

A philosophy and methodology for matching opposite sexes of one species, exemplified by a new synonym in *Myrmarachne* (Araneae: Salticidae)

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Abstract. Different philosophies concerning matching opposite sexes of one species, including descriptions of species from single sexes, are discussed. The idea that matching sexes of the same species is methodologically similar to placing species within a single genus is examined. In other words, while differences exist between intraspecific sexes as they do between intrageneric species, discovered intersexual shared autapomorphies or unique sets of characters must place them together as a single species until proven otherwise with new data. The description of separate new species for male and female individuals with similar morphology, especially if they have similar locality data, is untenable, as it generally results in the synonymy of one of the names when additional data is acquired. Separate sex descriptions hyper-inflate the species count for the family, giving a false sense of extant biodiversity. In such instances, the burden of proof must be to show that the sexes do not belong to one species, rather than to prove that they do. A methodology is proposed to be used as a guideline in making decisions about unmatched sexes and undescribed species. It incorporates an autapomorphy shared by both sexes as an intraspecific counterpart to an interspecific synapomorphy, as well as a geographic concept that places single types of intrageneric male and female specimens together as one species. This methodology is applied to the recent descriptions of two species of *Myrmarachne*, resulting in the following: *Myrmarachne gorontaloensis* Yamasaki 2012 is a **NEW SYNONYM** of *Myrmarachne bicuspidata* Yamasaki 2012.

Introduction

Presently, there are about 1.2-1.5 million described species (Mora *et al.* 2011, Costello *et al.* 2013). Most groups of life forms on the planet are incompletely known. Estimates of the total planetary arthropod diversity have reached as high as 30 million species (Erwin 1982) or more, although more recent estimates have revised this number downward [*e.g.*, 4.8-10.2 million (Ødegaard 2000); 5 ± 3 million (Costello *et al.* 2013)]. One of the major groups of arthropods is the sub-/infra-phylum Euchelicerata (Regier *et al.* 2010; level of taxon depending on validity of Chelicerata) containing classes Xyphosurida and Arachnida, the latter with approximately 102,000 described species (Anonymous 2009). The order Araneae alone, with over 44,000 described species (Platnick 2013), has been estimated to contain 125,000 (Agnarsson *et al.* 2013) to 170,000 species (Coddington and Levi 1991). Conservative estimates would double arachnid numbers to just over 200,000, whereas more recent estimates for Arachnida exceed 600,000 species (Anonymous 2009). The largest included order, the Acari at 45,000 described species, may only be 5% known (Walter *et al.* 1996). If true, this would project Arachnida to exceed one million species. At the other extreme, the sister group of Arachnida may consist of one of the few completely known higher taxa, *i.e.*, the class Xyphosurida (horseshoe crabs, family Limulidae), with four extant species worldwide (MarineBio 2013).

One instigation of this paper (although it is but the tip of the proverbial iceberg) happens to be a jumping spider of the genus *Myrmarachne*, family Salticidae. The genus belongs to the subfamily Myrmarachninae, part of a major Australasian radiation of salticids, the Astioida (Maddison *et al.* 2008). Jumping spiders form the largest family of spiders, with 592 genera and 5615 described species (Platnick 2013). The

Salticidae appears to be a young family that has rapidly radiated within the last 50 million years (Bodner and Maddison 2012). Despite its already large size that makes it a megadiverse group, salticids are thought at best to be only 50% known. However, one wonders if the present number of described species is truly representative of the known fauna.

Prószyński (2013) in his Database has a “state of knowledge” category (not including synonyms) that compiles numbers in five sections. As found on his main Database page, these sections include 1972 species accepted, 2479 species incomplete, 964 *species inquirenda*, 587 *nomen dubia* and 564 undescribed species, for a total of 6566 (not 6594 as reported) salticid species. Accepted means that both sexes are adequately described and illustrated, while incomplete is due to the description and illustration of only one sex. One wonders on what criteria the undescribed species are based, but they have no significant bearing on this discussion. His total is 947 species higher (6566/5615) than that listed by Platnick (2013), yet subtracting out the alleged undescribed species still leaves 6002 species, 387 species more than Platnick’s list. The addition of only accepted and incomplete sections gives a total 1164 less (4451/5615) than listed by Platnick (2013). No other combination of Prószyński’s categories match the 5615 species listed by Platnick, although the number of *species inquirenda* (964) is close to the difference (947) between the overall lists. However, adding these to the accepted plus incomplete sections still leaves a deficit of 200 species (5415/5615).

In his ‘About this database’ chapter, Prószyński (2013) reports his database totals in a slightly different way as follows: “it contains data on more than 6,420 nominal species - including 1,876 species having diagnostic illustrations for both sexes, 2,415 with drawings for only one sex; 1,577 species have no diagnostic drawings and cannot therefore be recognized.” These three sections combined total an excess of 253 species (5868/5615) more than the total given by Platnick (2013). It is not entirely clear why the numbers do not correlate between lists, although it appears that these numbers need to be updated, and perhaps also because in some cases the genera appear to be counted with the species, so maybe it is a simple database error that can be fixed. Regardless, Prószyński’s two versions average close enough to use as a reference point.

While it would take an analysis of all the species and the genera in which they are placed to get a complete picture of Prószyński’s section on incomplete species (or alternatively, species with drawings for only one sex), one can extrapolate, and state that if species described from only males or females are equally distributed within the same genera, potentially up to 50% of the incomplete species are synonyms (not counting possible same sex synonyms). Dividing either version from Prószyński (2479 or 2415) by 50% gives more than 1200 names that potentially are not valid. Is the number likely to be this high? Probably not, but that does not mean that inflated species numbers due to description of each sex as a separate species is not a problem, as is the failure to properly match males and females in many instances. As pointed out by Platnick and Raven (2013) in a historical analysis of spider systematics, the present high rate of species descriptions is partially offset by an apparent average 20% synonymy rate based on a sampling of major authors. Faunistic studies including new descriptions are by far the biggest contributor to the synonyms, as they do not generally take into account species outside the target area.

Knowledge bases. Taxonomy rarely occurs in a vacuum. Mostly the description of new species is done by experienced taxonomists or students under the supervision of experienced taxonomists, who impart their wisdom about how to make decisions on specimens of questionable placement. What is implicit in having experience is that the person with experience is familiar with the entire context in which a new species is being described. In other words, there is a hierarchical knowledge base consisting of: 1. all the other species in that genus, 2. all the other species in that species group [if more than one] or at least the closest other known species, 3. which species are known from both sexes and which are known from one sex, and 4. characters that match the sexes of species known from both sexes. Unfortunately, it is this latter category which is most often neglected and undocumented, even when the sexes are correctly

matched. How can one hope to accurately match sexes of poorly known species if the characters that match sexes of related well known species are not diagnosed? Without the knowledge base of all the above categories, it is very difficult to make educated decisions on the status of one or more specimens that don't fit the existing classification. Is a new specimen the opposite sex of a species described from one sex? Is it a new species? If the latter, is a different new specimen the opposite sex of it? How do you decide?

An equally pertinent question: What happens if experience and proper training are not requisites for publication? Generally this results in two types of problems. The first is the creation of descriptions that are useless for diagnostic purposes [*e.g.*, Makhan 2006; in the description of a holotype male, the following phrase was included, "epigynal spinnerets brown." Never mind that the phrase refers to the wrong sex, what does that even mean? No such structures exist.]. The second problem is the author may lack experience and diagnostic knowledge to be able to properly place species to genera, and match sexes within species. For example, Chickering (1946) described two species of *Metacyrba* from Panama from opposite sexes of the same species (he even acknowledged that they probably belonged together), while describing them in an unnecessary new genus (*Parkella*), later synonymized (Edwards 2006). Another source of similar problems is that of well-intentioned taxonomists who follow a flawed methodology, thereby preventing them from using their experience and useful diagnostic techniques to make optimal decisions about matching opposite sexes of species in various categories. These categories are: 1. matching undescribed forms of both sexes, 2. matching an undescribed sex to a described sex, and 3. matching two described species of opposite sex into a single species. I discuss philosophies pertaining to these categories below.

Philosophies

The faunas of most areas of the world are still incompletely known. Specimens come from various sources, and possibly are as much incidental as they are the result of organized expeditions. It was recently expressed to me that the largest source of undescribed biodiversity may occur in undetermined museum collections (W. Wesolowska, personal communication 2013). There is undoubtedly some truth to this. Museums are perennially understaffed and cannot keep up with full curation of specimens, thereby preventing examination of all available material by specialists. Not to mention that for most groups, insufficient specialists exist to keep up with the description of new taxa and analysis of phylogenetic relationships (knowledge of which is important to the placement of undescribed specimens). Lack of support for phylogenetic hypotheses and predictive classifications was previously decried by Platnick and Wheeler (2000), among others. I am sure that none of this is news to most practicing taxonomists. Regardless, existing specialists often encounter unknown specimens from poorly known areas of the world. How should they deal with these specimens? What criteria do they use to match sexes when they describe new species? Three philosophies on this subject are itemized below. I give them numbers for later referral.

[1] One philosophy is exemplified by Prószyński (2013) in Poland, and has been followed by his students, and perhaps other workers. Quoting directly from his website:

Males and females of a species could be considered matched only if the specimens were collected in the intimate situations (copulating, interacting, guarding their nests or brood), or at least in the same place, microhabitat, locality and time. In practice, specimens are taken as matched when kept preserved in the same vial in museum collections, but that is only hypothetic assumption at best. Matching specimens collected hundreds of kilometers apart has little sense, but that also happens in the literature. Diagnostic characters should be described and illustrated from the same specimen, but plates of pictures available in the literature are often composite from variable specimens, possibly even not conspecific, so may be misleading. Recognition of genera should be based on type species, or species obviously congeneric with types. In practice species cannot be, quite often, identified from existing

diagnostic documentation, while types are often not available. In tropics (especially in tropical mountains and archipelagoes) specimens of different but similarly looking species may live in a distance as small as a few hundred meters, but it often happens that genera are defined by type species living thousands of kilometers apart (New Caledonian species having type species in Sri Lanka, or the other way round). That could happen in the nature, but acceptance of these facts requires special care. There is a common practice of identifying species by external color pattern and shape, but similar pattern may occur in many unrelated species and genera. I do not believe automatically in conspecificity of incompletely documented specimens from distant populations.

To briefly summarize, essentially this philosophy states that specimens of opposite sex must be taken together or at least from the same location, habitat and time in order to be considered likely to be conspecific. The net result is it takes relatively little effort to find out if a new specimen fits one of these biological/geographical criteria; if it does not, then it must be a new species. In practice, if the two sexes are described as two different species, even if it is shown that they likely belong together, they are not united unless the two sexes are subsequently collected together. This seems to me to be an extraordinarily conservative viewpoint that does not take into account all possible data sources, and it certainly does not take into consideration the knowledge base that exists in the literature and presumably the experience that exists among most researchers.

[2] A simple way to avoid controversy and inflating species numbers is to only describe one sex if both sexes are present and there is uncertainty about whether or not specimens of the opposite sex belong together. The opposite sex can be described without formally assigning a name to it. One application of this would be for situations in which specimens of opposite sex were collected in the same or nearby localities, but the sexes were not collected together or at the same time. Subsequent research can confirm or refute the pairing, without having to make nomenclatorial changes. This is not an optimal option, but it is better than describing two species of opposite sex, and later having one of the names synonymized when the sexes are formally matched. It would be best if this option is used when there exists more than one type of at least one sex, as a single type of closely related male and female taken from one locality should always be matched lacking contradictory evidence (see argument below).

This methodology could have a more formal corollary, recently suggested (D. E. Hill, personal communication 2013). If specialists in a group were to agree that holotypes should be restricted to the one sex that typically gave the most morphological phylogenetic information (generally in the case of salticids, that would be males and their set of palpal characters), then such problems as superfluous names largely would be avoided. Conscientious experts sometimes have avoided describing new species when the only sex available was not the one which enabled phylogenetic placement (*e.g.*, Huber 2013, who declined to describe five new species of pholcids only known from females, as males have the characters necessary to place them to species groups).

On another level, there presently exist cases (*e.g.*, in India and Southeast Asia) where entire salticid genera are only known from one sex, whereas other similar genera in the same regions are only known from the opposite sex. Describing a new genus from a newly discovered species known only from one sex that gives little in the way of phylogenetic information (especially in salticids if that specimen is female and has a simple epigyne) has relatively little scientific value. The same is true for diagnoses of genera based on comparison of illustrations without a thorough written analysis of the characters being illustrated.

[3] While the previous method has its positive aspects (and perhaps the formal corollary should be implemented separately on its own merit), if both sexes are present (or one sex already may be known), my preference would be to try to find a character state (autapomorphy) or set of character states that are unique to both sexes, even if they were not collected together or exactly in the same place. If this is not readily apparent using traditional morphological methods, the option of molecular analysis is sometimes available, especially with freshly collected material. However, this option is not presently available for

older material that has not been preserved in a manner compatible with present affordable techniques for extracting DNA. In such cases, it would seem useful to have some criteria with which to judge the likelihood that two specimens of opposite sex belong to the same species. I discuss a methodology with such criteria below. In my 40+ years of experience, I have seen that unique matching morphological character states between sexes in salticids usually can be found. In such cases, a shared unique state is a species autapomorphy (a derived character/state unique to a terminal taxon), which must be used to match them. Even if lacking an autapomorphy, it is frequently possible to find sets of character states that are unique to a species.

While the definition of synapomorphy (a derived character/state shared by two or more taxa, *e.g.*, species) precludes its use in this situation, it might be useful to think of a unique shared state between the sexes as a sort of “intersexual species synapomorphy.” From a conceptual perspective, the sexes are two different entities, and a state linking them together would be similar to a state linking two species to a single genus; the term for this would be a shared autapomorphy. When making decisions about matching different sexes into single species, it seems necessary to look for such character states, otherwise, to paraphrase Prószyński (2013: About Salticidae), the effort made is more along the lines of collecting stamps than it is doing science. It similarly might be said that having as a goal describing as many species as possible without regard to existing knowledge of the genera in which they are placed is similar to collecting stamps, whereas the goal of discovering and properly documenting biodiversity (including matching both sexes of a species as well as possible using existing evidence) is doing real science. Diagnosing shared autapomorphies, or at least shared unique sets of character states, must be given priority when describing species and matching sexes.

I do not consider this viewpoint the opposite of [1] above, in fact I also consider it to be a conservative method. However, the purpose is different, in that it is intended to make the best possible decisions about intraspecific matching of sexes, in order to reduce the number of later corrections that must be made, and to prevent unrealistic inflation of the number of species. If an effort is made to get the matches right in the first place, chances are that no one will later have to make corrections. Obviously this only applies to situations in which both sexes are present (or potentially one sex is already known), and the decision must be made as to whether or not they belong together. The main difference in the implementation of this philosophy is that the emphasis is changed here, so that the burden of proof must be to show that congeneric opposite sexes of similar morphology (especially if they are in near proximity) represent different species, rather than having to prove that they belong together.

Along these same lines, it can be shown that the viewpoint in [1] is incomplete. For example, there is quoted, “Matching specimens collected hundreds of kilometers apart has little sense...” If this has any truth to it, and I would not argue that it does not (depending on the circumstances), then the inverse should also be true, “not matching specimens collected close together when no other clear options are available (such as single-sex related species) makes little sense either.” It is worth repeating that the burden of proof must be to show that congeneric specimens of opposite sex in near proximity do not belong together. What also is important to realize is that the presence of a shared autapomorphy is independent of distance, whether far or near. Opposite sexes exhibiting such a character state must be matched together until or unless better evidence becomes available indicating they are separate species.

Methodology

There are a number of potential information sources that can be utilized to make educated decisions on whether or not two individuals of opposite sex belong together as one species (assuming molecular data is not available). These can be divided into biological, geographical, morphological, and phenological data sources. While the non-morphological data sources are not character-based, these can be considered

attributes of a species (Dubois 2010). It is important to record details of such data when collecting specimens, otherwise the acquisition of specimens can again be compared to collecting stamps (Dubois 2010).

Biological data. As in [1] above, specimens of opposite sex which are found together in nature can generally be associated into a single species, despite rare exceptions (*e.g.*, see Edwards 2004 where a heterospecific cohabiting pair of *Phidippus* was reported, and heterospecific courtship in the same genus was observed). Spiderlings with their mother can be reared to discover the male. Specimens from unique habitats in the absence of congeneric species can be associated. In short, biological data at the time of collection which includes both sexes (or the potential to obtain both sexes) is a reliable indicator of conspecificity, even though it is not entirely foolproof. As noted in [1], specimens stored together in collections do not necessarily belong together, although it also is a reasonable indicator. It functions as a better indicator if only one species in a genus is locally involved. I know of one instance where two species in the same genus on an island had their sexes mismatched with each other, because the type vial for one of the species contained the holotype male and females of the other species. It was only when the species groups in the genus were analyzed that the mistake was discovered.

Geographical data. I include local as well as regional data here, and in local respects, there is some overlap with biological data. Occurring in the same location, and especially the same habitat, is a highly useful indicator. Lacking such local data, occurring in the same life zone or same elevation can be helpful; as these generally correspond, local knowledge of life zones and the elevations where they occur is very useful. Lack of a geographic isolating barrier would be a clue, which might result in enlarging any of the previous categories into a greater area, for example, a continuous area of lowland tropical rainforest might extend for many kilometers. Conversely, occurrence in a restricted geographic area, such as an island or isolated mountain top, might give a different picture, whereas recently formed islands might give a false suggestion of long term isolation and lead to wrong conclusions.

Morphological Data. This data type is usually the most reliable. However, it is imperative that documentation of and an understanding of the character states of the taxa in question be available for comparison. For example, in some genera, details of external somatic structure and color pattern are very species specific (this tends to be particularly true in some cases where the spider is a mimic of another organism), whereas in others, there may be differences between the sexes in certain somatic characteristics (particularly dimorphism associated with sexual selection and/or agonistic behavior), or conversely, the color patterns may be so similar among related species that no consistent differences may be discerned. Usually some unifying morphological character states can be found between the sexes, but it may take a very thorough search to find them. These states may be unexpected, *e.g.*, in recent research I have undertaken (Edwards 2010), I discovered that the ventral color patterns of the coxae and trochanters (along with lateral femoral color patterns) of *Myrmarachne* were similar or identical between sexes of the same species, and generally different from other species in the same geographic region. Richardson (2010) found similar correlation of leg color patterns among Chilean *Euophrys* species. States of sexual characters can be useful to match sexes as well, such as a short embolus with a short copulatory duct, or similarity in genital form to a related species known from both sexes. This is one area where experience and knowledge can be well utilized to make decisions beyond what is only available from biological data.

This points out why it is always better to describe new taxa in a revisionary work rather than in a faunistic work, or at least after the main revisionary work of a genus has already been done. In revisionary work, the opportunity usually exists to look at all known related taxa, and find the important characters which define species and match sexes. In faunistic work, the focus is not on one higher taxon (such as a genus), so it is easy to overlook already described taxa from other areas that might be relevant to the work in progress. No thorough analysis takes place that would allow matching of sexes, and

sometimes new species, and even new genera, are described that prove to be synonyms. It is a waste of time both for the describer and for some future researcher who has to make corrections, even if the opposite sex of a known species needed to be described [how much time did it take to decide on a superfluous new name for it?]. This is where knowing the context of an undescribed form as listed in the hierarchical knowledge base in the Introduction is important (a proper diagnosis including nearest relatives should be required for description of a new taxon: editors please take note). Furthermore, a revision is essentially a database of known forms, so a newly discovered form can be directly compared and placed in its proper context (*i.e.*, its closest relatives can be identified). In a faunistic study, no such information on relationships is usually given.

Phenological data. In temperate climates, spring and autumn faunas are often quite different due to difference in maturation times, so seasonal date of occurrence might be important in matching sexes. In the tropics, dry versus wet seasons could be important. One must keep in mind that sometimes females live much longer than males in the adult stage, which can reduce the usefulness of this category. The presence and timing of males may thus prove more valuable as a data source, particularly in the shorter temperate seasons, and matching females are more likely to be diagnosed when males are present or recently have been present (males often mature slightly earlier than females in such situations).

In addition to the above specific categories, the overall circumstances and probabilities should be taken into account when making decisions about describing species. I will not cite specific literature examples here, as I have no wish to disparage the work done by any of my colleagues, for whom I have great respect. But I will generalize a couple of examples to illustrate my point:

1. A species was described from one sex on an isolated island and is the only known species of that genus on the island; then later a specimen of the opposite sex in the same genus was found on the same island and was described as a different species – what is the probability of that? Isn't it much more likely to belong with the previously described species of opposite sex? In the second description, no discussion was given of the possibility of it being the opposite sex of the previously described species, nor was any evidence given that would prevent it from being matched with the other species. As noted above for such a situation, the sexes were collected from the same location with no other clear option, so matching them together should have been given priority unless there was clear countervailing evidence. It is more logical and more parsimonious to presume that they belong to the same species rather than to different species without such evidence.

2. Six species of one genus were described from a small group of islands, three known only from males, three known only from females; none were collected together, but some were collected on the same island. Just because the sexes were not matched does not mean there were more than three species. This is a conservative viewpoint, and is a good example of where [2] above could have been applied, and only three names given, which would avoid almost certain future synonymies and prevent species inflation. For that matter, [3] could have been applied, as the genus in question is not poorly known, and there exists comparative material of other species, including regional analyses, that could have assisted in matching the sexes. Making an analysis of character states at least would have given better support to not uniting, or provided evidence for uniting, some or all of the proposed species into pairs. Such data is needed when it is necessary to match multiple forms of different sexes in the same genus from one locality or a nearby set of localities.

While an argument could be made on which of the above categories is most important, and it seems like most of them could be given priority depending on the circumstances, character-based evidence should always be more heavily weighted when available (see below). My personal analysis is that the following hierarchy of importance usually will be applicable: 1. Genetic (if available), 2. Morphological, 3. Biological, 4. Geographical, 5. Phenological. I can envision instances where the order of categories 2-4

could change, but, on average based on my experience, this order will predominate. As can be seen from this, basing species on a limited set of biological and geographical conditions eliminates arguably more important data that can be used to match sexes. Therefore, it is not necessary to match opposite sexes only by collecting them together, when there is other data available that would make the same inference.

This does not mean that certain aspects of a lower rated category cannot be important. I present here a more formal geographical corollary of this methodology:

Previously unmatched opposite sexes from the same genus or subgeneric entity (whichever is smaller) found in the same general location (but not necessarily taken together or at the same time), lacking any evidence of other local congeneric species or morphological character states that would indicate they belonged in different taxa, must be considered conspecific until proven otherwise.

An example of belonging to different taxa would be clear evidence that the opposite sexes belong to different species groups. This of course does not alleviate the responsibility to find corresponding unique genetic and/or morphological matching character states uniting the two sexes. In fact, part of what this corollary represents is an indication that one should look for matching character states between two opposite sexes that occur at the same locale. However, it would not supercede a shared autapomorphy or otherwise matching set of unique characters, regardless of distance. An important aspect of this is to note that it is time independent. For example, if a male is described from a particular location as a new species, and 10 years later, a female of the same genus is found in the same location, the female belongs with the male, and is not a new species (in the absence of any contradictory or conflicting evidence that accrued during the intervening time period).

This would remain true even if multiple forms were present. For example, in a situation where one type of male and two types of female are found, the male should be matched with one of the females (and an effort should be made to match the other female if an unmatched male is already known). If there are two types of male and two types of female, character states must be found that will match at least one pair, and the other pair can be assumed (again, unless contrary evidence is available). For a given local fauna of a genus, the number of species normally should not exceed the sex with the most number of forms present. If the sexes are equal in number, then there is a high probability that the number of species is equal to the number of pairs. It becomes a matter of finding the character states that match them. To not do so could imply in some cases (*e.g.*, where differential somatic and genitalic character states exist among species) that the author did not have sufficient knowledge of a group (again see the hierarchical knowledge base in the Introduction), and should not have been describing new species.

Finally, some species may now only exist in museum collections (Wheeler and Platnick 2000b), due to the biodiversity crisis (*e.g.*, Wilson 1985, Platnick and Wheeler 2000). Prószyński (2013: About Salticidae) clearly implies that he follows Mayr's Biological Species Concept (*e.g.*, Mayr 2000). As in the case of fossils, extinct species (or, for that matter, extrapolation to any species that is only known from older preserved specimens, as we do not know if the species is now extinct) cannot have a Biological Species Concept that is based in the ability to interbreed applied to it, even though in practice, most species were never tested for this ability anyway, and the application of such a concept is speculative (Wheeler and Platnick 2000b). Furthermore, as quoted from Erchefsky (2010):

Adopting only an interbreeding approach to species... would exclude all asexual organisms from forming species. Interbreeding requires the genetic contributions of two sexual organisms. Asexual organisms reproduce by themselves, either through cloning, vegetative means or self fertilization. Some reptiles and amphibians reproduce asexually. Many insects reproduce asexually. And asexuality is rampant in plants, fungi and bacteria. In fact, asexual reproduction is the prominent form of reproduction on Earth (Hull 1988, Templeton 1989). If one adopts an interbreeding approach to species, then most organisms do not form species.

The philosophy followed in this paper is the Phylogenetic Species Concept exemplified by Wheeler and Platnick (2000a). As noted by Wheeler and Platnick (2000b), “Phylogenetic species, like other testable scientific hypotheses, should be based on and make predictions about observable (character) evidence.” These references (Wheeler and Platnick 2000a, b; Platnick and Wheeler 2000; Ercchefskey 2010) are highly recommended reading as background for the above discussion of philosophies for identifying opposite sexes of the same species.

The Genus *Myrmarachne* MacLeay 1839

Myrmarachne is one of the largest genera of salticid spiders, with well over 200 described species (Platnick 2013, Prószyński 2013). Much work remains to be done with the genus, particularly in areas such as Sundaland. A significant part of this area in Southeast Asia is now submerged, although formation of the islands in this region is a recent phenomenon (Amante and Eakins 2009). Hill (2010) documented the known salticid fauna of the Sunda region, and compared it to the salticid fauna of the Australasian region known as Sahul. Both are continental faunas, with a non-continental area and fauna between them (Wallacea, including Sulawesi). While descriptions of local continental and island faunas has continued (e.g., Edmunds and Prószyński 2003, Prószyński and Deeleman-Reinhold 2010), comparison of these different faunas is generally lacking.

Resolution of the *Myrmarachne* island fauna in Sulawesi and Sundaland has begun recently (Yamasaki 2012, Yamasaki and Ahmad 2013, Yamasaki and Edwards 2013). This fauna contains roughly an equal number of new species and new synonyms, the latter showing that many species have a much wider distribution than previously thought. However, in one recent instance, it appears that opposite sexes of one species were described as two different species. One purpose of this paper is to use the analytical tools as described above to match the sexes and make the synonymy.

Yamasaki (2012) described three new species of *Myrmarachne* from Sulawesi. One of these, *M. yamanei*, was described from both sexes. The other two species, *M. bicuspidata* (described from a male) and *M. gorontaloensis* (described from two females) appear likely candidates to be synonymous. Here I itemize my reasons for believing this based on the methodology outlined above.

Biological data	None, not collected together
Geographical data	Male and females collected on Mt. Tilongkabila, Gorontalo Province, Sulawesi. Elevation given for females (800m, 1200 m) but not given for male.
Phenological data	Females collected in January and February, male in March
Morphological data	Male and females have a similar overall appearance, for example, the coxal color pattern is relatively similar. Most importantly, Yamasaki (2012: 165) states “ <i>M. gorontaloensis</i> might be the female of <i>M. bicuspidatus</i> [sic] because they share a very unique shape of the thorax. However, <i>M. gorontaloensis</i> does not possess the protuberance on its carapace, which is a diagnostic character of <i>M. bicuspidatus</i> [sic].”

Analysing the evidence, we find that although the sexes were not collected together, they were taken from the same geographic locality (although we do not know if from the same approximate elevation or habitat). Phenological data are reasonable to match them given their tropical location. Morphological data are quite similar, especially the unique swollen shape of the thoracic area of the carapace. No other species of *Myrmarachne* is known to have this carapace shape. The closest is *M. malayana* Edmunds and Prószyński 2003 (Yamasaki and Ahmad 2013), but the swelling is less developed in *M. malayana*, and the species belongs to a different species group. The carapace shape is therefore a species shared autapomorphy, and the sexes must be matched based on this character, supported by geographic, phenological, and other morphological evidence.

Yamasaki (2012) stated that the reason he did not match the sexes was because of the distinctive anterolateral protuberance on each side of the male carapace, lacking in females. Based on the present author's experience, the presence of these protuberances is best regarded as a sex-specific character (*i.e.*, the sexes are dimorphic), occurring only in males, and is probably involved in intraspecific communication. Since only one male specimen is known, we do not know if this character varies. It could be part of an agonistic display, assisting males in evaluating their potential success against opposing males; or it could be part of a courtship display to females, advertising fitness in the male. Other genera of salticids are known in which some (but not all) species have anterior integumental modifications of the male carapace that are hypothesized to be used in intraspecific communication (*e.g.*, Bryant 1943: *Dinattus*; Edwards 2004: *Phidippus*). Enlarged chelicerae in males (a prominent feature in male *Myrmarachne*) is a well-known example in salticid spiders of a modified structure in one sex that is used in intraspecific communication and evaluation (*e.g.*, Tedore and Johnsen 2012).

The result is that we have the first known species in *Myrmarachne* that has a significant sexually dimorphic character other than cheliceral size, and we also have one species with two names. As first reviser, I choose *M. bicuspidata* Yamasaki 2012 as the name of the species; *M. gorontaloensis* Yamasaki 2012 becomes a **NEW SYNONYM**. Yamasaki (personal communication 2013), in recent correspondence, agrees with my assessment.

Discussion

While this discussion so far has been about describing new species or matching opposite sexes of species described from one sex, there is no reason why the methodologies described herein could not be retroactively applied to older cases where it is likely that males and females described as separate species could be matched together into one species. In many cases, this will require generic analyses that exceed what is presently available. While discovering and describing new species is a valuable addition to the knowledge base, perhaps a more valuable addition is analyzing genera, and defining species groups based on specific characters. It is this type of information that provides a basis and framework on which unknown forms can be placed. Most genera are inadequately defined and analyzed, not necessarily because the information does not exist, but too often because this type of research is not given priority, so no synthesis of information has been made. Perhaps this is because making a thorough analysis of characters takes more time than making decisions based on simple biological observations. It may seem more time efficient to simply describe a new form as a new species without taking the time to place it into proper context, but this is a false premise, as it will take somebody's time at a later date to make corrections to the status of superfluous species names. It is to be hoped that future research will better take into account the status of single sex species, and a reasonable attempt will be made to place new specimens into their proper context prior to making unneeded names for them (*e.g.*, comparison of characters with related species and single sex species of opposite sex in the same genus). This will avoid creating an inflated species count, and causing future workers to spend time making corrections when they could be doing more useful research.

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