid assessments may be sufficient to map species distributions and determine conservation priorities. The use of spider morphospecies identified by non-specialists is recommended only if adult spiders are used as surrogates. Spiders are a particularly large group and identification training is essential. Morphospecies level identifications do tend to improve with practice. However, if this approach is to be used then the same individual should sort a specific group and will thus become more experienced. If there is no alternative to using morphospecies, then a good knowledge of specific taxonomic characters of each group chosen is essential (Slotow and Hamer 2000).

Reference collections and good photographic records of identified species are essential and should be properly labeled and documented, and voucher specimens lodged at institutions with appropriate curatorial staff. This may allow comparisons with other sites at different times and more importantly allows for specimen verification.

In conclusion, as a first approximation, morphospecies based on adult specimens could be used, taking cognizance of the decline in agreement at larger spatial scales (Nipperess et al. 2008) and the limited application (Krell 2004). If higher degrees of resolution and precision are required, the study should focus on species level determinations. Thomisidae and Salticidae specimens proved to be appropriate in this instance. Generic determinations of specimens will provide a level of accuracy very similar to that of the identification of all species. Species-level identifications remain ideal if the data are to be used for conservation. Higher taxon data should only be used in situations where there are insufficient resources available for good species data to be a realistic alternative.

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Figure captions

Figure 1. Location of three surveys in the Limpopo Province, South Africa: LRS = Lajuma Research Station, BNR = Blouberg Nature Reserve, MNR = Mashovela Nature Reserve, , PNR = Polokwane Nature Reserve.

Figure 2. Relationship between total species richness and (a) generic richness and (b) family richness and (c) Thomisidae richness and (d) the two-indicator group in all 19 sites; relationship between total species richness and (e) bird species richness in 8 sites; relationship between total species richness and (f) woody plant species richness in 12 sites.

Figure 3. Comparison of the effect of the three surveys (geographic location and sampling effort based on (a) generic richness and total species richness, (b) family richness and total species richness between the different surveys, (c) Thomisidae richness and total species richness between the different surveys and (d) comparison of two-indicator group and total species richness.

Figure 4. Comparison of site ranking based on (a) generic richness and total species richness, b) family richness and total species richness, c) Thomisidae richness and total species richness and, d) two-indicator group richness and total species richness.

Figure 5. (a) Relationship between total species richness and morphospecies richness and (b) comparison of site ranking based on (b) morphospecies richness and total species richness at eight sites in Mashovela/Blouberg survey.

Figure 6. Qualitative comparison of the surrogate (Genus and Salticidae), Optimal and random curves at various spatial scales, a) Mashovela/Blouberg, b) Mashovela/Blouberg and Lajuma, c) Mashovela/Blouberg, Lajuma and Polokwane Nature Reserve, d) is the evaluation of Morphospecies as a surrogate and includes sites of Mashovela/Blouberg only.

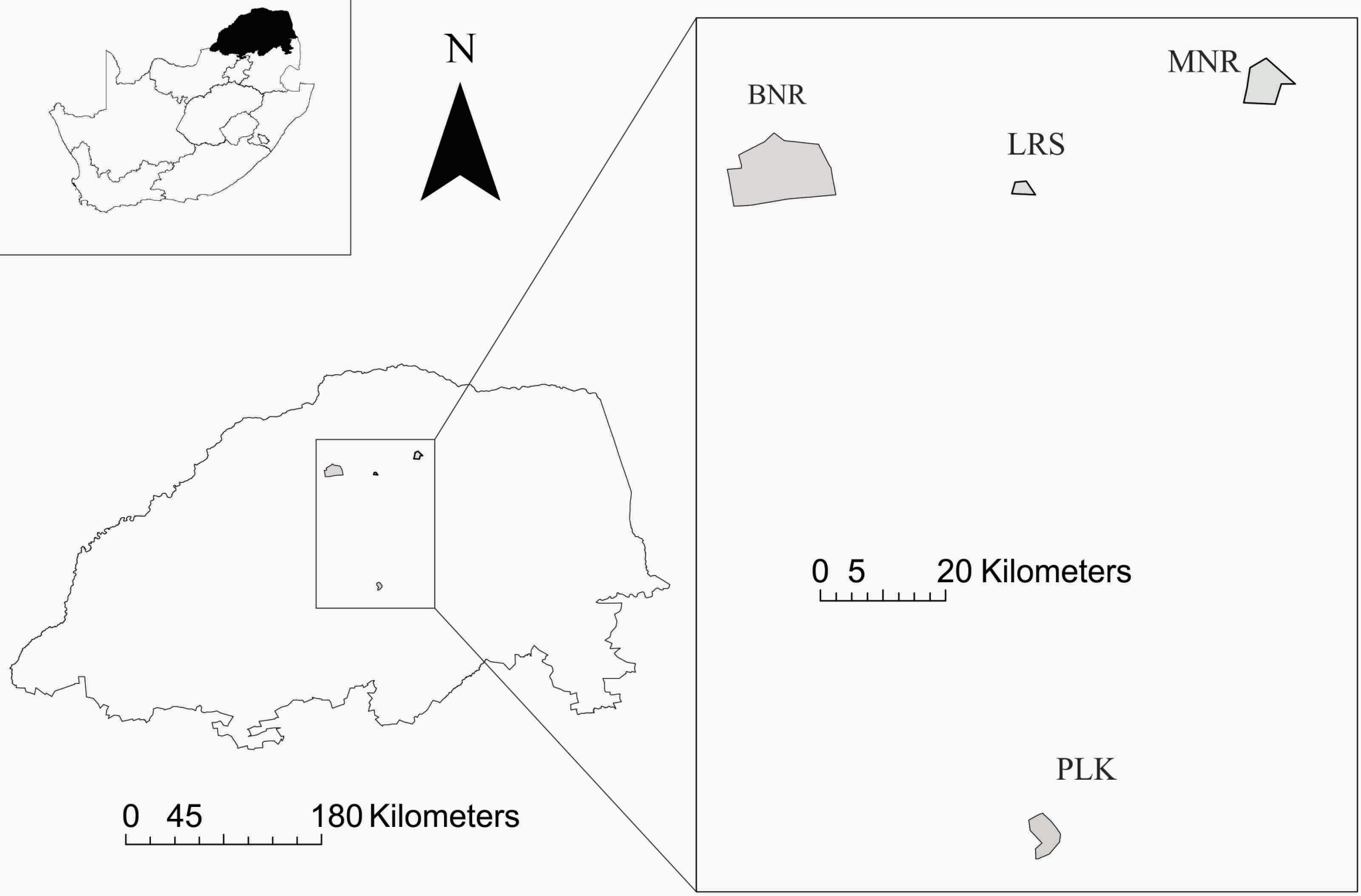


Fig. 1

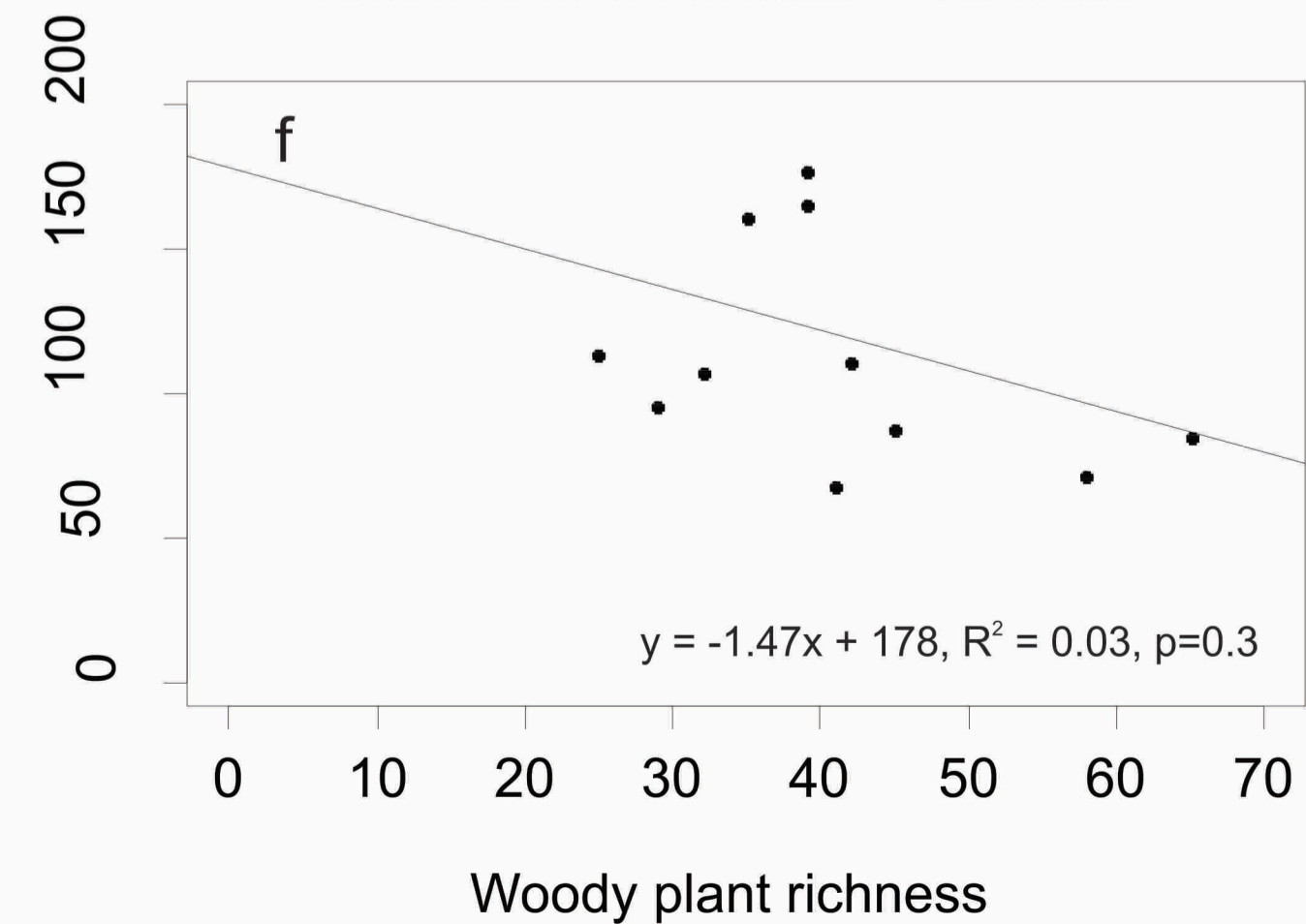
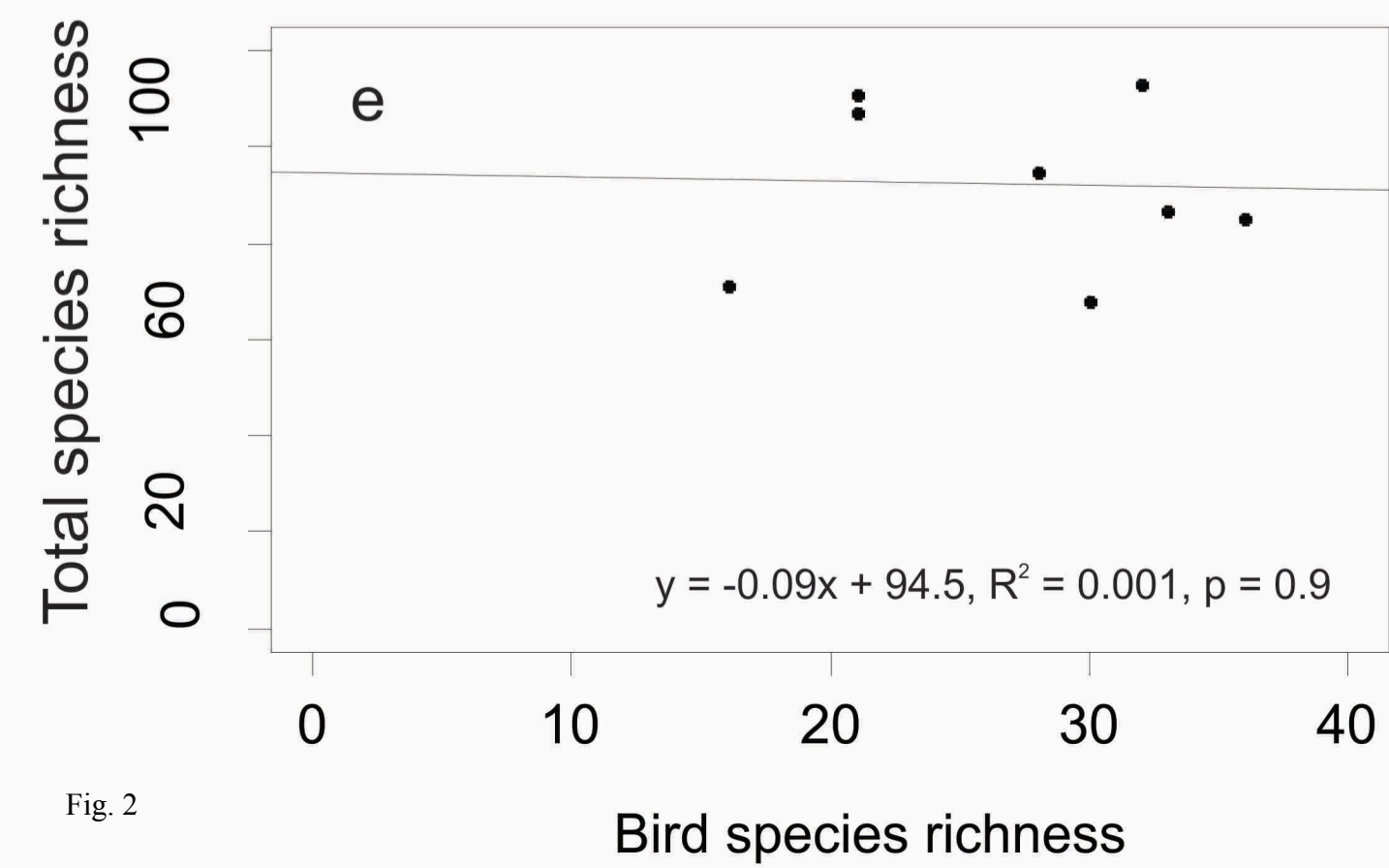
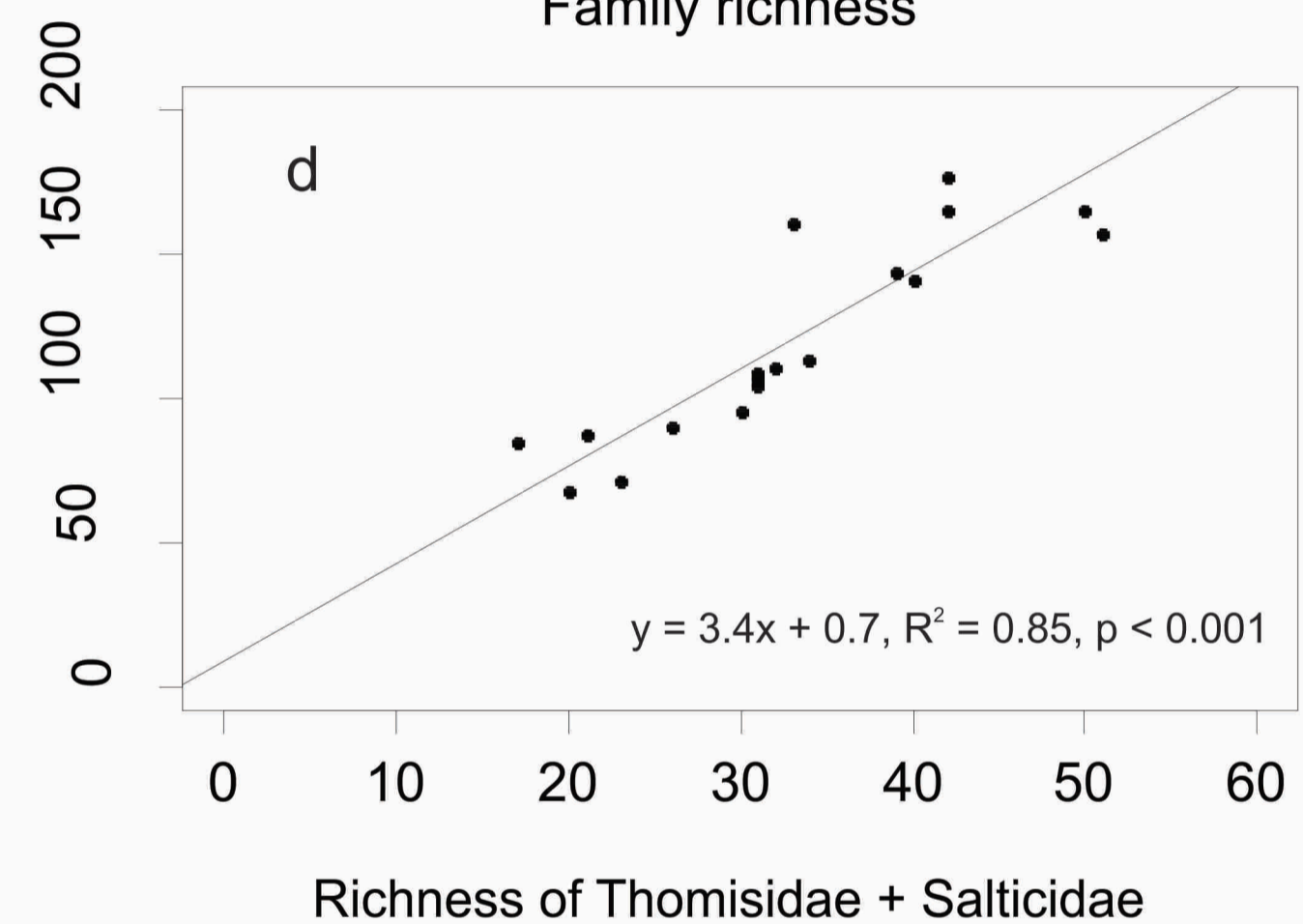
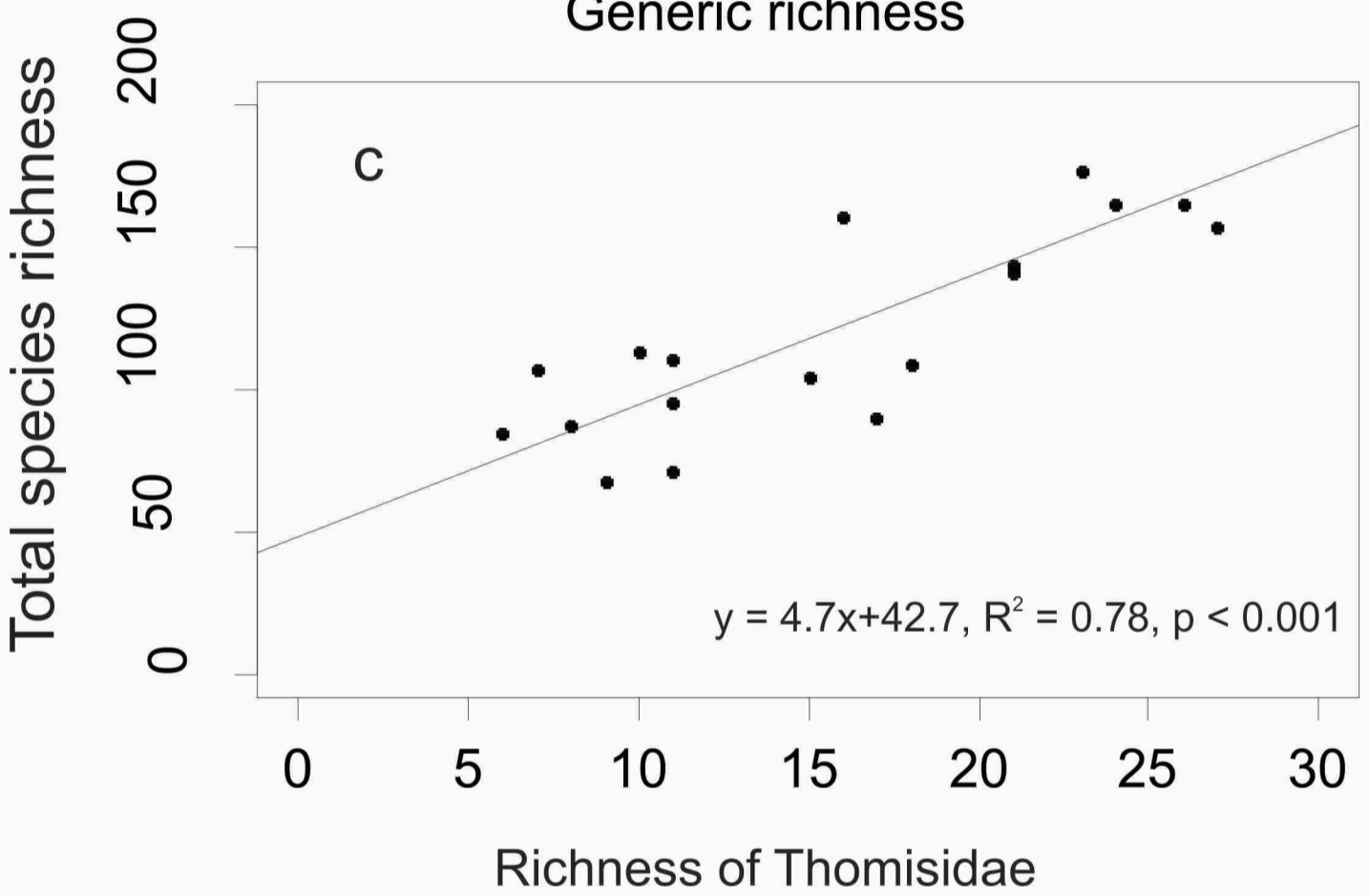
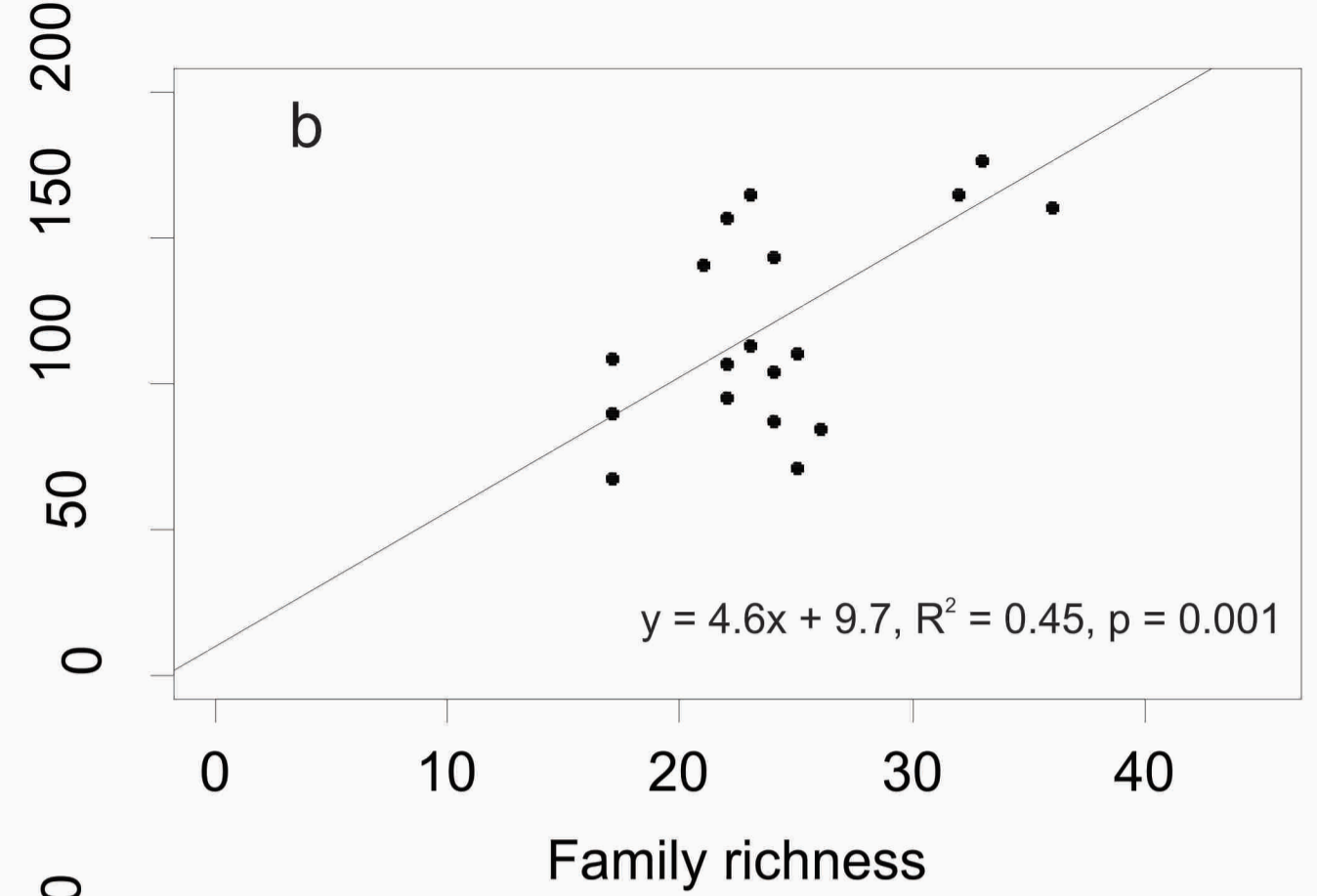
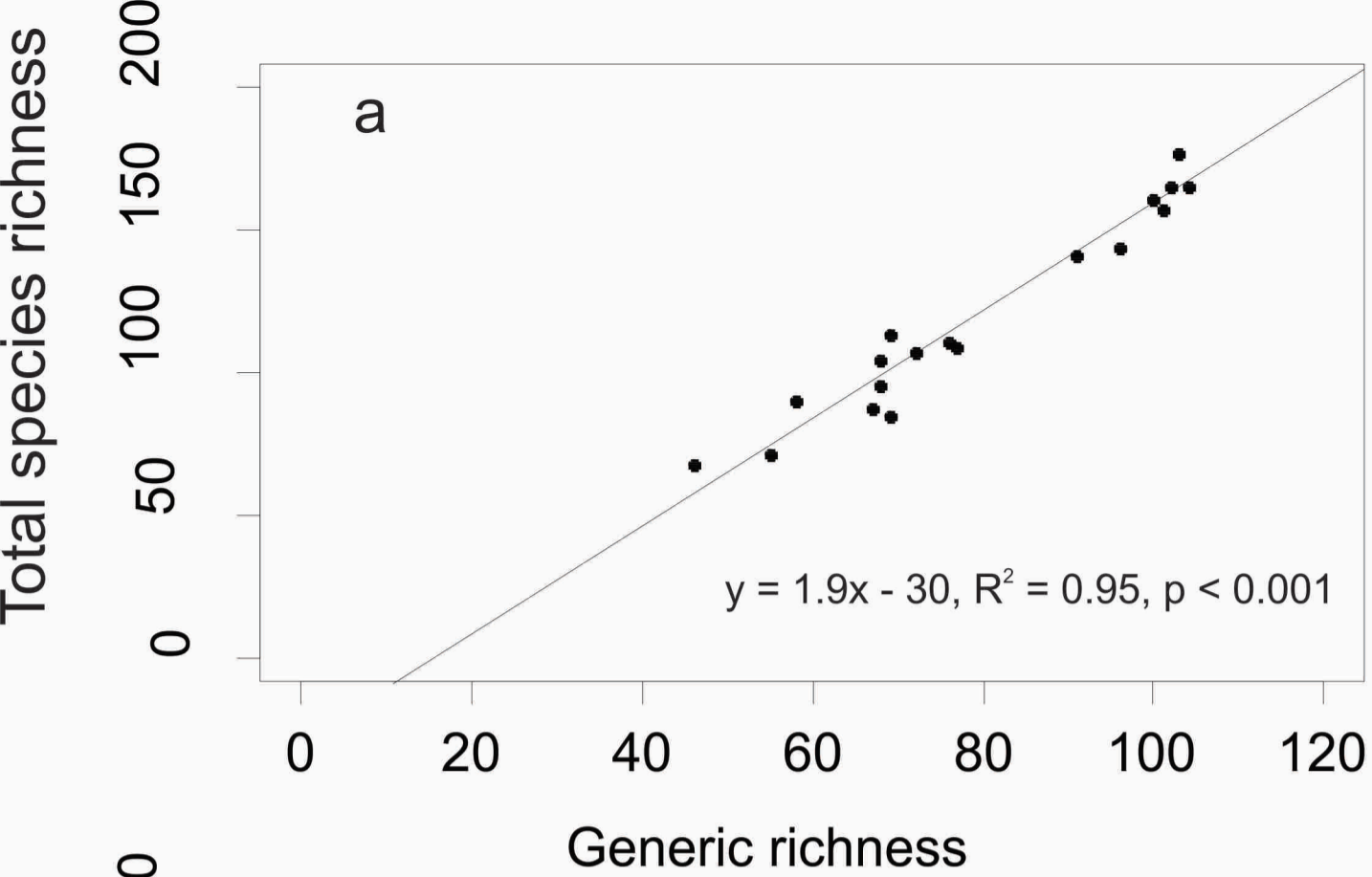


Fig. 2

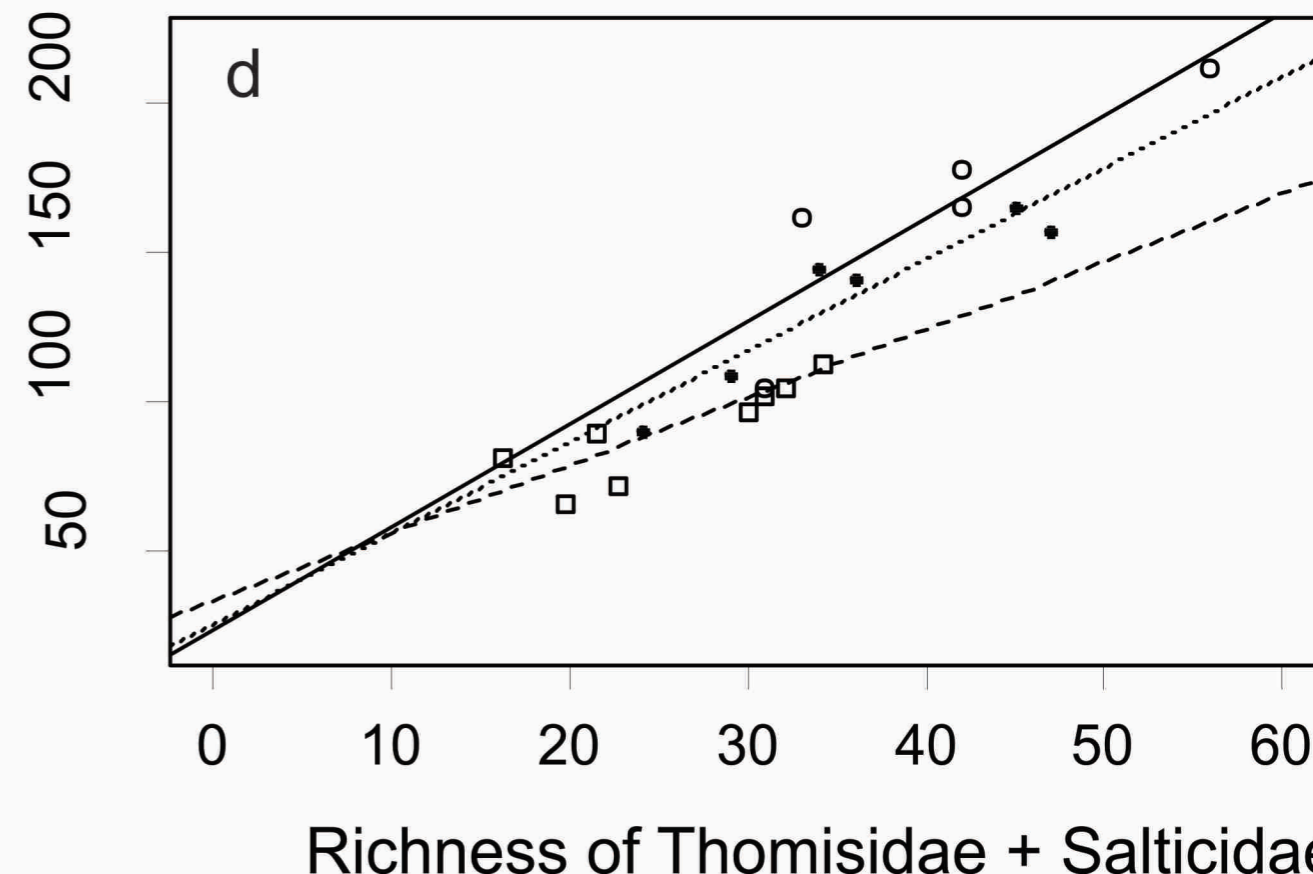
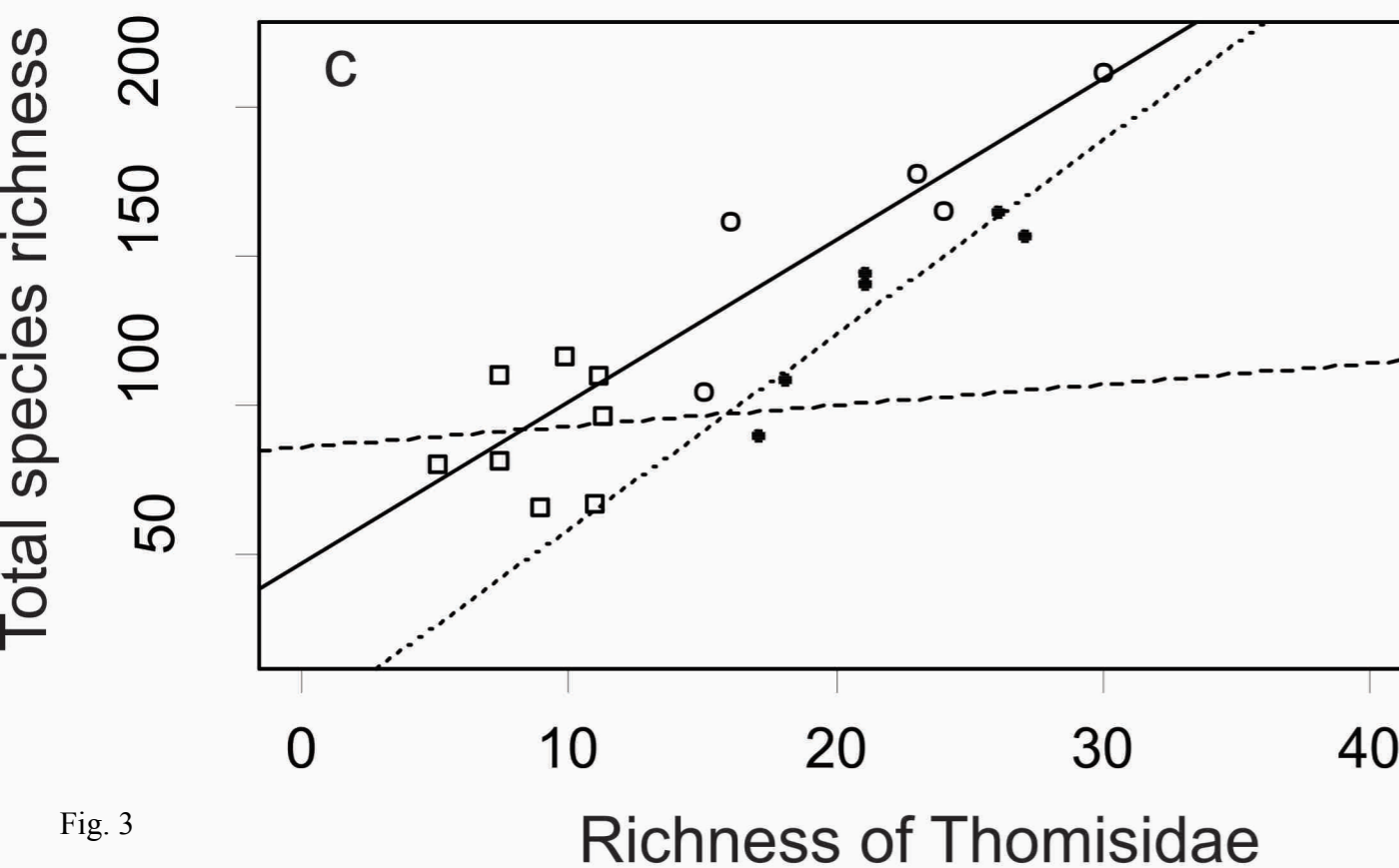
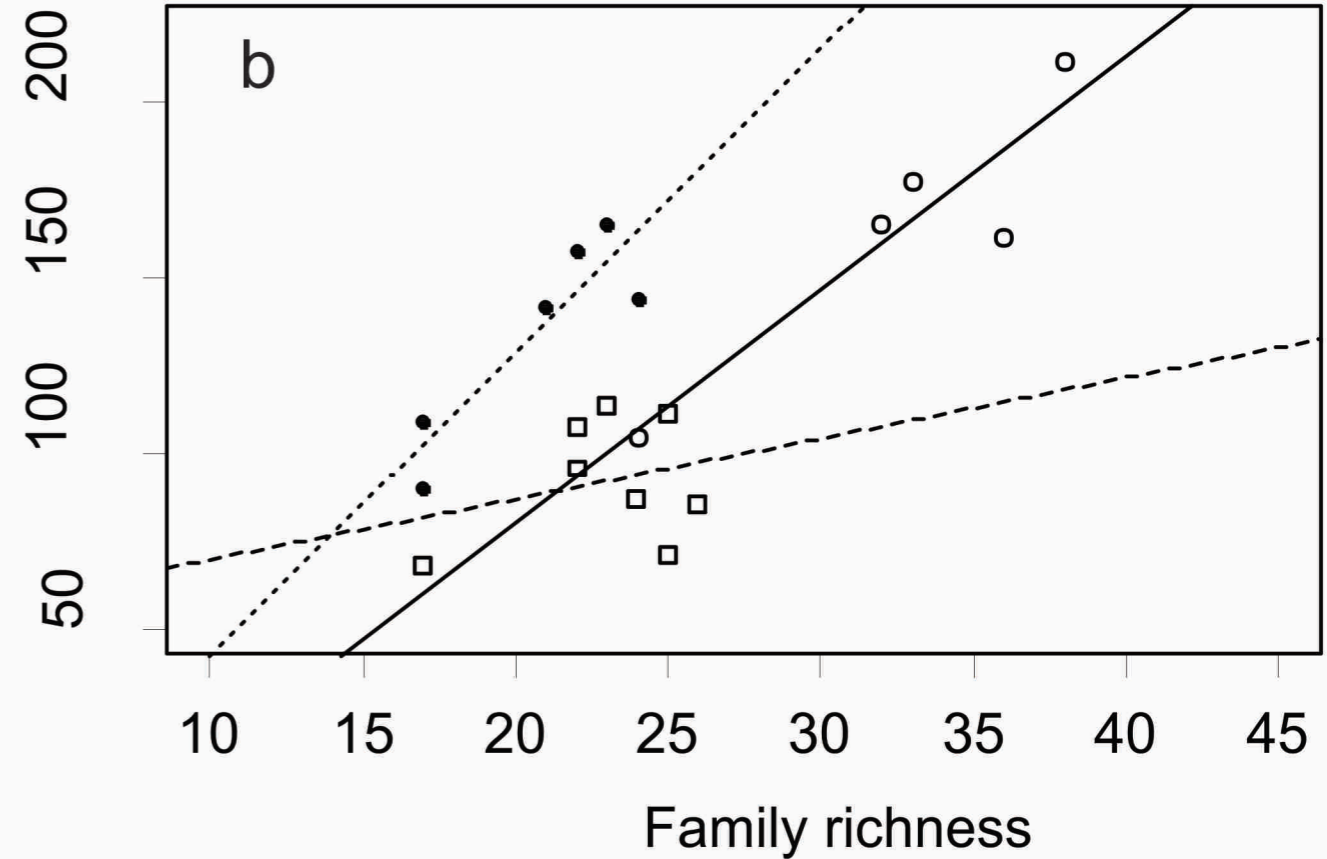
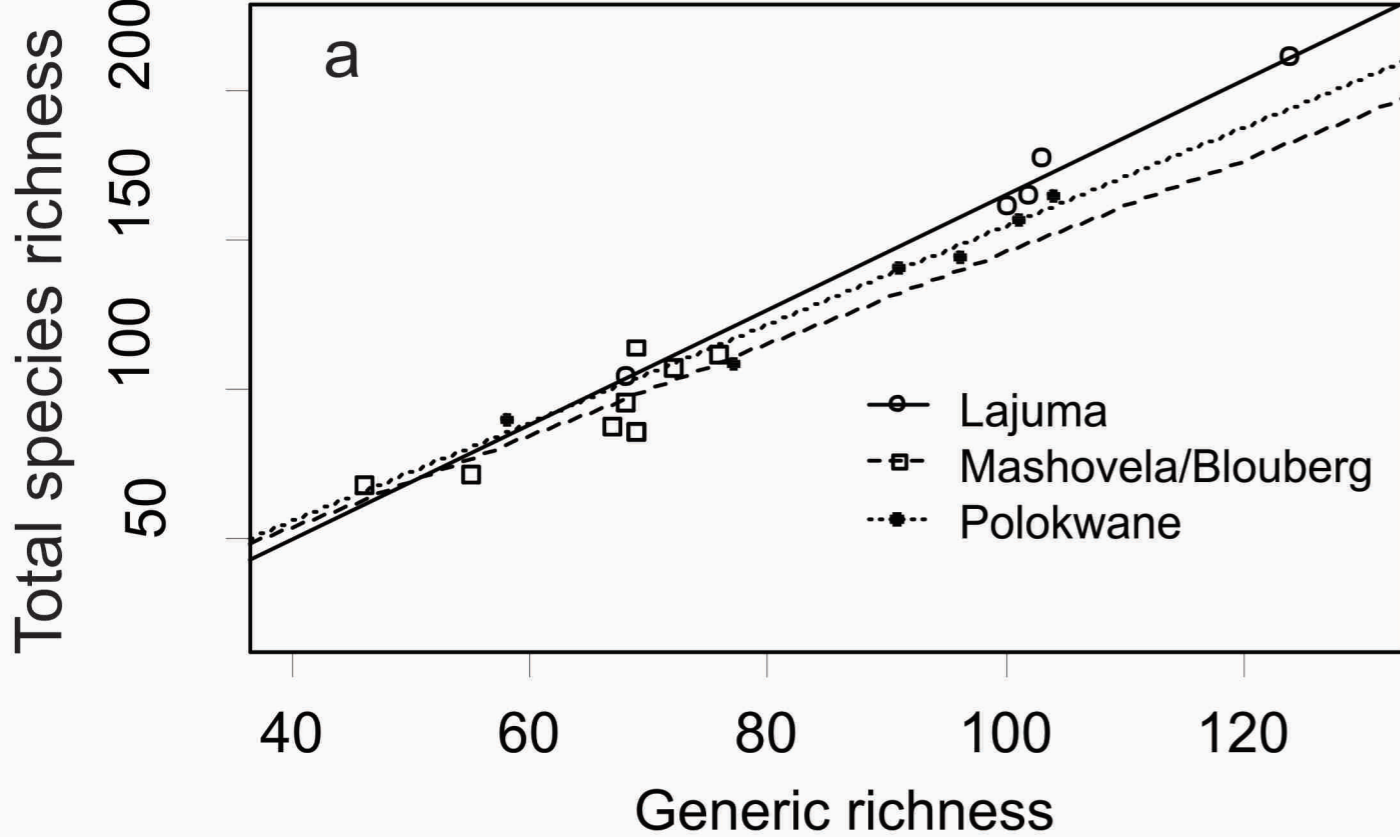


Fig. 3

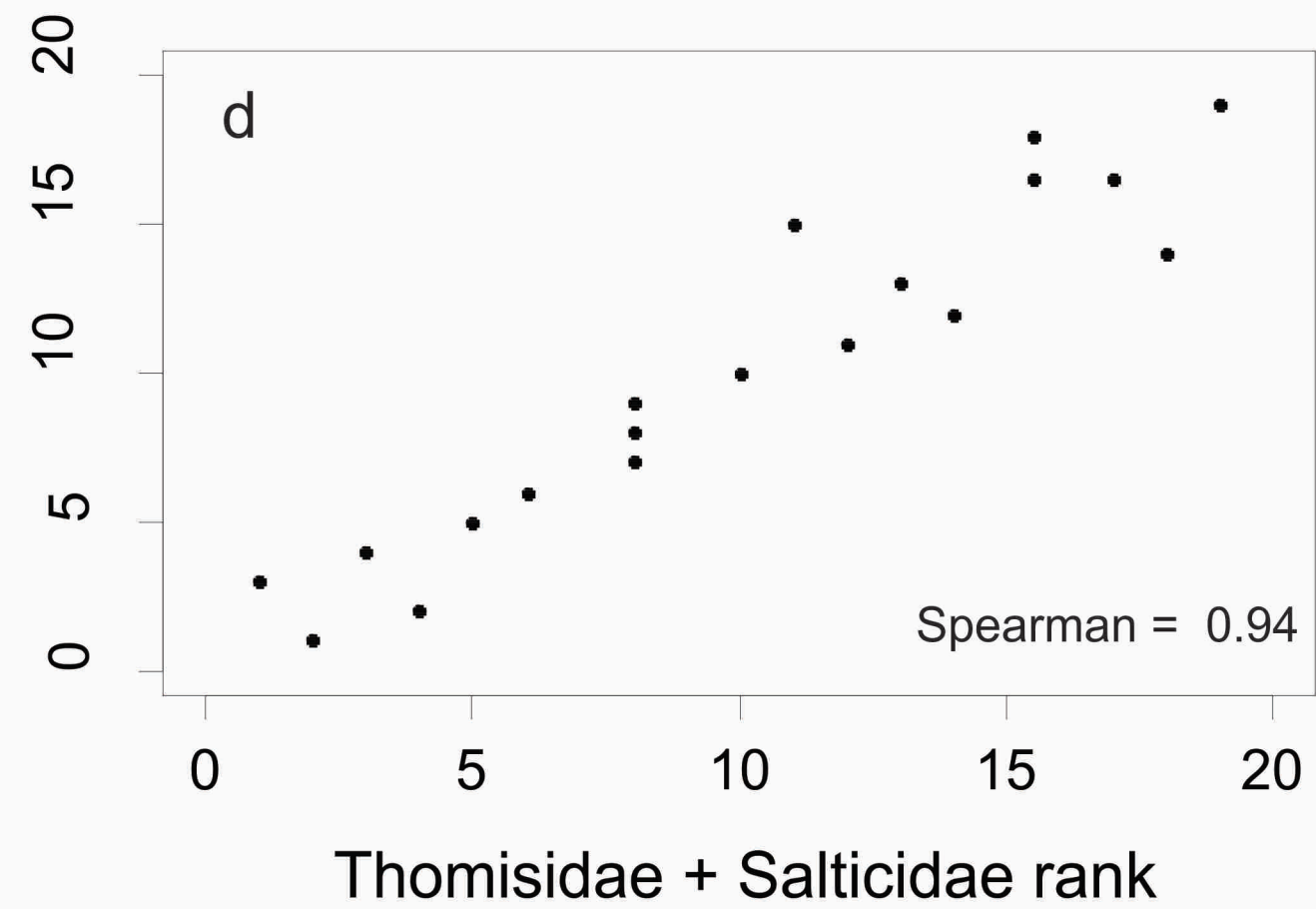
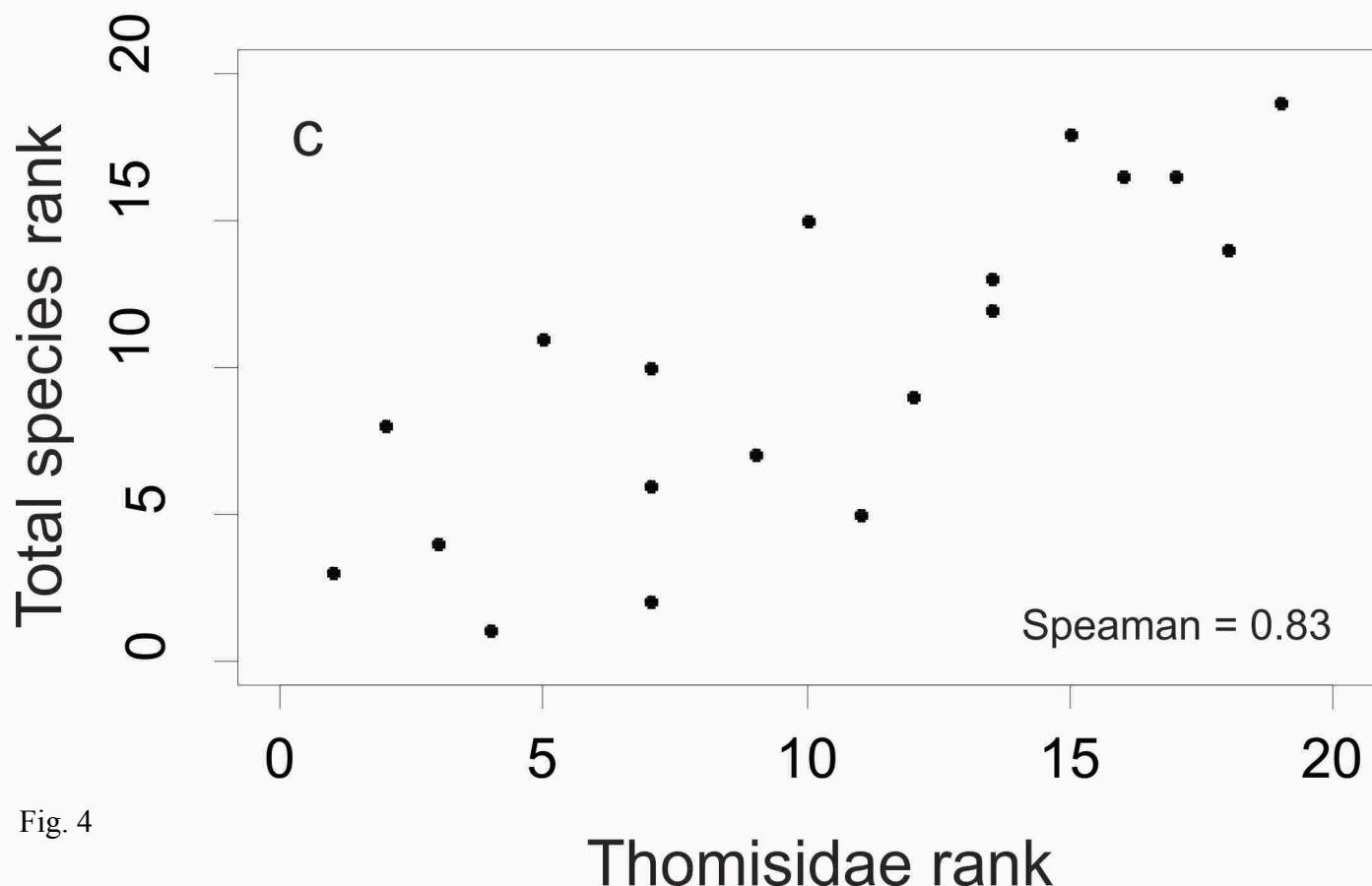
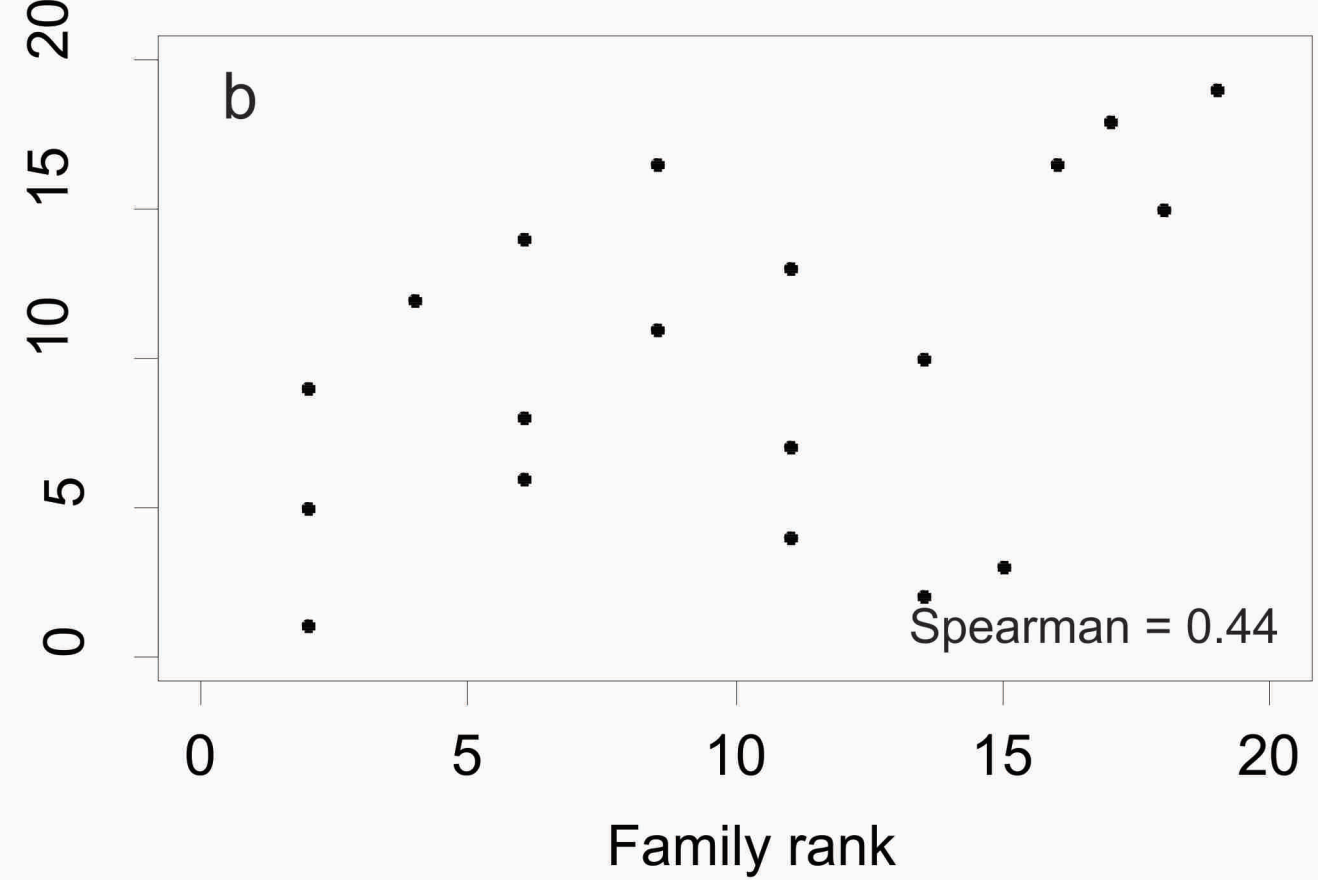
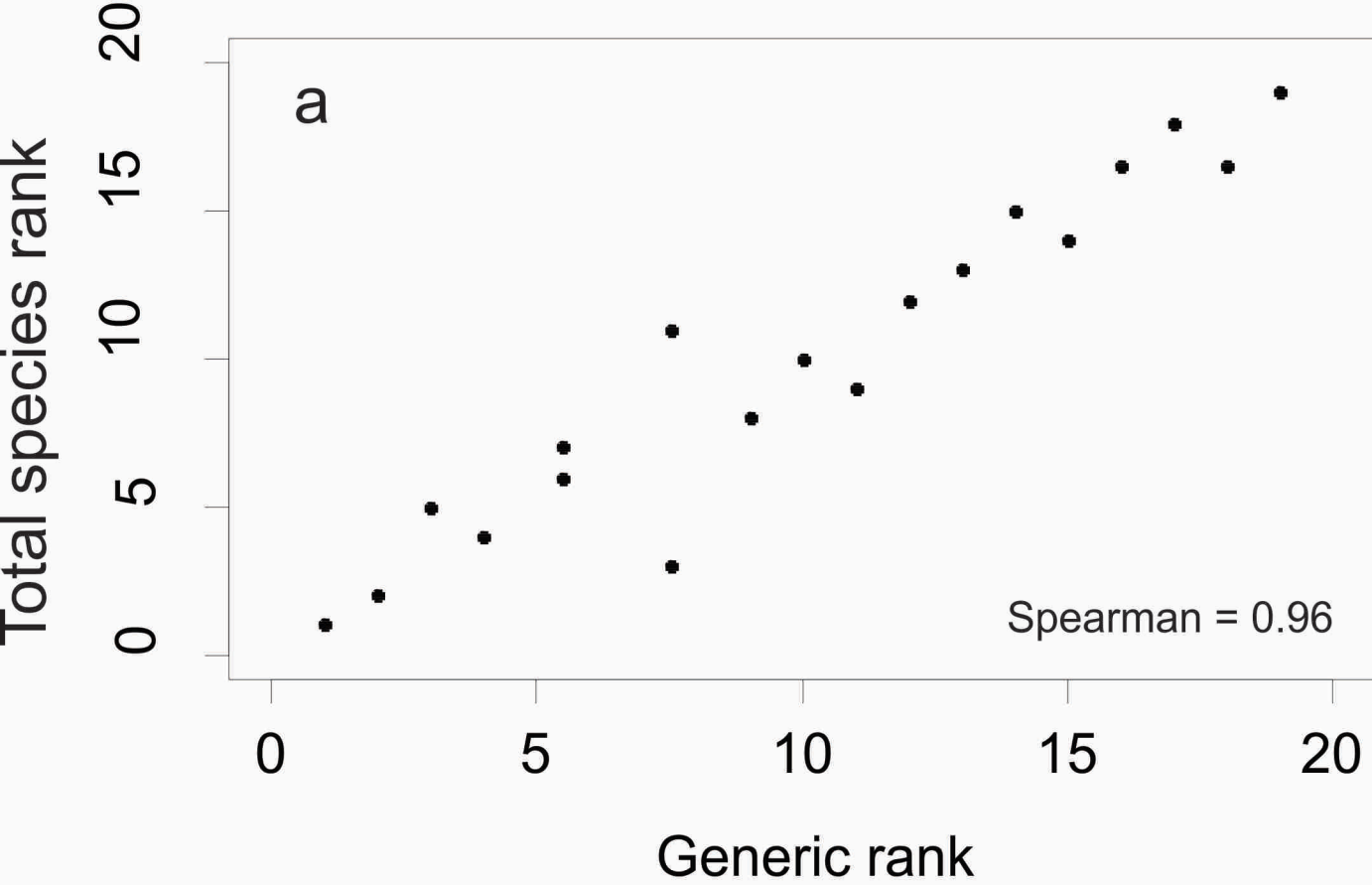


Fig. 4

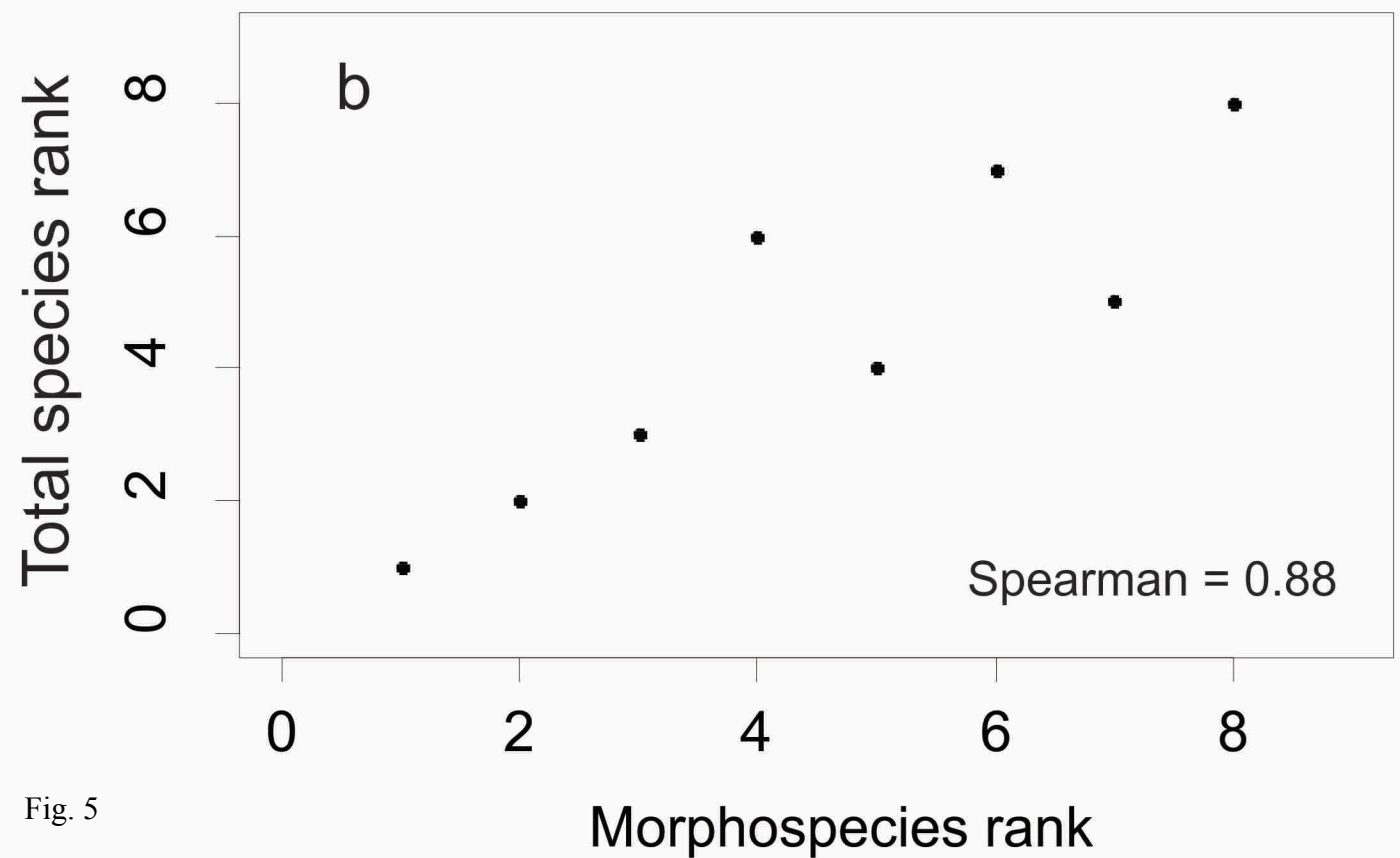
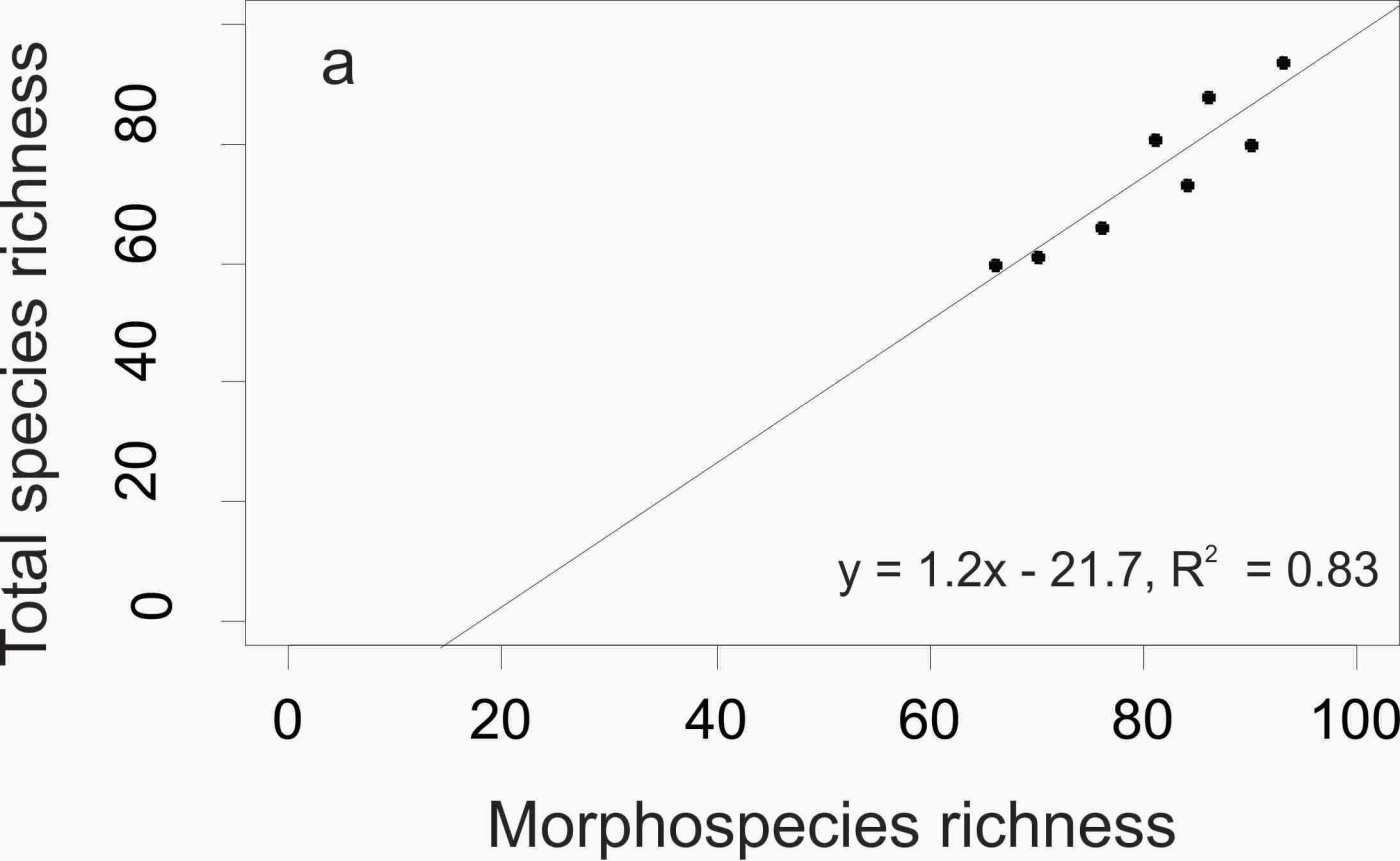


Fig. 5

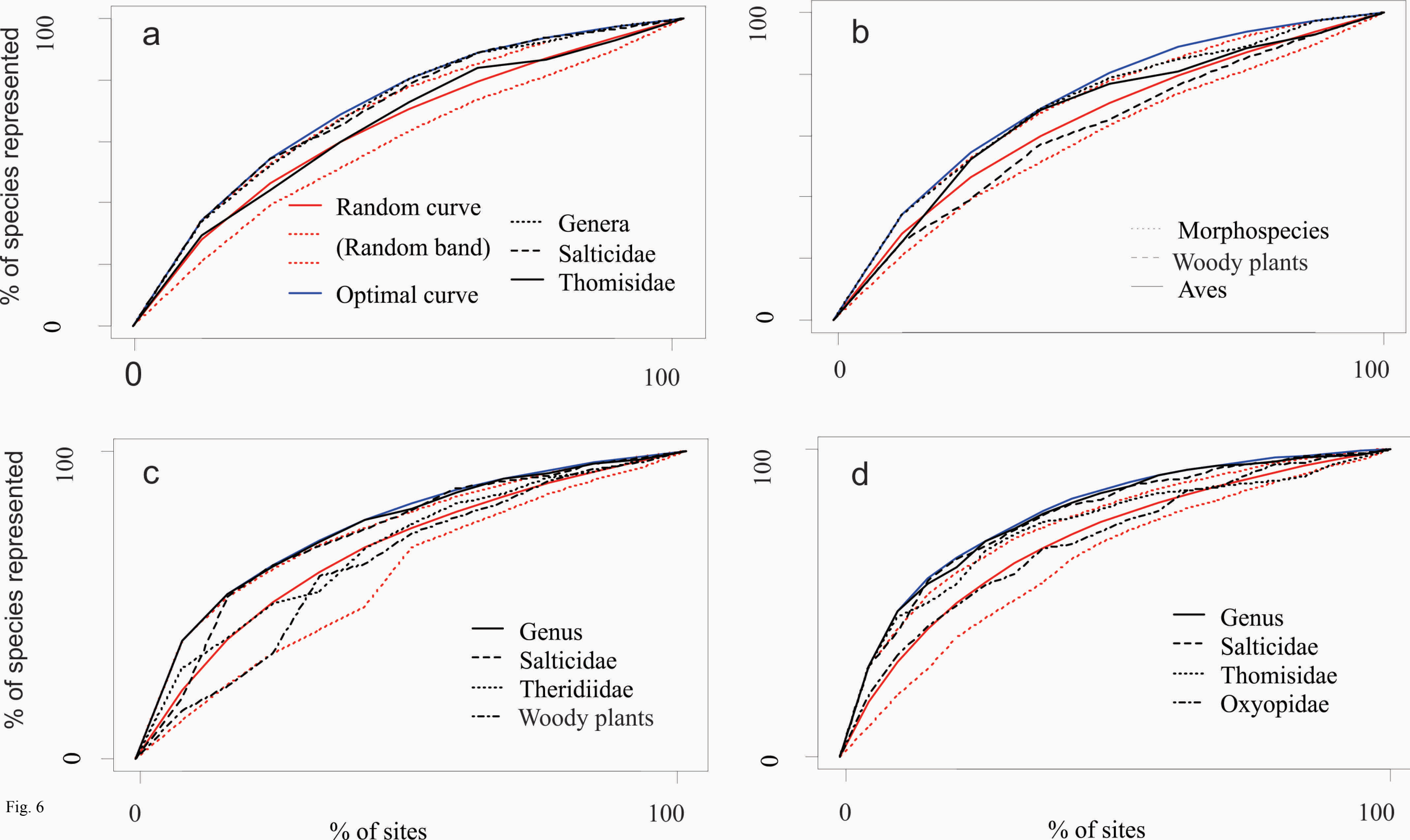


Fig. 6