

CHAPTER V

Endemicity lost: molecular homogeneity indicates multiple recent arrivals of megachilid bees in Pacific archipelagos with potential impacts on native ecosystems

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Abstract

When examining how the ecosystems of remote islands have developed, it is important to know the timing of when various elements arrived and whether they then diversified. Our understanding of the histories behind the biodiverse south west Pacific (SWP) archipelagos is limited, and further impeded by the complex geological histories of this region. Previous studies of the SWP short-tongued halictine bee fauna suggest their presence is much younger than the geological ages of these archipelagos, which is surprising given their critical role as pollinators in other terrestrial ecosystems. The long-tongued megachilid bees represent a considerable proportion of the known bee species for the region, yet little is known of their origin. Here we use genetic diversity within mitochondrial DNA to infer the likely ages and origins of megachilid species from Vanuatu, Fiji, and Samoa. Our results indicate a very recent origin for megachilids in the SWP, with many species exhibiting small intraspecific genetic distances. Three species share almost identical haplotypes with specimens from Southeast Asia, suggesting multiple human-aided introductions. Combined with data from recent studies on other bee groups present in the region, our results have broad implications for how the Pacific island biota developed and how we should approach its management.

Keywords: Vanuatu, Fiji, Samoa, pollinators, island biogeography, conservation

1.0 Introduction

Throughout the rise of angiosperms in terrestrial environments, bees have become increasingly important in ecosystem functioning (Engel 2001). As primary pollinators for a substantial number of flowering plants, their role is critical for a large proportion of floral diversity in terrestrial environments (Klein et al. 2007; Michener 2007; Ollerton et al. 2011). Island ecosystems often harbour low levels of species richness, but high levels of endemism (Whittaker and Fernandez-Palacios 2007). Low pollinator diversity on islands often results in broader host-plant ranges (Olesen et al. 2002), enabling pollinators to become keystone, ‘super generalist’ species that are responsible for pollinating a large suite of plants. The resulting pollinator network, involving few pollinators but many hosts, can become vulnerable to disruption from introduced species. In island systems, any disruption of interactions can have cascading impacts that result in considerable change in pollination networks (Kaiser-Bunbury et al. 2010).

The islands of the south west Pacific (SWP) represent a fragmented landscape of complex geological and climatic histories. Most islands are of volcanic origin, with the major archipelagos separated by hundreds of kilometres, increasing in isolation from west to east. Age estimates for islands vary but are relatively recent, with the largest subaerial land masses for Vanuatu, Fiji, and Samoa emerging at approximately 3 – 8 Mya (Crawford et al. 2003), 12.5 – 29 Mya (Taylor et al. 2000), and 5 Mya (Hart et al. 2004), respectively. Due to these volcanic origins most of the extant biodiversity is the result of long distance dispersal, likely aided by lowered sea levels during glacial periods with anthropogenic introductions occurring over the last

3000 years (Steadman and Martin 2003). The Australo-Papuan landmass provides a likely source region for many of the groups present in the SWP because of the island chains that link them with Melanesian and Polynesian archipelagos, but biogeographic histories are not always clear (*i.e.* Balke et al. 2007; Jönsson et al. 2010; Keogh et al. 2008; Keppel et al. 2008).

Humans arrived in the Pacific islands only very recently (~3000 years ago) (Bird et al. 2004), but moved relatively quickly across island groups. Their impact was very rapid, with widespread burning practices evident in sediment analyses in several areas of the region (Nunn 1990). This burning changed the landscape considerably, and with human-aided colonization of exotic species, the impact on native ecosystems would have been substantial (Hope et al. 2009). However, management of pre-human elements in these ecosystems depends on our ability to recognize which species are indigenous rather than anthropogenic, which is not straightforward. Taxonomic treatments of insects for likely source regions such as Southeast Asia and the Indo-Papuan region are often very poor, species biased, or non-existent (Sodhi et al. 2004). Reconstructing when key elements of these islands' flora and fauna arrived is, therefore, vital to our understanding of how current ecosystems function and provides insight into how best to manage populations in the future.

Studies of the bee fauna in the SWP are few, mostly from the first half of the 20th century (Perkins and Cheesman 1928; Perkins and Cheesman 1939), and were based purely on morphology (Michener 1979; Pauly and Munzinger 2003; Pauly and

Villemant 2009) until recently (Groom et al. 2013; Groom et al. 2014). Collectively, these studies describe a depauperate fauna largely represented by two families, Halictidae and Megachilidae, with Apidae comprising the introduced honeybee *Apis mellifera* and four other introduced species (Groom et al. 2014). Two very recent studies have used molecular data to provide important information regarding the history of both halictids and megachilids in Fiji. Firstly, Groom et al. (2013) found the Fijian halictine bees were entirely represented by the subgenus *Lasioglossum (Homalictus)* and colonised the archipelago during the middle to late Pleistocene. Although colonisation occurred at that time, during a period of warming climate after the last glacial maximum (LGM), the group experienced rapid diversification and population expansion resulting in a hyper-diverse haplotype clade prior to human arrival. Secondly, Davies et al. (2013) revealed that the Fijian megachilid bees represent even more recent dispersals, most or all of which were human-mediated arrivals from Southeast Asia. Considered concurrently, these two studies indicate that the Fijian bee fauna has only arrived recently relative to the geological age of this archipelago. This, in turn, suggests that bees were not important pollinators of the Fijian ecosystem until only recently, which has major implications for understanding the evolution of the islands' angiosperm communities.

To determine whether the patterns observed in Fijian megachilid bees reflect those seen in other regions of the SWP, we use mitochondrial DNA to assess the genetic diversity and infer the likely source regions of megachilid bees from Vanuatu, Fiji, and Samoa.

2.0 Methods

2.1. *Collecting localities*

Specimens were collected via sweep netting from inflorescences of both native and introduced plant species from both disturbed and undisturbed habitats. Specimens were transferred to 99% ethanol immediately after collection to ensure DNA preservation. The sampling regime sought to cover both habitat and geographic variability across all islands, to build on the dataset of Davies et al. (2013) and provide a greater regional context. Collection from the islands of Vanuatu occurred the between 30th January – 18th February 2011 across the islands of Santo, Malekula, Efate and the small neighbouring island of Pele, as well as the southern volcanic island of Tanna, covering an elevation range of 0 – 190m asl (above sea level). Higher elevations were unable to be sampled because of limited road access to peaks. Samoan samples were collected between 11th – 18th September 2011 from the two main islands of Upolu and Savaii covering an elevation range of 0 – 704m asl. The Fijian collection of Davies et al. (Davies et al. 2013) covered the four largest islands of Viti Levu, Vanua Levu, Taveuni, and Kadavu, and here we have expanded this to include the islands of the southern Lau group. Sampling in these islands was conducted between 6th July – 8th August 2011 from the islands of Ono-i-Lau, Vatoa, Ogea, Vulaga, Namuka, Kabara, Lakeba, Vanuavatu, Moala, Totoya, and Matuku. The resulting dataset comprises the greatest sampling coverage of the combined Fijian, Samoan and Vanuatu megachilid bees to date, covering an elevation range of 0 – 600m asl across 15 islands. Collecting localities are provided for all included haplotypes in Supplementary Table 1. Species identification followed Michener (2007) although we acknowledge there is much uncertainty among the relationships

within Megachilidae (Gonzalez et al. 2012), particularly at subgeneric level within the Asia Pacific region.

2.2. DNA sequencing

Tissue samples were processed at the Canadian Centre for DNA Barcoding (CCDB) at the Biodiversity Institute of Ontario, where DNA extraction, PCR, and mtDNA (COI) sequencing were carried out using standard protocols (Ivanova et al. 2006). Bidirectional sequencing was used with the universal primer pair of LepF1/LepR2 (Hebert et al. 2004), producing 687bp of cytochrome oxidase I (COI). Trace files were aligned using Geneious Pro v6.1.7 (Drummond et al. 2012), and consensus sequences were developed and genetic distances calculated. Sequences were screened via BLAST database search for potential *Wolbachia* contamination, but were also checked as part of CCDB sequencing quality controls. Sequences for outgroup taxa were acquired from GenBank and Barcode of Life Database (BOLD) systems through searches of public COI sequences for similar haplotypes. All specimens are stored in the Schwarz Bee Collection at Flinders University, South Australia.

2.3. Phylogenetic Analysis

We used a Bayesian MCMC technique for inferring phylogenetic relationships implemented in MrBayes v3.2 (Huelsenbeck and Ronquist 2001), including all available haplotypes. Data were split into two partitions, one comprising 1st and 2nd codons, and another of the 3rd position to accommodate the increased variation

common in mitochondrial DNA. We used a GTR + I + Γ model following a test for most appropriate substitution model using jModelTest 3.06 (Posada and Crandall 1998). We ran the analysis for 50 million generations, sampling every 10,000th generation. We used a burnin of 30 million generations, well beyond stationarity. An amino acid translation of the DNA dataset implemented using MacClade version 4.06 (Maddison and Maddison 2003) was used to identify the level of intraspecific genetic variability, correctly assign the codon reading frame, and confirm the absence of stop codons.

We also used a distance-based approach to reconstruct phylogenies. For this we used a neighbour-joining (NJ) technique applied to uncorrected 'p' distances implemented in PAUP* v4.0b (Swofford 1999). Missing gene fragments were not included when calculating pairwise distances and tree space was explored using a heuristic search. Node support using bootstrapping for these analyses was not estimated. Because most intraspecific haplotype variation involved only one to several nucleotide differences, bootstrapping procedures are very likely to omit these informative differences in pseudoreplicates. Instead, we relied on posterior probability (PP) values from our MrBayes analysis to estimate support for the nodes of interest in our analyses.

3.0 Results

3.1 Bayesian analyses

The consensus phylogram from our MrBayes analysis is summarized in Figure 1, where we have collapsed clades of maximum genetic distances less than 2.2% determined by our uncorrected p-distances matrix (Supplementary Table 2). A phylogeny without collapsed clades is presented in Supplementary Figure 1. Posterior probability (PP) values ≥ 0.90 are indicated by black diamonds on nodes, and maximum pairwise genetic distances for haplotypes within collapsed clades are provided. Clades are coloured by corresponding collection location with Vanuatu, Fiji, and Samoa of the Pacific represented as cyan, yellow, and green, respectively; Sarawak (Malaysia), Thailand, Vietnam, and Pakistan represented by pink, red, violet, and navy blue, respectively. Collection localities for species not closely related to our Pacific haplotypes are not coloured, but are included in Supplementary Table 1.

3.2 NJ Distance analyses

Our neighbour-joining tree based on uncorrected p-distances Supplementary Figure 2 demonstrates broad concordance with our Bayesian analysis in terms of tree topology. However, it also illustrates how the Bayesian model distorts branch lengths within clades where there are few or no differences in nucleotides. So where our Bayesian phylogeny of Supplementary Figure 1 suggests substantial intraspecific variation, the neighbour-joining distance-based tree of Supplementary Figure 2 reveals the amount of variation to be very low or absent.

3.3 Species delineation

Based on a threshold of 2.2% maximum genetic distance for species-level divergence (Ratnasingham and Hebert 2013), our analyses suggest the existence of 13 (or up to 14) species in total for the three archipelagos in our study, Vanuatu, Fiji, and Samoa. Vanuatu exhibits the largest number of species, comprising of: *Lithurgus scabrosus*, *Megachile rambutan*, *M. rangii*, *M. scutellata*, *M. similis*, *M. diligens*, *M. australis*, and *M. laticeps*. Although our sampling events in Fiji covered the widest geographical range in our study, we recovered only seven species from that archipelago, which were: *Heriades (Michenerella)* sp., *M. umbripenne*, *M. scutellata*, *M. laticeps*, *M. albomarginata*, and individuals each of *Lithurgus* nr. *bractipes* and *Heriades (Michenerella)* sp. that exceed the divergence threshold of their corresponding clades. Finally, our Samoan samples recovered only three species: *M. umbripenne* and *M. australis*, which both occur elsewhere in the Pacific, and *M. sp 3*, which had previously been reported only from Vanuatu (Pauly and Villemant 2009). Of the 13 species recovered from our SWP samples, four were found in two or more archipelagos, and three species from our SWP samples closely matched or were identical to haplotypes from the Southeast Asian species. Genetic distances for each species are summarised in Table 1 and illustrated as histograms in Figure 2. We also outline instances of multiple localities for individual species.

3.3.1 Multiple archipelago representatives

Of the four species found in multiple archipelagos, all were from the genus *Megachile*, three were from the subgenus *Eutricharea* and one from the subgenus *Callomegachile*. *Megachile*. (*E.*) *scutellata* and *M.* (*E.*) *laticeps* were recovered from both Vanuatu and Fiji and maximum genetic distances between specimens from the two archipelagos were 0.87% and 1.6% for the two species respectively. In addition, *M.* (*Eutricharea*) *australis* was collected from Samoa and Vanuatu, but also occurs in Southeast Asia, and *M.* (*Callomegachile*) *umbripenne* was recovered from Samoa and Fiji, but is also widespread in southern Asia.

3.3.2 SE Asian representatives

Lithurgus scabrosus has been previously referred to as a ‘tramp’ species, known to be distributed via human activity, and is found in many Pacific islands as well as Southeast Asia, the Indian subcontinent and the Indo-Malayan region (Krombein 1950; Michener 1965). We only recovered this species from Vanuatu along with what appears to be a second closely related species (distances from *L. scabrosus* clade range from 2.9% - 3.1%), *L.* nr. *bractipes* recovered from Kabara of the southern Lau group in Fiji. We feel confident that the presence of these two *Lithurgus* species in the SW Pacific is the result of human-aided introduction.

Representatives of the *Heriades* (*Michenerella*) species previously reported from Viti Levu of Fiji (Davies et al. 2013) were also collected in our study from the southern Lau group. Importantly, our specimens form two separate clades nested

within a larger clade that contains specimens from Thailand, Vietnam, Borneo and Pakistan. The genus *Heriades* had not been reported from the SWP prior to Davies et al. (2013), though species are known from Micronesia (Krombein 1950). Consequently, our data likely represents multiple recent dispersals into Fiji. Furthermore, specimen MSAPB1010-12 collected from the Fijian island of Lakeba in the southern Lau group ranges over the 2.2% threshold in pairwise comparison with some haplotypes and therefore likely represents a second closely related introduction.

Within the *Megachile* subgenus *Eutricharaea*, *M. australis* was found in both Fiji and Samoa, but genetic distances reveal (Figure 2) it is highly similar (max: 1.6%) to sequences from specimens of Thailand and Vietnam. Within the subgenus *Callomegachile*, specimens of *M. umbripenne* were recovered from Fiji in addition to those of Davies et al. (2013), which provided the first published record of the subgenus for this archipelago. Our analyses show that this haplotype falls into a strongly supported (1.00 PP) monophyletic clade with specimens collected from Fiji, Samoa, Borneo, Thailand and Vietnam with low genetic distances (Table 1; Figure 2), which strongly suggests a human-mediated introduction to the Pacific islands.

3.3.3 Single archipelago representatives

Species collected from single archipelagos with almost identical haplotypes (mean 0.0% - 0.31%) comprise the remaining six clades of our tree topology. The closely related species *Megachile rambutan* and *M. rangii*, of the subgenus

Callomegachile, are only known from Vanuatu and form monophyletic clades with almost identical haplotypes (Table 1). While in the subgenus *Eutricharea*, four species were revealed to be restricted to single archipelagos. *Megachile. similis* and *M. diligens* were only recovered from Vanuatu, with maximum genetic distances representing specimens from the southern island of Tanna. *Megachile. (E.) albomarginata* and *M. (E.)* sp 3 (Pauly and Munzinger 2003) were recovered from Fiji and Samoa respectively. Yet despite 72 sequenced specimens between the Fijian islands of northern Viti Levu and Ono-i-Lau, separated by some 500km, *M. albomarginata* shows less than 0.4% mean difference. While *M. sp 3* was recovered from Samoa, although previously reported in Vanuatu (Pauly and Munzinger 2003), with nearest neighbour distances suggest North American specimens as the closest related species rather than any of our Pacific collection.

4.0 Discussion

The range of species and geographical regions covered by our samples is the most comprehensive to date for a study of megachilid bees in the SWP. Moreover, the use of molecular data provides the opportunity to examine boundaries among known species and explore true species diversity, previously masked by morphology alone. In addition, due to the variation in our extensive haplotype dataset we are able to address the likely status of megachilids as endemics or exotics to the SWP. Below we discuss in more detail species diversity in the SWP before exploring the likely origins of megachilids and possible implications for recent large-scale introductions into the region.

4.1 Species status and molecular data

Delineating species boundaries on the basis of molecular data is not always straightforward. Magnacca and Brown (2012) found that the Irish bee fauna did not exhibit a clear ‘barcode gap’ between intraspecific and interspecific variation, although divergences within morphologically identified species were commonly <1%, and different morphological species mostly exhibited sequence divergences >1%. In a regional study of the bee fauna from Nova Scotia, Sheffield et al. (2009) reported an average intraspecific sequence divergence of 0.49%. Hebert et al. (2004) suggested that a threshold of 10x the level of average intraspecific variation sufficiently captures species level divergence, though such ‘rule of thumb’ criteria are fraught with difficulties. For example, recent beneficial mutations in mitochondrial genes can result in genetic sweeps (Bazin et al. 2006), where the resulting lack of mitochondrial variation does not match nuclear variation and where

this lack of variation may falsely suggest a recent origin of the species. However, more recently Ratnasingham and Hebert (2013) demonstrated a threshold of 2.2% provides consistent species identification in subsampled datasets of birds, fish, and invertebrates including bees.

Here we have implemented this approach where uncorrected patristic distances of less than 2.2% are regarded as indicating intraspecific variation, and divergence below 1% as low. Our data indicate that we have at least 13 megachilid species from the three archipelagos. Of these species, we found consistently low maximum genetic distances, with all mean intraspecific distances below 0.96% (Table 1). Given the threshold of 2.2% divergence, our identified species exhibit variation consistent with intraspecific levels but also identify a further two species in clades where individual specimens push above this threshold. Our phylogram also demonstrates that many of the Pacific haplotypes are shared between archipelagos of the region, and also specimens of Southeast Asia. Based on the lack of variation in these genetic distances, and the overlap of haplotypes of multiple regions, we now discuss the basis of inferring a recent megachilid bee fauna.

4.2 Known introductions vs. recent arrivals

Based on shared haplotypes and previous collection locations, we are able to determine that at least five of our species have been introduced into the Pacific via human activity. The remaining eight species demonstrate minimal haplotype variation, with *M. scutellata* and *M. laticeps* sharing haplotypes across multiple

archipelagos. In this regard we consider these two species as likely introductions or arrivals into the Pacific since the last glacial maximum.

Despite the six species being found only from single archipelagos, we remain confident in the proposed recency of their arrival based on minimal intraspecific variation and previous records. The two species of *M. albomarginata* and *M. sp 3* are found from Fiji and Samoa, respectively, with very small genetic variation despite a large number of sequenced specimens for *M. albomarginata*. While a comparison of the *M. sp 3* haplotypes indicates nearest neighbour species to have been collected from North America rather than the Pacific. Moreover, the maximum distances for both *M. similis* and *M. diligens* represent specimens collected from the southern Vanuatu island of Tanna. These species have both been recorded from elsewhere in the Pacific (Rasmussen et al. 2012; Rainbow 1896; Cockerell 1947), which suggests multiple arrivals given the proximity (250km) of Tanna to the Loyalty Islands of New Caledonia rather than a result of restricted interchange with the northern islands. In contrast, a short crown node separates the clades of *M. rambutan* and *M. rangii* with low within and between genetic divergence. Their apparent absence outside of Vanuatu may be the result of insufficient sampling, but the lack of genetic diversity within each of these clades suggests a recent origin for both. However, due to the short crown node, it is possible these species may be the result of insular speciation.

In summary, our data suggest the likely existence of two megachilid species endemic to the SWP (*M. (C.) rambutan* and *M. (C.) rangii*), five species that represent

recent dispersals into the SWP (*L. scabrosus*, *L. nr. bractipes*, *H. (M.) sp.*, *M. (E.) australis*, *M. (C.) umbripenne*) and six species where status as an endemic or exotic is unclear (*M. (E.) scutellata*, *M. (E.) similis*, *M. (E.) diligens*, *M. (E.) laticeps*, *M. (E.) sp 3*, *M. (E.) albomarginata*).

4.3 Endemicity of long-tongued bees in the SWP

The Megachilidae of the SWP represent a large proportion (~50%) of the recorded bee species for the region (Groom and Schwarz 2011). Yet our data indicate levels of intraspecific haplotype diversity that are much lower than reported for Fijian *Homalictus*, which represent a relatively recent (Pleistocene) dispersal. Groom et al. (Groom et al. 2013) found distances of up to 3.2% within the Fijian species *Lasioglossum (Homalictus) fijiensis*, with maximum distances of 1.4% among haplotypes that diverged after the last glacial maximum. Of the eight megachilid species in our study exclusively from within the Pacific, the maximum intraspecific variation was 1.2% for *M. laticeps*, recorded across Vanuatu and Fiji, while the mean intraspecific variation for these eight species was 0.22%. This has broad implications for the development of the region that will be explored below.

Groom et al. (2013) showed that halictines have only likely been present in Fiji since the Pleistocene, as well, Groom et al. (in review) indicated similar recent arrivals of this group in Vanuatu and Samoa. Davies et al. (2013) showed that Fijian megachilids had an even more recent origin compared to the halictines and that most, if not all species were the result of human-aided dispersal. Our results indicate that

megachilids are also recent arrivals for Samoa and Vanuatu, though there is evidence that post-dispersal insular speciation may have occurred for one clade (*M. rambutan* and *M. rangii*) in Vanuatu. If rates of sequence divergence in megachilids are similar to those of *Homalictus*, then none of the megachilid species in our study are likely to have arrived before the Pleistocene, and most will have much more recent origins, likely since human colonisation.

4.4 Implications for conservation of ecosystems

The region as a whole may have been largely absent of bees for the majority of its development, and the impact of their arrival is likely to have resulted in major disruptions of established species interactions. Being able to estimate the extent of these changes is important for determining how best to manage both pollinator populations and terrestrial ecosystems (Olesen et al. 2002).

A recent study by Groom et al. (2014) shows that in the Pacific, the bee family Apidae is represented by several anthropogenic introductions, the earliest of which likely occurred within the last century. Our data on megachilids suggests some dispersals are older than for Apidae, but no dispersals that likely pre-date the LGM. Consequently, most long-tongued bee species in the SWP are human introductions, and any pre-human dispersals are likely to have been since the LGM. Human dispersal across the SWP occurred rapidly and relatively recently compared to neighbouring regions, with considerable impact almost immediately through widespread burning practices (Nunn 1990; Fall and Drezner 2013). As many apid

species are stem-nesting, and most megachilids nest in wood, the establishment of maritime trade routes would have likely aided inter-island introductions (Sheffield et al. 2011) and will continue to do so if left unmonitored. The combination of widespread disturbance of vegetation and a suite of new long-tongued bee pollinators would provide ideal conditions for invasive plant species to expand their current ranges and colonize, particularly those with long corolla tubes (Goulson 2003).

Despite the obviously negative impacts of introduced pollinators on endemic ecosystems, long-tongued bees are known to be of benefit to agricultural production (Garibaldi et al. 2013). As many agricultural crops are exotic species, long-tongued bees in the SW Pacific may also fulfil the pollinator requirements of exotic plants where native short-tongued *Homalictus* are unable. Furthermore, megachilid bees comprise the majority of non-*Apis* managed pollinators; these megachilids have easily managed nesting substrates which makes them suitable as alternative pollinators of certain crops (Gonzalez et al. 2013). With the increasing importance of food security in the region combined with the susceptibility of the honeybee *Apis mellifera* to the mite *Varroa destructor*, using established populations of polylectic pollinators should become a key priority of agricultural developments.

As a primary pollinator in almost all terrestrial ecosystems, the results presented here considered with previous studies of Pacific bees suggest a very alarming and perhaps puzzling scenario for the SWP. The two predominant bee families in the region exhibit recent histories relative the age of the archipelagos. The Megachilidae appear to have arrived or been introduced since the LGM, while the Halictidae has dispersed

and speciated across the region since the late Pleistocene (Groom et al. 2013). This has major implications for our understanding of how the Pacific island biota developed and how we should continue to manage it. These results suggest that bees in the south west Pacific were not a key part of early island ecosystem development and, furthermore, were not abundant until after the last glacial maximum (> 23 kya). Future research must focus on determining the role of pollinators, primarily bees, in Pacific island ecosystems to highlight specialist indigenous interactions and determine the utility of generalist pollinators in agriculture.

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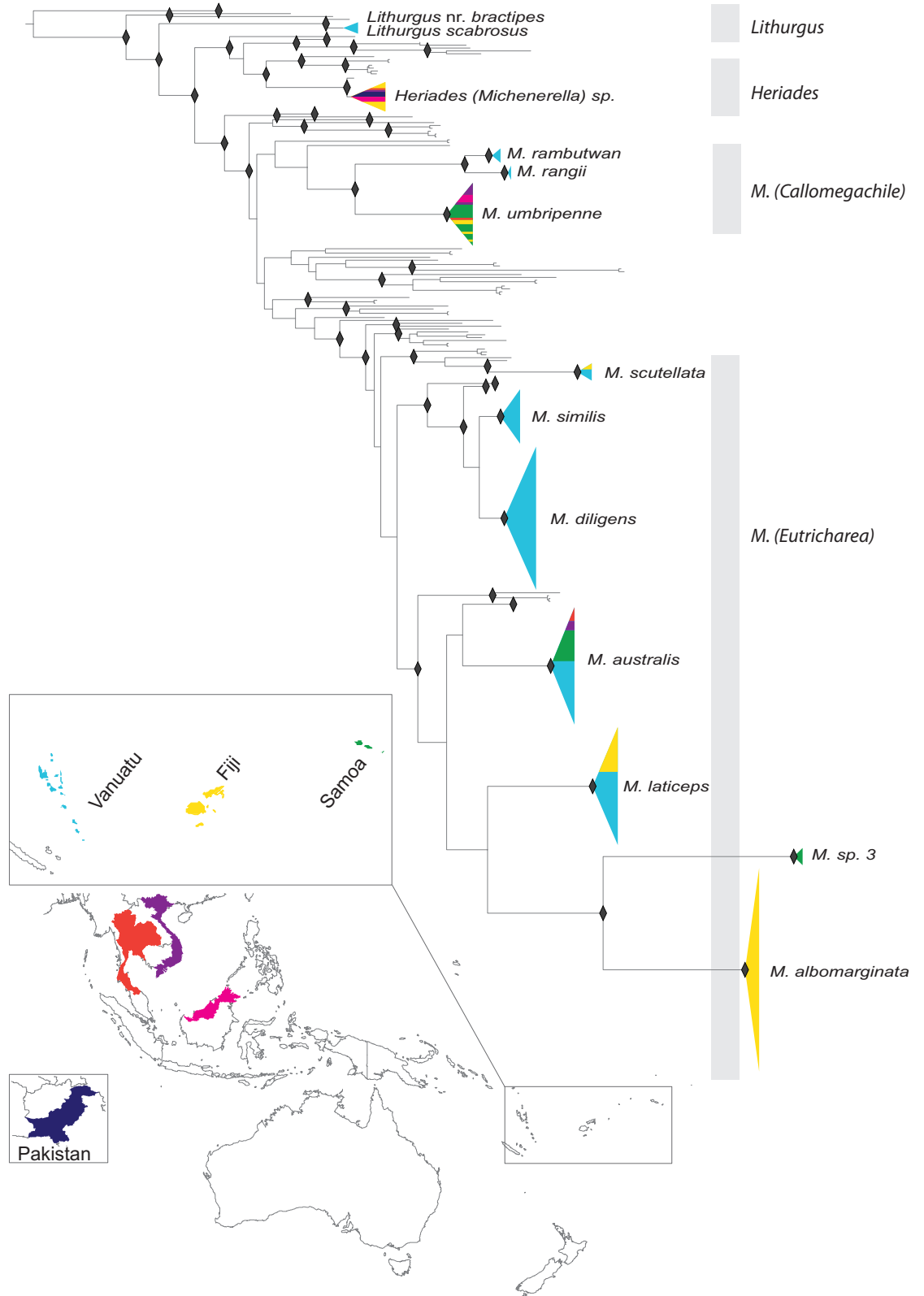


Figure 1: Bayesian phylogeny based on mtDNA (COI) dataset. Phylogeny estimated via MrBayes with GTR + I + Γ substitution prior for a dataset partitioned by 1st + 2nd, and 3rd codon position. Clades have been collapsed based on a maximum genetic distance of 2.2% as indicating intraspecific divergence levels. Collapsed clades are then coloured as per corresponding collection location: light blue = Vanuatu, yellow = Fiji, green = Samoa, red = Thailand, violet = Vietnam, pink = Sarawak (Malaysia), and navy blue = Pakistan. Diamonds on nodes indicate posterior probability support above 0.90%.

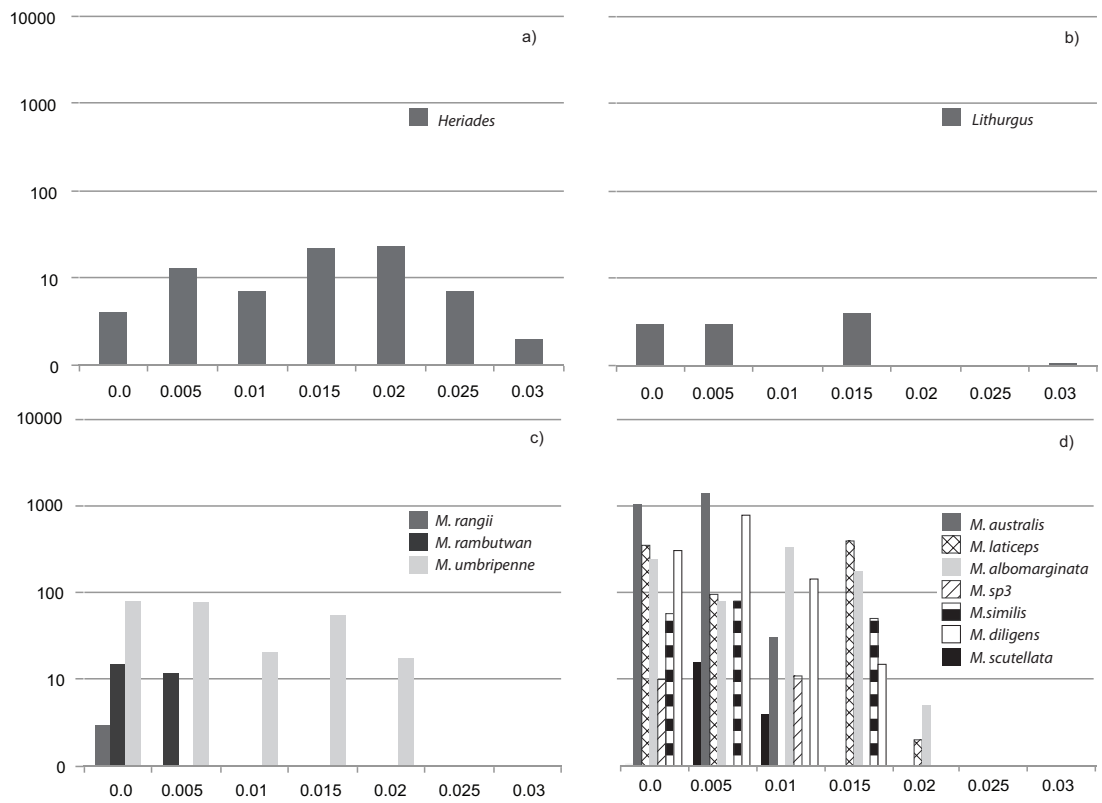
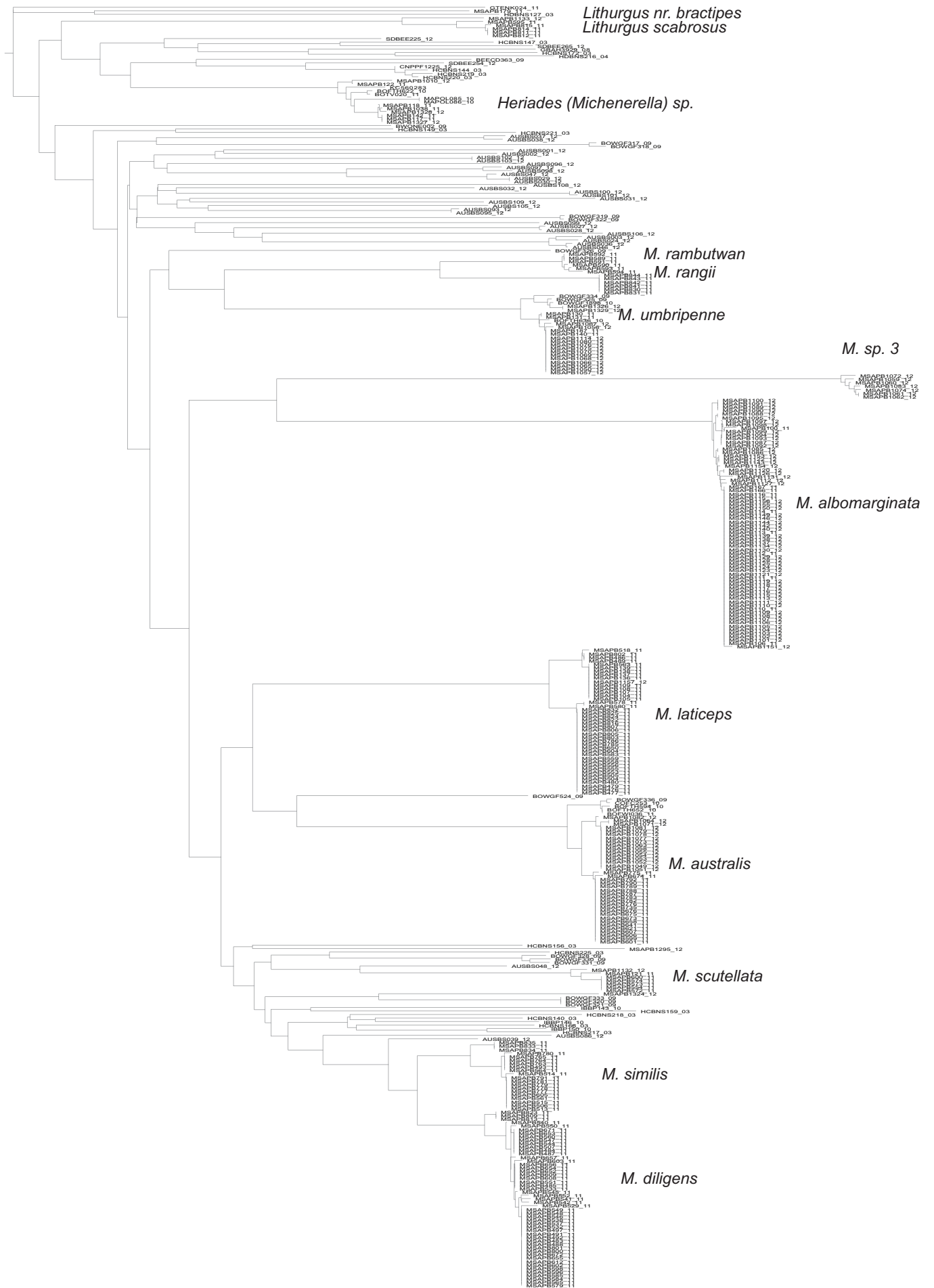


Figure 2: Histograms illustrating distribution of genetic divergence within each species clade. Graphs are provided for *Lithurgus*, *Heriades*, *Megachile* (*Callomegachile*) and *M. (Eutricharaea)* separately for clades containing Pacific representatives to aid visual clarity.

Table 1: Summary of uncorrected pairwise genetic distances for Pacific megachilid species. *Lithurgus* and *Heriades* columns comprise all individuals of their corresponding clades to indicate max genetic distance including two specimens that exceed the intraspecific divergence threshold.

	<i>Lithurgus</i>	<i>H. (M.) sp.</i>	<i>M ramburwan</i>	<i>M rangii</i>	<i>M umbripenne</i>	<i>M scutellata</i>	<i>M similis</i>	<i>M ditigens</i>	<i>M australis</i>	<i>M laticeps</i>	<i>M sp. 3</i>	<i>M albomarginata</i>
Average	0.0069	0.0121	0.0020	0.0000	0.0048	0.0042	0.0037	0.0024	0.0054	0.0059	0.0033	0.0015
Min	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Max	0.0291	0.0277	0.0044	0.0000	0.0175	0.0087	0.0131	0.0116	0.0160	0.0160	0.0073	0.0073
Representatives	6	11	6	6	20	7	18	51	42	42	7	72

Supplementary Figure 1: Bayesian phylogeny with clades not collapsed as presented in Figure 1 based on mtDNA (COI) dataset. Phylogeny estimated via MrBayes with dataset partitioned by 1st + 2nd, and 3rd codon positions.



Supplementary Figure 2: Neighbour-joining phylogram based on uncorrected 'p' genetic distances between COI haplotypes. Scale bar indicates substitutions per nucleotide.

Supplementary Table 1: Locality data and sequence ID numbers for all included sequences. Sequence ID correspond to BOLD Systems database records except where underlined to indicate Genbank accession numbers.

Sequence ID	Species	Country	Latitude	Longitude
AUSBS001-12	<i>Megachile sp. RLCR1</i>	Australia	-22.014	115.631
AUSBS002-12	<i>Megachile sp. RLCR2</i>	Australia	-22.014	115.631
AUSBS003-12	<i>Megachile sp. RLCR3</i>	Australia	-21.977	115.658
AUSBS024-12	<i>Megachile sp. RLCR3</i>	Australia	-21.977	115.658
AUSBS027-12	<i>Megachile sp. RLCR4</i>	Australia	-22.382	115.441
AUSBS028-12	<i>Megachile sp. RLCR4</i>	Australia	-22.382	115.441
AUSBS029-12	<i>Megachile sp. RLCR7</i>	Australia	-22.382	115.441
AUSBS030-12	<i>Megachile sp. RLCR7</i>	Australia	-22.382	115.441
AUSBS031-12	<i>Megachile sp. RLCR10</i>	Australia	-21.977	115.658
AUSBS032-12	<i>Megachile sp. RLCR9</i>	Australia	-21.977	115.658
AUSBS036-12	<i>Megachile sp. RLCR3</i>	Australia	-21.977	115.658
AUSBS037-12	<i>Megachile sp. RLCR5</i>	Australia	-21.977	115.658
AUSBS038-12	<i>Megachile sp. RLCR5</i>	Australia	-21.977	115.658
AUSBS039-12	<i>Megachile sp. RLCR11</i>	Australia	-22.014	115.631
AUSBS046-12	<i>Megachile sp. RLCR3</i>	Australia	-22.382	115.441
AUSBS047-12	<i>Megachile sp. RLCR7</i>	Australia	-22.002	115.861
AUSBS048-12	<i>Megachile sp. RLCR12</i>	Australia	-22.002	115.861
AUSBS086-12	<i>Megachile sp. RLWB1</i>	Australia	-30.124	137.907
AUSBS093-12	<i>Megachile sp. RLWB2</i>	Australia	-30.844	135.539
AUSBS095-12	<i>Megachile sp. RLWB2</i>	Australia	-30.844	135.539
AUSBS096-12	<i>Megachile sp. RLWB4</i>	Australia	-29.9777	137.877
AUSBS097-12	<i>Megachile sp. RLWB5</i>	Australia	-30.305	135.434
AUSBS098-12	<i>Megachile sp. RLWB5</i>	Australia	-30.423	138.077
AUSBS099-12	<i>Megachile sp. RLWB6</i>	Australia	-30.844	135.539
AUSBS100-12	<i>Megachile sp. RLWB7</i>	Australia	-30.076	137.84
AUSBS101-12	<i>Megachile sp. RLWB7</i>	Australia	-30.305	135.434
AUSBS102-12	<i>Megachile sp. RLWB8</i>	Australia	-30.305	135.434
AUSBS103-12	<i>Megachile sp. RLWB8</i>	Australia	-30.293	135.418
AUSBS105-12	<i>Megachile sp. RLWB10</i>	Australia	-30.305	135.434
AUSBS106-12	<i>Megachile sp. RLWB11</i>	Australia	-30.305	135.434
AUSBS108-12	<i>Megachile sp. RLWB13</i>	Australia	-30.076	137.84
AUSBS109-12	<i>Megachile sp. RLWB14</i>	Australia	-30.802	135.432
BEECD363-09	<i>Megachile sp. RLWB15</i>	Canada	43.158	-79.247
BOFTH594-10	<i>Megachile australis</i>	Thailand	16.91	103.904
BOFTH622-10	<i>Megachile sp. RLWB17</i>	Thailand	15.636	101.399
BOFTH636-10	<i>Megachile sp. RLWB18</i>	Thailand	18.883	98.861
BOFTH652-10	<i>Megachile australis</i>	Thailand	16.654	101.132
BOFWI036-11	<i>Megachile australis</i>	Vietnam	12.912	108.184
BOTV020-11	<i>Megachile sp. RLWB21</i>	Vietnam	12.8819	108.644
BOWGF1898-10	<i>Megachile sp. RLWB22</i>	Thailand	12.268	99.944
BOWGF317-09	<i>Megachile sp. RLWB23</i>	Vietnam		
BOWGF318-09	<i>Megachile sp. RLWB24</i>	Vietnam		
BOWGF319-09	<i>Megachile sp. RLWB25</i>	Vietnam		
BOWGF320-09	<i>Megachile sp. RLWB26</i>	Vietnam		
BOWGF321-09	<i>Megachile sp. RLWB27</i>	Vietnam		
BOWGF322-09	<i>Megachile sp. RLWB28</i>	Vietnam		
BOWGF325-09	<i>Megachile sp. RLWB29</i>	Vietnam		
BOWGF326-09	<i>Megachile sp. RLWB30</i>	Vietnam		
BOWGF328-09	<i>Megachile sp. RLWB31</i>	Vietnam		
BOWGF330-09	<i>Megachile sp. RLWB32</i>	Vietnam		
BOWGF331-09	<i>Megachile sp. RLWB33</i>	Vietnam		
BOWGF333-09	<i>Megachile sp. RLWB34</i>	Vietnam	12.512	108.372
BOWGF334-09	<i>Megachile sp. RLWB35</i>	Vietnam	12.512	108.372
BOWGF336-09	<i>Megachile australis</i>	Vietnam	12.512	108.372
BOWGF524-09	<i>Megachile sp. RLWB37</i>	Thailand	16.6598	101.136
BWONE002-09	<i>Megachile sp. RLWB38</i>	Serbia	45.16	19.648
CNPPF1225-12	<i>Heriades carinatus</i>	Canada	41.939	-82.516
COFC253-10	<i>Megachile australis</i>	Thailand	19.36	97.988
GBAH3929-08	<i>Osmia cornifrons</i>			
GTENK024-11	<i>Apis mellifera</i>	United States		
HCBNS140-03	<i>Megachile gemula</i>	Canada	43.876	-66.101

HCBNS144-03	<i>Heriades carinatus</i>	Canada	45.12	-64.273
HCBNS147-03	<i>Hoplitis spoliata</i>	Canada	45.087	-64.668
HCBNS149-03	<i>Coelioxys moesta</i>	Canada	45.12	-64.273
HCBNS156-03	<i>Megachile pugnata</i>	Canada	44.966	-65.058
HCBNS159-03	<i>Megachile inermis</i>	Canada	45.084	-64.732
HCBNS166-03	<i>Megachile melanophaea</i>	Canada		
HCBNS172-03	<i>Osmia atriventris</i>	Canada	45.135	-64.489
HCBNS217-03	<i>Megachile frigida</i>	Canada	45.119	-64.263
HCBNS218-03	<i>Megachile latimanus</i>	Canada	45.119	-64.263
HCBNS219-03	<i>Heriades carinatus</i>	Canada	45.085	-64.234
HCBNS220-03	<i>Heriades carinatus</i>	Canada	45.085	-64.234
HCBNS221-03	<i>Coelioxys sodalis</i>	Canada	45.119	-64.263
HCBNS225-03	<i>Megachile rotundata</i>	Canada		
HDBNS127-03	<i>Nomada pygmaea</i>	Canada	45.12	-64.2
HDBNS216-04	<i>Osmia virga</i>	Canada	44.319	-64.016
IBBP143-10	<i>Megachile centuncularis</i>	Ireland	53.296	-6.3015
IBBP146-10	<i>Megachile maritima</i>	Ireland	52.888	-6.059
IBBP150-10	<i>Megachile willughbiella</i>	Ireland	52.341	-9.831
KC560283	<i>Heriades sp.</i>	China	40.103983	115.912883
MAPOL085-10	<i>Heriades sp.</i>	Pakistan	30.25	71.5
MAPOL086-10	<i>Heriades sp.</i>	Pakistan	30.25	71.5
MSAPB100-11	<i>Megachile albomarginata</i>	Fiji	-18.15	178.443
MSAPB1010-12	<i>Heriades sp.</i>	Fiji	-18.237	-178.809
MSAPB1038-11	<i>Heriades sp.</i>	Fiji	-18.3629	-179.278
MSAPB104-11	<i>Megachile laticeps</i>	Fiji	-18.149	178.424
MSAPB1049-12	<i>Megachile australis</i>	Samoa	-13.8329	-171.772
MSAPB105-11	<i>Megachile laticeps</i>	Fiji	-18.149	178.424
MSAPB1050-12	<i>Megachile umbripenne</i>	Samoa	-13.8239	-171.774
MSAPB1051-12	<i>Megachile australis</i>	Samoa	-13.8239	-171.774
MSAPB1052-12	<i>Megachile australis</i>	Samoa	-13.8239	-171.774
MSAPB1053-12	<i>Megachile australis</i>	Samoa	-13.8239	-171.774
MSAPB1054-12	<i>Megachile australis</i>	Samoa	-13.8239	-171.774
MSAPB1055-12	<i>Megachile australis</i>	Samoa	-13.8239	-171.774
MSAPB1056-12	<i>Megachile umbripenne</i>	Samoa	-13.8239	-171.774
MSAPB1057-12	<i>Megachile umbripenne</i>	Samoa	-13.8239	-171.774
MSAPB1058-12	<i>Megachile australis</i>	Samoa	-13.8239	-171.774
MSAPB1059-12	<i>Megachile sp. 3</i>	Samoa	-14.0138	-171.608
MSAPB106-11	<i>Megachile albomarginata</i>	Fiji	-18.149	178.424
MSAPB1060-12	<i>Megachile sp. 3</i>	Samoa	-14.0093	-171.602
MSAPB1061-12	<i>Megachile sp. 3</i>	Samoa	-14.0093	-171.602
MSAPB1062-12	<i>Megachile sp. 3</i>	Samoa	-14.0093	-171.602
MSAPB1063-12	<i>Megachile australis</i>	Samoa	-13.5669	-172.232
MSAPB1064-12	<i>Megachile australis</i>	Samoa	-13.5669	-172.232
MSAPB1065-12	<i>Megachile umbripenne</i>	Samoa	-13.5925	-172.281
MSAPB1066-12	<i>Megachile umbripenne</i>	Samoa	-13.5925	-172.281
MSAPB1067-12	<i>Megachile umbripenne</i>	Samoa	-13.5925	-172.281
MSAPB1068-12	<i>Megachile umbripenne</i>	Samoa	-13.5925	-172.281
MSAPB1069-12	<i>Megachile umbripenne</i>	Samoa	-13.5925	-172.281
MSAPB107-11	<i>Megachile laticeps</i>	Fiji	-18.15	178.453
MSAPB1070-12	<i>Megachile umbripenne</i>	Samoa	-13.5925	-172.281
MSAPB1071-12	<i>Megachile australis</i>	Samoa	-13.4601	-172.321
MSAPB1072-12	<i>Megachile sp. 3</i>	Samoa	-13.4601	-172.321
MSAPB1073-12	<i>Megachile australis</i>	Samoa	-13.4601	-172.321
MSAPB1074-12	<i>Megachile sp. 3</i>	Samoa	-13.4821	-172.404
MSAPB1075-12	<i>Megachile umbripenne</i>	Samoa	-13.4483	-172.374
MSAPB1076-12	<i>Megachile umbripenne</i>	Samoa	-13.4502	-172.333
MSAPB1077-12	<i>Megachile australis</i>	Samoa	-13.4502	-172.333
MSAPB1078-12	<i>Megachile australis</i>	Samoa	-13.4502	-172.333
MSAPB1079-12	<i>Megachile australis</i>	Samoa	-13.4502	-172.333
MSAPB108-11	<i>Megachile laticeps</i>	Fiji	-18.15	178.453
MSAPB1080-12	<i>Megachile umbripenne</i>	Samoa	-13.4502	-172.333
MSAPB1081-12	<i>Megachile australis</i>	Samoa	-13.4502	-172.333
MSAPB1082-12	<i>Megachile australis</i>	Samoa	-13.4502	-172.333
MSAPB1083-12	<i>Megachile sp. 3</i>	Samoa	-13.5148	-172.396
MSAPB1085-12	<i>Megachile albomarginata</i>	Fiji	-20.6682	-178.722
MSAPB1086-12	<i>Megachile albomarginata</i>	Fiji	-20.6682	-178.722
MSAPB1087-12	<i>Megachile albomarginata</i>	Fiji	-20.6682	-178.722
MSAPB1088-12	<i>Megachile albomarginata</i>	Fiji	-20.5804	-178.72
MSAPB1089-12	<i>Megachile albomarginata</i>	Fiji	-20.6639	-178.73

MSAPB1090-12	<i>Megachile albomarginata</i>	Fiji	-20.6635	-178.725
MSAPB1091-12	<i>Megachile albomarginata</i>	Fiji	-20.6635	-178.725
MSAPB1092-12	<i>Megachile albomarginata</i>	Fiji	-20.6635	-178.725
MSAPB1093-12	<i>Megachile albomarginata</i>	Fiji	-20.6682	-178.722
MSAPB1094-12	<i>Megachile albomarginata</i>	Fiji	-20.6635	-178.725
MSAPB1095-12	<i>Megachile albomarginata</i>	Fiji	-20.6731	-178.696
MSAPB1097-12	<i>Megachile albomarginata</i>	Fiji	-20.6731	-178.696
MSAPB1098-12	<i>Megachile albomarginata</i>	Fiji	-20.6731	-178.696
MSAPB1099-12	<i>Megachile albomarginata</i>	Fiji	-20.6731	-178.696
MSAPB110-11	<i>Megachile albomarginata</i>	Fiji	-18.15	178.453
MSAPB1100-12	<i>Megachile albomarginata</i>	Fiji	-20.6731	-178.696
MSAPB1101-12	<i>Megachile albomarginata</i>	Fiji	-19.8086	-178.241
MSAPB1102-12	<i>Megachile albomarginata</i>	Fiji	-19.8086	-178.241
MSAPB1103-12	<i>Megachile albomarginata</i>	Fiji	-19.8086	-178.241
MSAPB1104-12	<i>Megachile albomarginata</i>	Fiji	-19.8086	-178.241
MSAPB1105-12	<i>Megachile albomarginata</i>	Fiji	-19.8075	-178.24
MSAPB1106-12	<i>Megachile albomarginata</i>	Fiji	-19.8082	-178.239
MSAPB1107-12	<i>Megachile albomarginata</i>	Fiji	-19.8082	-178.239
MSAPB1108-12	<i>Megachile albomarginata</i>	Fiji	-19.8113	-178.237
MSAPB1109-12	<i>Megachile albomarginata</i>	Fiji	-19.1567	-178.408
MSAPB111-11	<i>Megachile albomarginata</i>	Fiji	-18.15	178.453
MSAPB1110-12	<i>Megachile albomarginata</i>	Fiji	-19.1567	-178.408
MSAPB1111-12	<i>Megachile albomarginata</i>	Fiji	-18.237	-178.809
MSAPB1112-12	<i>Megachile albomarginata</i>	Fiji	-18.237	-178.809
MSAPB1113-12	<i>Megachile albomarginata</i>	Fiji	-18.237	-178.809
MSAPB1114-12	<i>Megachile umbripenne</i>	Fiji	-18.237	-178.809
MSAPB1115-12	<i>Megachile albomarginata</i>	Fiji	-18.237	-178.809
MSAPB1116-12	<i>Megachile albomarginata</i>	Fiji	-18.237	-178.809
MSAPB1117-12	<i>Megachile albomarginata</i>	Fiji	-18.237	-178.809
MSAPB1118-12	<i>Megachile albomarginata</i>	Fiji	-18.8493	-178.669
MSAPB1119-12	<i>Megachile albomarginata</i>	Fiji	-18.8493	-178.669
MSAPB112-11	<i>Megachile albomarginata</i>	Fiji	-18.15	178.453
MSAPB1120-12	<i>Megachile albomarginata</i>	Fiji	-18.8493	-178.669
MSAPB1121-12	<i>Megachile albomarginata</i>	Fiji	-18.8493	-178.669
MSAPB1122-12	<i>Megachile albomarginata</i>	Fiji	-18.8493	-178.669
MSAPB1123-12	<i>Megachile albomarginata</i>	Fiji	-18.8474	-178.661
MSAPB1124-12	<i>Megachile albomarginata</i>	Fiji	-18.8474	-178.661
MSAPB1125-12	<i>Megachile albomarginata</i>	Fiji	-18.8474	-178.661
MSAPB1126-12	<i>Megachile albomarginata</i>	Fiji	-19.145	-178.599
MSAPB1127-12	<i>Megachile albomarginata</i>	Fiji	-19.145	-178.599
MSAPB1128-12	<i>Megachile albomarginata</i>	Fiji	-19.145	-178.599
MSAPB1129-12	<i>Megachile albomarginata</i>	Fiji	-19.1308	-178.536
MSAPB113-11	<i>Megachile albomarginata</i>	Fiji	-18.15	178.453
MSAPB1130-12	<i>Megachile albomarginata</i>	Fiji	-19.1308	-178.536
MSAPB1131-12	<i>Megachile albomarginata</i>	Fiji	-19.1308	-178.536
MSAPB1132-12	<i>Megachile scutellata</i>	Fiji	-19.143	-178.57
MSAPB1133-12	<i>Lithurgus nr. bractipes</i>	Fiji	-18.919	-178.945
MSAPB1134-12	<i>Megachile albomarginata</i>	Fiji	-18.9184	-178.952
MSAPB1137-12	<i>Megachile albomarginata</i>	Fiji	-18.9681	-179.883
MSAPB1138-13	<i>Megachile albomarginata</i>	Fiji	-18.9681	-179.883
MSAPB1139-12	<i>Megachile albomarginata</i>	Fiji	-18.9681	-179.883
MSAPB114-11	<i>Megachile albomarginata</i>	Fiji	-18.15	178.453
MSAPB1140-12	<i>Megachile albomarginata</i>	Fiji	-18.9681	-179.883
MSAPB1142-12	<i>Megachile albomarginata</i>	Fiji	-19.1663	179.756
MSAPB1143-12	<i>Megachile albomarginata</i>	Fiji	-19.1668	179.763
MSAPB1144-12	<i>Megachile albomarginata</i>	Fiji	-19.1668	179.763
MSAPB1146-12	<i>Megachile albomarginata</i>	Fiji	-18.3629	-179.278
MSAPB1149-12	<i>Megachile albomarginata</i>	Fiji	-18.3751	-179.27
MSAPB115-11	<i>Megachile albomarginata</i>	Fiji	-18.15	178.453
MSAPB1150-12	<i>Megachile albomarginata</i>	Fiji	-18.3751	-179.27
MSAPB1151-12	<i>Megachile albomarginata</i>	Fiji	-18.3751	-179.27
MSAPB1153-12	<i>Megachile albomarginata</i>	Fiji	-18.5617	179.928
MSAPB1154-12	<i>Megachile albomarginata</i>	Fiji	-18.5617	179.928
MSAPB1155-12	<i>Megachile albomarginata</i>	Fiji	-18.5617	179.928
MSAPB1156-12	<i>Megachile albomarginata</i>	Fiji	-18.5617	179.928
MSAPB1157-12	<i>Megachile laticeps</i>	Fiji	-16.9349	179.901
MSAPB116-11	<i>Megachile albomarginata</i>	Fiji	-18.15	178.453
MSAPB117-11	<i>Heriades sp.</i>	Fiji	-18.15	178.453
MSAPB118-11	<i>Heriades sp.</i>	Fiji	-17.422	177.996

MSAPB122-11	<i>Heriades sp.</i>	Fiji	-17.592	177.755
MSAPB1295-12	<i>Heriades sp.</i>	Australia	-20.7245	139.495
MSAPB130-11	<i>Megachile umbripenne</i>	Fiji	-16.78	179.33
MSAPB131-11	<i>Megachile umbripenne</i>	Fiji	-16.78	179.33
MSAPB1324-12	<i>Megachile sp. serian</i>	Malaysia	1.17273	110.564
MSAPB1326-12	<i>Megachile umbripenne</i>	Malaysia	1.17273	110.564
MSAPB1327-12	<i>Heriades sp.</i>	Malaysia	1.17273	110.564
MSAPB1328-12	<i>Heriades sp.</i>	Malaysia	1.17273	110.564
MSAPB1329-12	<i>Megachile umbripenne</i>	Malaysia	1.17273	110.564
MSAPB136-11	<i>Megachile laticeps</i>	Fiji	-16.432	179.365
MSAPB137-11	<i>Megachile laticeps</i>	Fiji	-16.432	179.365
MSAPB138-11	<i>Megachile laticeps</i>	Fiji	-16.432	179.365
MSAPB139-11	<i>Megachile laticeps</i>	Fiji	-16.432	179.365
MSAPB140-11	<i>Megachile umbripenne</i>	Fiji	-16.432	179.365
MSAPB142-11	<i>Heriades sp.</i>	Fiji	-16.434	179.363
MSAPB166-11	<i>Megachile albomarginata</i>	Fiji	-17.385	179.392
MSAPB167-11	<i>Megachile albomarginata</i>	Fiji	-19.816	-178.239
MSAPB179-11	<i>Braunsapis sp.</i>	India	13.424	77.73
MSAPB187-11	<i>Megachile umbripenne</i>	Fiji	-16.432	179.365
MSAPB476-11	<i>Megachile laticeps</i>	Vanuatu	-17.706	168.317
MSAPB477-11	<i>Megachile laticeps</i>	Vanuatu	-17.706	168.317
MSAPB479-11	<i>Megachile laticeps</i>	Vanuatu	-17.706	168.317
MSAPB480-11	<i>Megachile laticeps</i>	Vanuatu	-17.706	168.317
MSAPB483-11	<i>Megachile diligens</i>	Vanuatu	-17.771	168.303
MSAPB484-11	<i>Megachile diligens</i>	Vanuatu	-17.771	168.303
MSAPB485-11	<i>Megachile diligens</i>	Vanuatu	-17.771	168.303
MSAPB486-11	<i>Megachile laticeps</i>	Vanuatu	-17.771	168.303
MSAPB487-11	<i>Megachile diligens</i>	Vanuatu	-17.771	168.303
MSAPB488-11	<i>Megachile diligens</i>	Vanuatu	-17.771	168.303
MSAPB489-11	<i>Megachile laticeps</i>	Vanuatu	-17.771	168.303
MSAPB491-11	<i>Megachile diligens</i>	Vanuatu	-17.771	168.303
MSAPB492-11	<i>Megachile diligens</i>	Vanuatu	-17.771	168.303
MSAPB493-11	<i>Megachile similis</i>	Vanuatu	-17.771	168.303
MSAPB497-11	<i>Megachile diligens</i>	Vanuatu	-17.728	168.304
MSAPB504-11	<i>Megachile laticeps</i>	Vanuatu	-17.697	168.3
MSAPB505-11	<i>Megachile laticeps</i>	Vanuatu	-17.697	168.3
MSAPB506-11	<i>Megachile similis</i>	Vanuatu	-17.673	168.302
MSAPB507-11	<i>Megachile diligens</i>	Vanuatu	-17.673	168.302
MSAPB513-11	<i>Megachile similis</i>	Vanuatu	-17.546	168.306
MSAPB514-11	<i>Megachile similis</i>	Vanuatu	-17.546	168.306
MSAPB515-11	<i>Megachile similis</i>	Vanuatu	-17.546	168.306
MSAPB518-11	<i>Megachile laticeps</i>	Vanuatu	-17.557	168.461
MSAPB529-11	<i>Megachile diligens</i>	Vanuatu	-17.731	168.312
MSAPB532-11	<i>Megachile diligens</i>	Vanuatu	-17.731	168.312
MSAPB533-11	<i>Megachile diligens</i>	Vanuatu	-17.731	168.312
MSAPB537-11	<i>Megachile diligens</i>	Vanuatu	-17.731	168.312
MSAPB538-11	<i>Megachile diligens</i>	Vanuatu	-17.731	168.312
MSAPB540-11	<i>Megachile diligens</i>	Vanuatu	-17.731	168.312
MSAPB541-11	<i>Megachile diligens</i>	Vanuatu	-17.498	168.419
MSAPB542-11	<i>Megachile diligens</i>	Vanuatu	-17.498	168.419
MSAPB544-11	<i>Megachile diligens</i>	Vanuatu	-17.498	168.419
MSAPB545-11	<i>Megachile diligens</i>	Vanuatu	-17.498	168.419
MSAPB546-11	<i>Megachile diligens</i>	Vanuatu	-17.498	168.419
MSAPB547-11	<i>Megachile diligens</i>	Vanuatu	-17.498	168.419
MSAPB548-11	<i>Megachile diligens</i>	Vanuatu	-17.498	168.419
MSAPB549-11	<i>Megachile diligens</i>	Vanuatu	-17.498	168.419
MSAPB550-11	<i>Megachile diligens</i>	Vanuatu	-17.498	168.419
MSAPB551-11	<i>Megachile diligens</i>	Vanuatu	-17.498	168.419
MSAPB552-11	<i>Megachile diligens</i>	Vanuatu	-17.498	168.419
MSAPB553-11	<i>Megachile laticeps</i>	Vanuatu	-17.498	168.419
MSAPB554-11	<i>Megachile scutellata</i>	Vanuatu	-17.498	168.419
MSAPB555-11	<i>Megachile laticeps</i>	Vanuatu	-17.498	168.419
MSAPB556-11	<i>Megachile laticeps</i>	Vanuatu	-17.498	168.419
MSAPB558-11	<i>Megachile laticeps</i>	Vanuatu	-17.498	168.419
MSAPB559-11	<i>Megachile laticeps</i>	Vanuatu	-17.498	168.419
MSAPB560-11	<i>Megachile diligens</i>	Vanuatu	-17.498	168.419
MSAPB561-11	<i>Megachile similis</i>	Vanuatu	-17.498	168.403
MSAPB563-11	<i>Megachile laticeps</i>	Vanuatu	-16.078	167.404
MSAPB564-11	<i>Megachile similis</i>	Vanuatu	-16.078	167.404

MSAPB572-11	<i>Megachile scutellata</i>	Vanuatu	-16.127	167.284
MSAPB573-11	<i>Megachile scutellata</i>	Vanuatu	-16.127	167.284
MSAPB574-11	<i>Megachile scutellata</i>	Vanuatu	-16.127	167.284
MSAPB578-11	<i>Megachile laticeps</i>	Vanuatu	-16.115	167.316
MSAPB579-11	<i>Megachile diligens</i>	Vanuatu	-16.115	167.316
MSAPB580-11	<i>Megachile laticeps</i>	Vanuatu	-16.115	167.316
MSAPB583-11	<i>Megachile laticeps</i>	Vanuatu	-16.114	167.32
MSAPB584-11	<i>Megachile diligens</i>	Vanuatu	-16.111	167.332
MSAPB585-11	<i>Megachile diligens</i>	Vanuatu	-16.111	167.332
MSAPB589-11	<i>Megachile rambutan</i>	Vanuatu	-16.111	167.332
MSAPB590-11	<i>Megachile rambutan</i>	Vanuatu	-16.111	167.332
MSAPB591-11	<i>Megachile rambutan</i>	Vanuatu	-16.111	167.332
MSAPB592-11	<i>Megachile rambutan</i>	Vanuatu	-16.111	167.332
MSAPB593-11	<i>Megachile rambutan</i>	Vanuatu	-16.111	167.332
MSAPB594-11	<i>Megachile rambutan</i>	Vanuatu	-16.111	167.332
MSAPB595-11	<i>Lithurgus scabrosus</i>	Vanuatu	-16.111	167.332
MSAPB596-11	<i>Megachile diligens</i>	Vanuatu	-16.112	167.332
MSAPB598-11	<i>Megachile diligens</i>	Vanuatu	-16.182	167.389
MSAPB599-11	<i>Megachile australis</i>	Vanuatu	-15.932	167.177
MSAPB600-11	<i>Megachile scutellata</i>	Vanuatu	-15.932	167.177
MSAPB601-11	<i>Megachile australis</i>	Vanuatu	-15.932	167.177
MSAPB602-11	<i>Megachile diligens</i>	Vanuatu	-15.932	167.177
MSAPB603-11	<i>Megachile diligens</i>	Vanuatu	-15.932	167.177
MSAPB604-11	<i>Megachile laticeps</i>	Vanuatu	-15.932	167.177
MSAPB605-11	<i>Megachile similis</i>	Vanuatu	-15.932	167.177
MSAPB606-11	<i>Megachile australis</i>	Vanuatu	-15.932	167.177
MSAPB607-11	<i>Megachile australis</i>	Vanuatu	-15.932	167.177
MSAPB608-11	<i>Megachile diligens</i>	Vanuatu	-15.932	167.177
MSAPB609-11	<i>Megachile diligens</i>	Vanuatu	-15.932	167.177
MSAPB612-11	<i>Megachile diligens</i>	Vanuatu	-15.932	167.177
MSAPB621-11	<i>Megachile australis</i>	Vanuatu	-15.95	167.182
MSAPB641-11	<i>Megachile australis</i>	Vanuatu	-15.906	167.18
MSAPB650-11	<i>Megachile laticeps</i>	Vanuatu	-15.902	167.183
MSAPB652-11	<i>Megachile diligens</i>	Vanuatu	-15.902	167.183
MSAPB653-11	<i>Megachile diligens</i>	Vanuatu	-15.902	167.183
MSAPB654-11	<i>Megachile diligens</i>	Vanuatu	-15.902	167.183
MSAPB655-11	<i>Megachile diligens</i>	Vanuatu	-15.902	167.183
MSAPB656-11	<i>Megachile diligens</i>	Vanuatu	-15.902	167.183
MSAPB657-11	<i>Megachile diligens</i>	Vanuatu	-15.897	167.209
MSAPB658-11	<i>Megachile australis</i>	Vanuatu	-15.897	167.209
MSAPB671-11	<i>Megachile diligens</i>	Vanuatu	-15.906	167.295
MSAPB672-11	<i>Megachile diligens</i>	Vanuatu	-15.906	167.295
MSAPB673-11	<i>Megachile australis</i>	Vanuatu	-16.017	167.396
MSAPB674-11	<i>Megachile australis</i>	Vanuatu	-16.164	167.537
MSAPB675-11	<i>Megachile australis</i>	Vanuatu	-16.164	167.537
MSAPB676-11	<i>Megachile australis</i>	Vanuatu	-16.164	167.537
MSAPB735-11	<i>Megachile australis</i>	Vanuatu	-15.402	167.11
MSAPB763-11	<i>Megachile similis</i>	Vanuatu	-15.145	167.119
MSAPB764-11	<i>Megachile similis</i>	Vanuatu	-15.145	167.119
MSAPB765-11	<i>Megachile similis</i>	Vanuatu	-15.104	167.052
MSAPB775-11	<i>Megachile australis</i>	Vanuatu	-15.494	167.171
MSAPB776-11	<i>Megachile australis</i>	Vanuatu	-15.494	167.171
MSAPB777-11	<i>Megachile similis</i>	Vanuatu	-15.497	167.172
MSAPB778-11	<i>Megachile similis</i>	Vanuatu	-15.497	167.172
MSAPB779-11	<i>Megachile similis</i>	Vanuatu	-15.497	167.172
MSAPB780-11	<i>Megachile similis</i>	Vanuatu	-15.497	167.172
MSAPB781-11	<i>Megachile similis</i>	Vanuatu	-15.497	167.172
MSAPB782-11	<i>Megachile australis</i>	Vanuatu	-15.595	167.111
MSAPB783-11	<i>Megachile australis</i>	Vanuatu	-15.595	167.111
MSAPB785-11	<i>Megachile laticeps</i>	Vanuatu	-15.595	167.111
MSAPB786-11	<i>Megachile laticeps</i>	Vanuatu	-15.595	167.111
MSAPB787-11	<i>Megachile australis</i>	Vanuatu	-15.595	167.111
MSAPB788-11	<i>Megachile australis</i>	Vanuatu	-15.595	167.111
MSAPB789-11	<i>Megachile australis</i>	Vanuatu	-15.595	167.111
MSAPB790-11	<i>Megachile australis</i>	Vanuatu	-15.595	167.111
MSAPB791-11	<i>Megachile similis</i>	Vanuatu	-15.588	166.99
MSAPB792-11	<i>Megachile australis</i>	Vanuatu	-15.559	166.966
MSAPB800-11	<i>Megachile diligens</i>	Vanuatu	-15.561	166.961
MSAPB801-11	<i>Megachile diligens</i>	Vanuatu	-15.561	166.961

MSAPB803-11	<i>Megachile laticeps</i>	Vanuatu	-15.556	166.95
MSAPB805-11	<i>Megachile laticeps</i>	Vanuatu	-19.528	169.262
MSAPB806-11	<i>Megachile laticeps</i>	Vanuatu	-19.528	169.262
MSAPB807-11	<i>Megachile laticeps</i>	Vanuatu	-19.528	169.262
MSAPB809-11	<i>Megachile diligens</i>	Vanuatu	-19.528	169.262
MSAPB811-11	<i>Lithurgus scabrosus</i>	Vanuatu	-19.528	169.262
MSAPB812-11	<i>Lithurgus scabrosus</i>	Vanuatu	-19.528	169.262
MSAPB813-11	<i>Megachile diligens</i>	Vanuatu	-19.528	169.262
MSAPB814-11	<i>Lithurgus scabrosus</i>	Vanuatu	-19.528	169.262
MSAPB815-11	<i>Lithurgus scabrosus</i>	Vanuatu	-19.528	169.262
MSAPB816-11	<i>Megachile laticeps</i>	Vanuatu	-19.528	169.262
MSAPB822-11	<i>Megachile laticeps</i>	Vanuatu	-19.528	169.262
MSAPB823-11	<i>Megachile diligens</i>	Vanuatu	-19.528	169.262
MSAPB824-11	<i>Megachile laticeps</i>	Vanuatu	-19.528	169.262
MSAPB825-11	<i>Megachile laticeps</i>	Vanuatu	-19.537	169.279
MSAPB830-11	<i>Megachile rangii</i>	Vanuatu	-19.512	169.263
MSAPB831-11	<i>Megachile rangii</i>	Vanuatu	-19.512	169.263
MSAPB832-11	<i>Megachile laticeps</i>	Vanuatu	-19.512	169.263
MSAPB833-11	<i>Megachile similis</i>	Vanuatu	-19.502	169.274
MSAPB834-11	<i>Megachile similis</i>	Vanuatu	-19.502	169.274
MSAPB835-11	<i>Megachile similis</i>	Vanuatu	-19.502	169.274
MSAPB841-11	<i>Megachile rangii</i>	Vanuatu	-19.502	169.274
MSAPB842-11	<i>Megachile rangii</i>	Vanuatu	-19.502	169.274
MSAPB843-11	<i>Megachile rangii</i>	Vanuatu	-19.502	169.274
MSAPB844-11	<i>Megachile rangii</i>	Vanuatu	-19.502	169.274
SDBEE225-12	<i>Ashmeadiella buconis</i>	United States	32.7339	-116.951
SDBEE254-12	<i>Heriades SanDiego Sp.A</i>	United States	32.7329	-116.955
SDBEE265-12	<i>Hoplitis fulgida platyura</i>	United States	32.7201	-117.078

Supplementary Table 2: Pairwise comparison of uncorrected p-distances for all representatives included in both distance-based and Bayesian analyses.

75	HCBSN225_03	16.3	16.1	17.4	17.1	17.4	17.4	18	18	18.6	16.3	17.3	17.4	17.6	13.6	17.1	17.4	10.7	14.4	16	16	16.1	17.4	17.3	18.3	18	18.2	15	15	15.1	19.2	17	17.1	22.7	16.3	17.4	17.4	16.3	16.3	17.4	17.6	20.1	19.8	18	14.4	14.4	18	17.9	17.6	11	11.3	11.2	14.4	17.9
76	HDBSN127_03	25.9	27.1	27.4	27.3	25.9	25.9	28.1	28.1	27.4	25.1	27.4	26.1	26.4	26.8	27.3	27.8	26.4	25.9	24.6	24.6	26.7	27.5	27.8	26.8	27.8	27.8	26.7	26.7	25.9	28.7	27.7	25.8	25.4	28.1	24.3	25.8	28.1	28.1	24.2	25.4	28.6	28.3	27.1	26.1	26.1	27	25.4	25.9	27.1	27.1	27.1	26.1	25.4
77	HDNSL216_04	22.5	23.4	22.3	22.2	21.9	22.1	21.8	21.8	25.4	21.2	22.2	22.9	22.9	22.3	22.1	21.6	23.4	24.4	22.3	22.3	22.9	21.6	21.9	21.6	24.5	24.5	21.6	21.6	22.1	22.2	23.4	22.8	23.3	25.3	18.4	23.5	25.3	18.3	23.8	22.9	22.9	24.1	22.9	22.9	23.9	23.5	23.4	25.1	25.5	25.4	22.9	23.4	
78	IBBP143_10	16.8	16.4	18.4	18.2	17	17	19	19.3	16.8	18.4	19.6	19.8	12.6	18.3	18.6	14.1	14.2	16.4	16.4	17.6	18	18.4	19.2	19.2	19.3	15.2	15.2	17.4	19	18.3	17.3	23.1	15.2	18.2	18.3	15.2	15.2	18.3	18.2	21.4	21.1	19.2	15	15	19	18	18.3	13.8	14.2	14.1	15	17.9	
79	IBBP146_10	16.4	15.1	19.7	19.7	19	18.9	17.8	17.8	19.7	18.3	19.7	17.2	17.2	11.6	19.6	17.4	12.6	12.9	15.6	15.2	16.8	17.5	17.8	19.9	18.3	18.3	15.5	15.5	17.5	19.3	19.1	17.7	21.1	14.8	18.2	16.2	14.8	14.8	18.6	16.4	21	21.3	19.3	13.8	13.8	19.3	16.4	18.6	13	13	13.2	13.8	16.7
80	IBBP150_10	17.7	16.8	19.6	19.4	18.9	18.9	17.1	17.1	18	16.5	19.6	17.8	18	13	19.4	16.2	12.9	12.6	15.5	15.5	16.1	15.6	15.9	18.7	18.7	14.6	14.6	16.4	19.6	18.1	15.8	21.4	14.9	17.8	17	14.9	14.9	17.7	17	20	20	19.6	15.2	15.2	19.6	16.2	13.2	13.2	15.2	17			
81	KC560283	21.7	21.7	21.5	21.4	21.4	21.3	21.5	21.5	23.4	21.5	21.5	21.8	22	20.8	21.4	21.5	20.2	19.7	20.5	20.5	21.7	22.3	22.6	21.7	23.4	23.4	20.7	20.7	20.1	22.1	21.8	20.1	23.1	9.5	23	23.1	9.3	23.1	21.8	21.8	24	21.8	21.8	24	23.1	21.3	22	22.1	22.1	21.8	23.3		
82	MAPOL085_10	15	15.3	15.3	15.3	15.1	15	15	15	17.5	15.1	15.3	15	15.1	15	15.1	14.7	14.6	14.7	14	13.8	16	15.3	15.6	15.3	16.7	16.9	14.6	14.6	14.4	14.7	16.3	15.4	13.4	17.9	1.6	17.3	17.8	17.8	1.7	16.9	15.4	15.6	17.6	15.4	15.4	17.6	16.9	15.3	16.6	16.9	16.7	15.4	17.2
83	MAPOL086_10	15	15.3	15.3	15.3	15.1	15	15	15	17.5	15.1	15.3	15	15.1	15	15.1	14.7	14.6	14.7	14	13.8	16	15.3	15.6	15.3	16.7	16.9	14.6	14.6	14.4	14.7	16.3	15.4	13.4	17.9	1.6	17.3	17.8	17.8	1.7	16.9	15.4	15.6	17.6	15.4	15.4	17.6	16.9	15.3	16.6	16.9	16.7	15.4	17.2
84	MSAPB100_11	20.9	18.7	20.3	20.3	19.3	19.4	19	19.6	18.6	19.9	19.4	19	16.4	20	18.9	16.8	17.7	17.7	19.7	19.3	19.4	20.3	20.2	20.2	18.7	18.7	19.1	21.2	19.1	18.3	24.2	19.1	18.9	19.7	19	19	19	20	19.9	20	20.6	18.4	18.4	20.5	20	19.6	18.4	18.3	18.3	18.4	20		
85	MSAPB1010_12	14.8	14.3	14.7	14.6	14.4	14.6	14.6	17.2	14	14.7	14.7	14.8	14.7	14.6	14.3	14.1	15	13.2	13.1	15.3	15.4	15.7	15	16.7	16.9	13.5	13.5	13.4	14	15.3	14.8	13.7	17.2	1.6	16.9	17	17	1.6	16.9	15.4	15.6	17.2	14.8	14.8	17.2	16.9	14.7	15.1	15.7	15.6	14.8	17	
86	MSAPB1038_11	14.4	14.6	14.8	14.8	14.6	14.4	14.6	14.6	16.4	14.3	14.7	14.6	14.7	14.1	14.6	14.3	13.7	14.3	13.1	13	15.3	14.8	15.1	14.7	16.7	16.9	13.2	13.2	14	14.4	15.1	14.3	13.4	17.2	0.9	16.7	17	17	0.7	16.6	14.8	15	17.3	14.8	14.8	17.3	16.6	14.1	15.6	16	15.7	14.8	16.7
87	MSAPB1049_12	14.8	15.4	17.3	17.3	16.7	16.6	15.7	15.7	16.9	15.6	17.3	15.4	15.3	11.5	17.2	15.6	12.7	13	14.4	14.3	16.6	15.1	15.1	14.8	16.4	16.6	15.4	15.4	15.1	18.6	16.2	15.7	21	1.2	17	14.4	1	1	17	14.7	18.9	19.2	16.4	13.5	13.5	16.4	14.6	16.4	13.4	13.4	13.5	13.5	14.8
88	MSAPB104_11	15.1	16.7	18	18	16.2	16.2	15.6	15.6	17.6	15	18	14.6	15	10.6	17.9	15.3	12.8	11.9	16	15.9	15.9	16.3	16.7	15.6	16.6	16.7	15.6	15.6	16.4	17	15.6	14.8	21.5	12.8	17	15	12.7	16.9	15	17.9	18.3	15.3	13.1	13.1	15.4	15	14.8	12.1	12.1	13.1	14.7		
89	MSAPB1050_12	15.3	14	16.4	16.6	16.2	16	15.1	15.1	15.4	12.8	16.2	15.9	15.6	13.5	16	15.3	14.1	15.3	12.8	11.9	16	15.9	15.9	16.3	16.7	15.6	16.6	16.7	15.6	15.6	16.4	17	15.6	14.8	21.5	12.8	17	15	12.7	16.9	15	17.9	18.3	15.3	13.1	13.1	15.4	15	14.8	12.1	12.1	13.1	14.7
90	MSAPB1051_12	14.8	15.4	17.3	17.3	16.7	16.6	15.7	15.7	16.9	15.6	17.3	15.4	15.3	11.5	17.2	15.6	12.7	13	14.4	14.3	16.6	15.1	15.1	14.8	16.4	16.6	15.4	15.4	15.1	18.6	16.2	15.7	21	1.2	17	14.4	1	1	17	14.7	18.9	19.2	16.4	13.5	13.5	16.4	14.6	16.4	13.4	13.4	13.5	13.5	14.8
91	MSAPB1052_12	14.8	15.4	17.3	17.3	16.7	16.6	15.7	15.7	16.9	15.6	17.3	15.4	15.3	11.5	17.2	15.6	12.7	13	14.4	14.3	16.6	15.1	15.1	14.8	16.4	16.6	15.4	15.4	15.1	18.6	16.2	15.7	21	1.2	17	14.4	1	1	17	14.7	18.9	19.2	16.4	13.5	13.5	16.4	14.6	16.4	13.4	13.4	13.5	13.5	14.8
92	MSAPB1053_12	14.8	15.4	17.3	17.3	16.7	16.6	15.7	15.7	16.9	15.6	17.3	15.4	15.3	11.5	17.2	15.6	12.7	13	14.4	14.3	16.6	15.1	15.1	14.8	16.4	16.6	15.4	15.4	15.1	18.6	16.2	15.7	21	1.2	17	14.4	1	1	17	14.7	18.9	19.2	16.4	13.5	13.5	16.4	14.6	16.4	13.4	13.4	13.5	13.5	14.8
93	MSAPB1054_12	14.8	15.4	17.3	17.3	16.7	16.6	15.7	15.7	16.9	15.6	17.3	15.4	15.3	11.5	17.2	15.6	12.7	13	14.4	14.3	16.6	15.1	15.1	14.8	16.4	16.6	15.4	15.4	15.1	18.6	16.2	15.7	21	1.2	17	14.4	1	1	17	14.7	18.9	19.2	16.4	13.5	13.5	16.4	14.6	16.4	13.4	13.4	13.5	13.5	14.8
94	MSAPB1055_12	14.8	15.4	17.3	17.3	16.7	16.6	15.7	15.7	16.9	15.6	17.3	15.4	15.3	11.5	17.2	15.6	12.7	13	14.4	14.3	16.6	15.1	15.1	14.8	16.4	16.6	15.4	15.4	15.1	18.6	16.2	15.7	21	1.2	17	14.4	1	1	17	14.7	18.9	19.2	16.4	13.5	13.5	16.4	14.6	16.4	13.4	13.4	13.5	13.5	14.8
95	MSAPB1056_12	15.4	14.1	16.6	16.7	16.3	16.2	15.3	15.3	15.6	13	16.3	16	15.7	13.7	16.2	15.4	14.3	15.4	13	12.8	14.8	16.3	16.4	14.7	14.7	14.8	14.4	14.4	13.5	16.9	13.5	15	19.4	14.8	16.7	0.4	14.7	14.7	16.6	0.9	16.6	16.6	15.9	14.4	14.4	15.9	1.2	13.7	13.8	14	14.1	14.4	17
96	MSAPB1057_12	15.3	14	16.4	16.6	16.2	16	15.1	15.1	15.4	12.8	16.2	15.9	15.6	13.5	16	15.3	14.1	15.3	12.8	11.9	16	15.9	15.9	16.3	16.7	15.6	16.6	16.7	15.6	15.6	16.4	17	15.6	14.8	21.5	12.8	17	15	12.7	16.9	15	17.9	18.3	15.3	13.1	13.1	15.4	15	14.8	12.1	12.1	13.1	14.7
97	MSAPB1058_12	14.8	15.4	17.3	17.3	16.7	16.6	15.7	15.7	16.9	15.6	17.3	15.4	15.3	11.5	17.2	15.6	12.7	13	14.4	14.3	16.6	15.1	15.1	14.8	16.4	16.6	15.4	15.4	15.1	18.6	16.2	15.7	21	1.2	17	14.4	1	1	17	14.7	18.9	19.2	16.4	13.5	13.5	16.4	14.6	16.4	13.4	13.4	13.5	13.5	14.8
98	MSAPB1059_12	21.1	19.2	20.8	20.7	20.7	20.5	20.1	20.1	21.5	19.4	20.4	21.7	21.7	18.3	20.5	19.9	17.6	19.2	18.3	18.2	22.3	19.2	19.7	19.8	21	21.1	19.5	19.5	20.5	19.9	18.9	18.5	25	18.5	21.1	21	18.3	18.3	21.1	20.8	21	21.3	20.7	19.1	19.1	20.7	20.8	19.5	18.9	18.5	18.5	19.1	21
99	MSAPB105_11	15.1	16.7	18	18	16.2	16.2	15.6	15.6	17.6	15	18	14.6	15	10.6	17.9	15.3	12.8	11.9	16	15.9	15.9	16.3	16.7	15.6	16.6	16.7	15.6	15.6	16.4	17	15.6	14.8	21.5	12.8	17	15	12.7	16.9	15	17.9	18.3	15.3	13.1	13.1	15.4	15	14.8	12.1	12.1	13.1	14.7		
100	MSAPB1060_12	21	19.1	21	20.8	20.4	20.2	19.9	19.9	21.5	19.4	20.5	21.7	21.7	18.3	20.7	19.8	17.6	19.1	18.3	18.2	22.1	19.1	19.5	19.7	21.1	21.3	19.4	19.																									

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53		
223 MSAPB477_11	14.6	16.4	17.6	17.6	16	16	15.1	15.1	17.3	14.6	17.6	14.3	14.7	10.8	17.5	14.8	12.7	12.1	15.9	15.7	15.7	15.9	16.3	15.1	16.6	16.7	15.3	15.3	16.2	16.9	15.1	14.6	21.4	12.2	16.7	14.8	12.1	12.1	16.6	14.8	17.8	18.2	14.8	12.8	12.8	15	14.8	14.8	11.9	11.9	11.9	12.8	14.6		
224 MSAPB479_11	14.6	16.4	17.6	17.6	16	16	15.1	15.1	17.3	14.6	17.6	14.3	14.7	10.8	17.5	14.8	12.7	12.1	15.9	15.7	15.7	15.9	16.3	15.1	16.6	16.7	15.3	15.3	16.2	16.9	15.1	14.6	21.4	12.2	16.7	14.8	12.1	12.1	16.6	14.8	17.8	18.2	14.8	12.8	12.8	15	14.8	14.8	11.9	11.9	11.9	12.8	14.6		
225 MSAPB480_11	14.6	16.4	17.6	17.6	16	16	15.1	15.1	17.3	14.6	17.6	14.3	14.7	10.8	17.5	14.8	12.7	12.1	15.9	15.7	15.7	15.9	16.3	15.1	16.6	16.7	15.3	15.3	16.2	16.9	15.1	14.6	21.4	12.2	16.7	14.8	12.1	12.1	16.6	14.8	17.8	18.2	14.8	12.8	12.8	15	14.8	14.8	11.9	11.9	11.9	12.8	14.6		
226 MSAPB483_11	13.8	13	15	14.7	15.1	15	13.5	13.5	16.6	13.7	14.8	14.1	14.1	4.1	14.7	13.2	9.2	7.9	13.4	13.2	13.2	12.2	12.5	15.7	15.4	15.6	13.1	13.1	14	15.1	14.4	13.5	20.2	12.4	14.7	14	12.2	12.2	14.6	14.1	16.2	16.3	15	9.5	9.5	15	14.1	13.5	9.6	9.8	9.5	14.1			
227 MSAPB484_11	13.7	12.8	14.8	14.6	15.3	15.1	13.4	13.4	16.4	13.5	14.7	14	14	3.9	14.6	13.1	9	7.7	13.2	13.1	13.1	12.1	12.4	15.6	15.3	15.4	13	13	13.8	15	14.3	13.4	20.1	12.2	14.6	13.8	12.1	12.1	14.4	14	16	16.2	14.8	9.3	9.3	14.8	14	13.7	9.5	9.8	9.6	9.3	14		
228 MSAPB485_11	13.7	13.1	15.1	14.8	15	14.8	13.4	13.4	16.4	13.5	15	14	14	3.9	14.8	13.1	9	8	13.2	13.1	13.1	12.4	12.7	15.6	15.3	15.4	13	13	13.8	15	14.6	13.4	20.1	12.2	14.6	13.8	12.1	12.1	14.4	14	16	16.2	15.1	9.3	9.3	15.1	14	13.4	9.5	9.8	9.6	9.3	14		
229 MSAPB486_11	15	16.6	17.9	17.9	16	16	15.4	15.4	17.5	15.1	17.9	14.4	14.8	10.5	17.8	15.1	12.7	11.8	15.9	15.7	15.7	16.2	16.6	15.4	16.4	16.6	15.4	15.4	16.3	17.2	15.6	14.7	21.4	12.7	16.9	15.1	12.5	12.5	16.7	15.1	17.9	18.3	15.3	13.1	13.1	15.4	15.1	15	12.2	12.2	12.2	13.1	14.8		
230 MSAPB487_11	13.7	12.8	14.8	14.6	15.3	15.1	13.4	13.4	16.4	13.5	14.7	14	14	3.9	14.6	13.1	9	7.7	13.2	13.1	13.1	12.1	12.4	15.6	15.3	15.4	13	13	13.8	15	14.3	13.4	20.1	12.2	14.6	13.8	12.1	12.1	14.4	14	16	16.2	14.8	9.3	9.3	14.8	14	13.7	9.5	9.8	9.6	9.3	14		
231 MSAPB488_11	13.8	13	15	14.7	15.1	15	13.5	13.5	16.6	13.7	14.8	14.1	14.1	4.1	14.7	13.2	9.2	7.9	13.4	13.2	13.2	12.2	12.5	15.7	15.4	15.6	13.1	13.1	14	15.1	14.4	13.5	20.2	12.4	14.7	14	12.2	12.2	14.6	14.1	16.2	16.3	15	9.5	9.5	15	14.1	13.5	9.6	9.8	9.5	14.1			
232 MSAPB489_11	15	16.6	17.9	17.9	16	16	15.4	15.4	17.5	15.1	17.9	14.4	14.8	10.5	17.8	15.1	12.7	11.8	15.9	15.7	15.7	16.2	16.6	15.4	16.4	16.6	15.4	15.4	16.3	17.2	15.6	14.7	21.4	12.7	16.9	15.1	12.5	12.5	16.7	15.1	17.9	18.3	15.3	13.1	13.1	15.4	15.1	15	12.2	12.2	12.2	13.1	14.8		
233 MSAPB491_11	13.8	13	15	14.7	15.1	15	13.5	13.5	16.6	13.7	14.8	14.1	14.1	4.1	14.7	13.2	9.2	7.9	13.4	13.2	13.2	12.2	12.5	15.7	15.4	15.6	13.1	13.1	14	15.1	14.4	13.5	20.2	12.4	14.7	14	12.2	12.2	14.6	14.1	16.2	16.3	15	9.5	9.5	15	14.1	13.5	9.6	9.8	9.5	14.1			
234 MSAPB492_11	13.8	13	15	14.7	15.1	15	13.5	13.5	16.6	13.7	14.8	14.1	14.1	4.1	14.7	13.2	9.2	7.9	13.4	13.2	13.2	12.2	12.5	15.7	15.4	15.6	13.1	13.1	14	15.1	14.4	13.5	20.2	12.4	14.7	14	12.2	12.2	14.6	14.1	16.2	16.3	15	9.5	9.5	15	14.1	13.5	9.6	9.8	9.5	14.1			
235 MSAPB493_11	13.4	13.5	16.3	16	15.6	15.4	14.1	14.1	16.9	14.3	16.2	14.3	14.3	3.5	16	13.8	9	7	13.4	13.2	13.2	13.2	12.5	15.7	15.4	15.6	13.1	13.1	13.4	15	14.8	13.7	20.4	12.7	14.6	13.5	12.5	12.5	14.4	13.7	15.9	16	14.6	9.8	9.8	14.6	13.7	13.5	9.2	9.5	9.5	9.8	13.8		
236 MSAPB497_11	13.8	13	15	14.7	15.1	15	13.5	13.5	16.6	13.7	14.8	14.1	14.1	4.1	14.7	13.2	9.2	7.9	13.4	13.2	13.2	12.2	12.5	15.7	15.4	15.6	13.1	13.1	14	15.1	14.4	13.5	20.2	12.4	14.7	14	12.2	12.2	14.6	14.1	16.2	16.3	15	9.5	9.5	15	14.1	13.5	9.6	9.8	9.5	14.1			
237 MSAPB504_11	14.6	16.4	17.6	17.6	16	16	15.1	15.1	17.3	14.6	17.6	14.3	14.7	10.8	17.5	14.8	12.7	12.1	15.9	15.7	15.7	15.9	16.3	15.1	16.6	16.7	15.3	15.3	16.2	16.9	15.1	14.6	21.4	12.2	16.7	14.8	12.1	12.1	16.6	14.8	17.8	18.2	14.8	12.8	12.8	15	14.8	14.8	11.9	11.9	11.9	12.8	14.6		
238 MSAPB505_11	14.6	16.4	17.6	17.6	16	16	15.1	15.1	17.3	14.6	17.6	14.3	14.7	10.8	17.5	14.8	12.7	12.1	15.9	15.7	15.7	15.9	16.3	15.1	16.6	16.7	15.3	15.3	16.2	16.9	15.1	14.6	21.4	12.2	16.7	14.8	12.1	12.1	16.6	14.8	17.8	18.2	14.8	12.8	12.8	15	14.8	14.8	11.9	11.9	11.9	12.8	14.6		
239 MSAPB506_11	13.5	13.4	16.4	16.2	15.7	15.6	14	14	16.7	14.4	16.3	14.1	14.1	3.6	16.2	13.7	9.2	6.8	13.5	13.4	13.4	13.1	13.1	15.4	14.7	14.8	13.2	13.2	14.8	14.7	13.8	20.2	12.5	14.7	13.7	12.4	12.4	14.6	13.8	16	16.2	14.4	9.9	9.9	14.4	13.8	13.7	9	9.3	9.3	9.9	14			
240 MSAPB507_11	13.7	12.8	14.8	14.6	15.3	15.1	13.4	13.4	16.4	13.5	14.7	14	14	3.9	14.6	13.1	9	7.7	13.2	13.1	13.1	12.1	12.4	15.6	15.3	15.4	13	13	13.8	15	14.3	13.4	20.1	12.2	14.6	13.8	12.1	12.1	14.4	14	16	16.2	14.8	9.3	9.3	14.8	14	13.7	9.5	9.8	9.6	9.3	14		
241 MSAPB513_11	13.5	13.4	16.4	16.2	15.7	15.6	14	14	16.7	14.4	16.3	14.1	14.1	3.6	16.2	13.7	9.2	6.8	13.5	13.4	13.4	13.1	13.1	15.4	14.7	14.8	13.2	13.2	14.8	14.7	13.8	20.2	12.5	14.7	13.7	12.4	12.4	14.6	13.8	16	16.2	14.4	9.9	9.9	14.4	13.8	13.7	9	9.3	9.3	9.9	14			
242 MSAPB514_11	13.7	13.5	16.6	16.3	15.9	15.7	14.1	14.1	16.9	14.6	16.4	14.3	14.3	3.8	16.3	13.8	9.3	6.7	13.7	13.5	13.5	13.2	13.2	15.6	14.6	14.7	13.4	13.4	13.4	15	14.8	14	20.2	12.7	14.8	13.8	12.5	12.5	14.7	14	16.2	16.3	14.6	10	10	14.6	14	13.8	9.2	9.5	9.5	10	14.1		
243 MSAPB515_11	13.5	13.4	16.4	16.2	15.7	15.6	14	14	16.7	14.4	16.3	14.1	14.1	3.6	16.2	13.7	9.2	6.8	13.5	13.4	13.4	13.1	13.1	15.4	14.7	14.8	13.2	13.2	14.8	14.7	13.8	20.2	12.5	14.7	13.7	12.4	12.4	14.6	13.8	16	16.2	14.4	9.9	9.9	14.4	13.8	13.7	9	9.3	9.3	9.9	14			
244 MSAPB518_11	15.1	16.4	17.8	17.8	16.2	16.2	15.3	15.3	17.6	15.3	17.8	14.6	15	10.6	17.6	15.3	12.8	11.8	16	15.9	15.9	16.3	16.7	15.6	16.6	16.7	15.6	15.6	16.4	17	15.7	14.8	21.5	12.5	17	15	12.4	12.4	16.9	15.3	18	18.5	15.4	13.2	13.2	15.6	15.1	12.4	12.4	13.2	15.5	10.2	10	9.8	14.4
245 MSAPB529_11	14.1	13.2	15.3	15	15.4	15.3	13.8	13.8	16.9	14	15.1	14.4	14.4	4.4	15	13.5	9.5	8.2	13.7	13.5	13.5	13.2	12.5	15.7	15.4	15.6	13.1	13.1	14	15.1	14.4	13.5	20.1	12.2	14.6	13.8	12.1	12.1	14.4	14	16	16.2	15.1	9.3	9.3	15.1	14	13.4	9.5	9.8	9.6	9.3	14		
246 MSAPB532_11	13.8	13	15	14.7	15.1	15	13.5	13.5	16.6	13.7	14.8	14.1	14.1	4.1	14.7	13.2	9.2	7.9	13.4	13.2	13.2	12.2	12.5	15.7	15.4	15.6	13.1	13.1	14	15.1	14.4	13.5	20.2	12.4	14.7	14	12.2	12.2	14.6	14.1	16.2	16.3	15	9.5	9.5	15	14.1	13.5	9.6	9.8	9.5	14.1			
247 MSAPB533_11	13.7	13.1	15.1	14.8	15	14.8	13.4	13.4	16.4	13.5	15	14	14	3.9	14.8	13.1	9	8	13.2	13.1	13.1	12.4	12.7	15.6	15.3	15.4	13	13	13.8	15	14.6	13.4	20.1	12.2	14.6	13.8	12.1	12.1	14.4	14	16	16.2	15.1	9.3	9.3	15.1	14	13.4	9.5	9.8</					

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76 28.1 30.1 25.8 25.5 28.1 25.8 25.4 25.9 25.9 25.4 24.5 24.2 25.9 28.1 25.5 24.6 27 26.7 25.8 25.7 25.7 26.2

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89 14.7 22.5 15.3 16.2 14.7 19.1 19.8 17 17.4 19.6 24.9 16.1 17.9 20.7 17.5 21.9 18.2 18.2 21.9 19.7 18.2 17.4 25.8 23.5 18.2 16.2 17 23 17.2 17.2 19.9 16.7 16.6 14.3 14.8

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99 12.8 20.1 15.6 16.2 12.8 19.4 20.1 16.6 16.9 19.8 26.8 17.9 16.3 19.3 17.4 23.3 17.1 18.5 22.3 19.9 20.9 17.1 27.7 24.7 16.4 16.7 15.4 23.4 17.8 17.8 18.4 17.6 17 12.5 0 14.8 12.5 12.5 12.5 12.5 12.5 15 14.8 12.5 19.2

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101 18.6 27.9 20.2 21.4 18.6 24.3 23.8 23.7 24.1 24.6 30.4 22.1 21.2 24.6 22.6 26.7 24.3 22.2 26.8 24.5 24.7 21.1 32.4 27.6 21.9 22.9 22.6 26.6 21.5 21.5 20.5 20.8 21.3 18.2 19.2 21 18.2 0.3 19.2 0.1

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103 1.2 19.6 16.2 15 1.2 20.9 21.1 16 16.3 18.3 26.1 17 15.8 17.6 16.5 24.8 16.5 17.4 20.7 18.5 20.1 16.1 28.3 25.4 15.1 14.8 14.9 23.4 17.9 17.9 19 17.3 17.3 0 12.5 14.3 0 0 0 14.4 14.3

104 1.3 19.8 16.3 15.1 1.3 20.9 21.1 16 16.3 18.3 26.1 17 15.8 17.6 16.5 24.8 16.5 17.4 20.7 18.5 20.1 16.1 28.3 25.4 15.1 14.8 14.9 23.4 17.9 17.9 19 17.3 17.3 0 12.7 14.4 0.1 0.1 0.1 0.1 14.6 14.4 0.1 18.2 12.7 18.2 18.3 18.3 0.1

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116 14.7 22.5 15.3 16.2 14.7 19.1 19.8 17 17.4 19.6 24.9 16.1 17.9 20.7 17.5 21.9 18.2 18.2 21.9 19.7 18.2 17.4 25.8 23.5 18.2 16.2 17 23 17.2 17.2 19.9 16.7 16.6 14.3 14.8 0 14.3 14.3 14.3 14.3 14.3 0.1 0 14.3 20.8 14.8 20.8 21 21 14.3 14.4 0 0 0.1 0

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118 1.2 19.6 16.2 15 1.2 20.9 21.1 16 16.3 18.3 26.1 17 15.8 17.6 16.5 24.8 16.5 17.4 20.7 18.5 20.1 16.1 28.3 25.4 15.1 14.8 14.9 23.4 17.9 17.9 19 17.3 17.3 0 12.5 14.3 0 0 0 14.4 14.3 0 18 12.5 18 18.2 18.2 0 0.1 14.3 14.3 14.1 14.3

119 1.2 19.6 16.2 15 1.2 20.9 21.1 16 16.3 18.3 26.1 17 15.8 17.6 16.5 24.8 16.5 17.4 20.7 18.5 20.1 16.1 28.3 25.4 15.1 14.8 14.9 23.4 17.9 17.9 19 17.3 17.3 0 12.5 14.3 0 0 0 14.4 14.3 0 18 12.5 18 18.2 18.2 0 0.1 14.3 14.3 14.1 14.3

120 1.2 19.6 16.2 15 1.2 20.9 21.1 16 16.3 18.3 26.1 17 15.8 17.6 16.5 24.8 16.5 17.4 20.7 18.5 20.1 16.1 28.3 25.4 15.1 14.8 14.9 23.4 17.9 17.9 19 17.3 17.3 0 12.5 14.3 0 0 0 14.4 14.3 0 18 12.5 18 18.2 18.2 0 0.1 14.3 14.3 14.1 14.3

121 12.8 20.1 15.6 16.2 12.8 19.4 20.1 16.6 16.9 19.8 26.8 17.9 16.3 19.3 17.4 23.3 17.1 18.5 22.3 19.9 20.9 17.1 27.7 24.7 16.4 16.7 15.4 23.4 17.8 17.8 18.4 17.6 17 12.5 0 14.8 12.5 12.5 12.5 12.5 12.5 15 14.8 12.5 19.2 0 19.1 19.2 19.2 12.5 12.7 14.8 14.8 15 14.8

122 14.7 22.5 15.3 16.2 14.7 19.1 19.8 17 17.4 19.6 24.9 16.1 17.9 20.7 17.5 21.9 18.2 18.2 21.9 19.7 18.2 17.4 25.8 23.5 18.2 16.2 17 23 17.2 17.2 19.9 16.7 16.6 14.3 14.8 0 14.3 14.3 14.3 14.3 14.3 0.1 0 14.3 20.8 14.8 20.8 21 21 14.3 14.4 0 0 0.1 0

123 1.2 19.6 16.2 15 1.2 20.9 21.1 16 16.3 18.3 26.1 17 15.8 17.6 16.5 24.8 16.5 17.4 20.7 18.5 20.1 16.1 28.3 25.4 15.1 14.8 14.9 23.4 17.9 17.9 19 17.3 17.3 0 12.5 14.3 0 0 0 14.4 14.3 0 18 12.5 18 18.2 18.2 0 0.1 14.3 14.3 14.1 14.3

124 1.3 19.8 16.3 15.1 1.3 20.7 21 16.2 16.5 18.4 25.9 17.1 16 17.8 16.8 24.6 16.6 17.2 20.7 18.5 19.9 16 28.1 25.4 15.2 14.6 15.1 23.4 18 18 18.9 17.5 17.5 0.1 12.7 14.1 0.1 0.1 0.1 0.1 14.3 14.1 0.1 17.9 12.7 17.9 18 18 0.1 0.3 14.1 14.1 14 14.1

125 18.6 27.9 20.2 21.4 18.6 24.2 23.8 23.7 24.1 24.6 30.3 22.1 21.2 24.6 22.6 26.7 24.3 22.2 26.8 24.5 24.7 20.9 32.4 27.4 21.9 22.9 22.6 26.6 21.5 21.5 20.6 20.8 21.3 18.2 19.2 21 18.2 0.2 18.2 18.2 18.2 18.2 21.3 21.1 18.2 0.4 19.2 0.3 0.1 0.1 18.2 18.3 21.1 21.1 21 21.1

126 17.2 25.7 19.5 19.7 17.2 22.7 20.9 20.8 21.1 23.1 28.2 19 19 21.9 20.4 25.8 21.1 21.9 25.4 23.1 21.4 18.3 29 27.1 19.5 19 19.6 24.2 17.9 17.9 2 18 17.3 17 16.4 17.9 17 17 17 17 18 17.9 17 18.3 16.4 18.3 18.5 18.5 17 17.2 17.9 17.9 18 17.9

127 17.2 25.7 19.5 19.7 17.2 22.7 20.9 21 21.3 23.1 28.2 19 19 21.9 20.4 25.8 21.1 21.9 25.4 23.1 21.4 18.3 29 27.1 19.5 19 19.6 24.2 17.9 17.9 2 18 17.3 17 16.4 17.9 17 17 17 17 18 17.9 17 18.3 16.4 18.3 18.5 18.5 17 17.2 17.9 17.9 18 17.9

128 17.2 25.7 19.5 19.7 17.2 22.7 20.9 21 21.3 23.1 28.2 19 19 21.9 20.4 25.8 21.1 21.9 25.4 23.1 21.4 18.3 29 27.1 19.5 19 19.6 24.2 17.9 17.9 2 18 17.3 17 16.4 17.9 17 17 17 17 18 17.9 17 18.3 16.4 18.3 18.5 18.5 17 17.2 17.9 17.9 18 17.9

129 17 25.6 19.7 19.5 17 22.7 21 20.8 21.1 23 28.2 18.9 19 21.7 20.3 25.8 21 21.9 25.2 23 21.4 18.3 29.1 27.1 19.5 19 19.4 24.3 18 18 2.3 18.2 17.5 16.9 16.3 17.8 16.9 16.9 16.9 16.9 17.9 17.8 16.9 18.2 16.3 18.2 18.3 18.3 16.9 17 17.8 17.8 17.9 17.8

130 17.2 25.7 19.5 19.7 17.2 22.7 20.9 20.8 21.1 23.1 28.2 19 19 21.9 20.4 25.8 21.1 21.9 25.4 23.1 21.4 18.3 29 27.1 19.5 19 19.6 24.2 17.9 17.9 2 18 17.3 17 16.4 17.9 17 17 17 17 18 17.9 17 18.3 16.4 18.3 18.5 18.5 17 17.2 17.9 17.9 18 17.9

131 12.8 20.1 15.6 16.2 12.8 19.4 20.1 16.6 16.9 19.8 26.8 17.9 16.3 19.3 17.4 23.3 17.1 18.5 22.3 19.9 20.9 17.1 27.7 24.7 16.4 16.7 15.4 23.4 17.8 17.8 18.4 17.6 17 12.5 0 14.8 12.5 12.5 12.5 12.5 15 14.8 12.5 19.2 0 19.1 19.2 19.2 12.5 12.7 14.8 14.8 15 14.8

132 17.2 25.7 19.5 19.7 17.2 22.7 20.9 20.8 21.1 23.1 28.2 19 19 21.9 20.4 25.8 21.1 21.9 25.4 23.1 21.4 18.3 29 27.1 19.5 19 19.6 24.2 17.9 17.9 2 18 17.3 17 16.4 17.9 17 17 17 17 18 17.9 17 18.3 16.4 18.3 18.5 18.5 17 17.2 17.9 17.9 18 17.9

133 17.2 25.7 19.5 19.7 17.2 22.7 20.9 21 21.3 23.1 28.2 19 19 21.9 20.4 25.8 21.1 21.9 25.4 23.1 21.4 18.3

223	12.2	19.9	15.1	16.2	12.2	19.1	20	16.6	16.9	19.8	26.8	17.6	16	19.1	17.4	23.2	16.9	18.5	22.3	19.9	20.9	17	27.7	24.4	16.4	16.7	15.2	23.6	17.5	17.5	18.3	17.3	16.7	11.9	1.2	14.7	11.9	11.9	11.9	11.9	11.9	11.9	14.8	14.7	11.9	19.1	1.2	18.9	19.1	19.1	11.9	12.1	14.7	14.7	14.8	14.7
224	12.2	19.9	15.1	16.2	12.2	19.1	20	16.6	16.9	19.8	26.8	17.6	16	19.1	17.4	23.2	16.9	18.5	22.3	19.9	20.9	17	27.7	24.4	16.4	16.7	15.2	23.6	17.5	17.5	18.3	17.3	16.7	11.9	1.2	14.7	11.9	11.9	11.9	11.9	11.9	14.8	14.7	11.9	19.1	1.2	18.9	19.1	19.1	11.9	12.1	14.7	14.7	14.8	14.7	
225	12.2	19.9	15.1	16.2	12.2	19.1	20	16.6	16.9	19.8	26.8	17.6	16	19.1	17.4	23.2	16.9	18.5	22.3	19.9	20.9	17	27.7	24.4	16.4	16.7	15.2	23.6	17.5	17.5	18.3	17.3	16.7	11.9	1.2	14.7	11.9	11.9	11.9	11.9	11.9	14.8	14.7	11.9	19.1	1.2	18.9	19.1	19.1	11.9	12.1	14.7	14.7	14.8	14.7	
226	12.5	19.6	13	14.7	12.4	19.8	20	12.8	13.1	18	25.5	16.7	12.6	15.5	13.9	21	14.2	14	20.1	17.9	17.7	13.4	25.8	22.8	13.1	11.1	12.3	21	15.6	15.6	18.1	14.3	14.8	12.2	11.8	14	12.2	12.2	12.2	12.2	12.2	14.1	14	12.2	18	11.8	18	18.2	18.2	12.2	12.4	14	14	14.1	14	
227	12.4	19.5	12.8	14.6	12.2	19.7	19.8	12.7	13	17.9	25.3	16.6	12.5	15.3	13.7	20.9	14	13.9	20	17.8	17.9	13.2	25.7	22.6	12.9	11	12.2	20.8	15.4	15.4	18.1	14.1	14.7	12.1	11.6	13.8	12.1	12.1	12.1	12.1	12.1	14	13.8	12.1	17.9	11.6	17.9	18	18	12.1	12.2	13.8	13.8	14	13.8	
228	12.4	19.5	13.1	14.6	12.2	19.7	19.8	12.7	13	17.9	25.3	16.6	12.5	15.3	13.7	20.9	14	13.9	20	17.8	17.9	13.2	25.7	22.6	12.9	11	12.2	20.8	15.4	15.4	18.1	14.1	14.7	12.1	11.6	13.8	12.1	12.1	12.1	12.1	12.1	14	13.8	12.1	18.2	18.3	18.3	12.1	12.2	13.8	13.8	14	13.8			
229	12.7	19.9	15.1	16.2	12.2	19.3	20.1	16.4	16.8	19.8	26.8	17.9	16.1	19.1	17.2	23.5	16.9	18.4	22.3	19.9	20.9	17	27.5	24.5	16.3	16.5	15.2	23.3	17.6	17.6	18.3	17.5	16.9	12.4	0.1	15	12.4	12.4	12.4	12.4	12.4	15.1	15	12.4	19.4	0.1	19.2	19.4	19.4	12.4	12.5	15	15	15.1	15	
230	12.4	19.5	12.8	14.6	12.2	19.7	19.8	12.7	13	17.9	25.3	16.6	12.5	15.3	13.7	20.9	14	13.9	20	17.8	17.9	13.2	25.7	22.6	12.9	11	12.2	20.8	15.4	15.4	18.1	14.1	14.7	12.1	11.6	13.8	12.1	12.1	12.1	12.1	12.1	14	13.8	12.1	17.9	11.6	17.9	18	18	12.1	12.2	13.8	13.8	14	13.8	
231	12.5	19.6	13	14.7	12.4	19.8	20	12.8	13.1	18	25.5	16.7	12.6	15.5	13.9	21	14.2	14	20.1	17.9	17.7	13.4	25.8	22.8	13.1	11.1	12.3	21	15.6	15.6	18.1	14.3	14.8	12.2	11.8	14	12.2	12.2	12.2	12.2	12.2	14.1	14	12.2	18	11.8	18	18.2	18.2	12.2	12.4	14	14	14.1	14	
232	12.7	19.9	15.4	16.2	12.7	19.3	20.1	16.4	16.8	19.8	26.8	17.9	16.1	19.1	17.2	23.5	16.9	18.4	22.3	19.9	20.9	17	27.5	24.5	16.3	16.5	15.2	23.3	17.6	17.6	18.3	17.5	16.9	12.4	0.1	15	12.4	12.4	12.4	12.4	12.4	15.1	15	12.4	19.4	0.1	19.2	19.4	19.4	12.4	12.5	15	15	15.1	15	
233	12.5	19.6	13	14.7	12.4	19.8	20	12.8	13.1	18	25.5	16.7	12.6	15.5	13.9	21	14.2	14	20.1	17.9	17.7	13.4	25.8	22.8	13.1	11.1	12.3	21	15.6	15.6	18.1	14.3	14.8	12.2	11.8	14	12.2	12.2	12.2	12.2	12.2	14.1	14	12.2	18	11.8	18	18.2	18.2	12.2	12.4	14	14	14.1	14	
234	12.5	19.6	13	14.7	12.4	19.8	20	12.8	13.1	18	25.5	16.7	12.6	15.5	13.9	21	14.2	14	20.1	17.9	17.7	13.4	25.8	22.8	13.1	11.1	12.3	21	15.6	15.6	18.1	14.3	14.8	12.2	11.8	14	12.2	12.2	12.2	12.2	12.2	14.1	14	12.2	18	11.8	18	18.2	18.2	12.2	12.4	14	14	14.1	14	
235	12.8	19.2	13.4	15	12.7	19.7	20.1	12.8	13.1	18.6	25.3	16.4	13.8	16	13.7	21	14.6	14.6	20.7	18.5	17.6	13.1	25.8	23.2	13.9	11.4	12.6	21	15.6	15.6	17.1	14.7	14.6	12.5	11.2	13.5	12.5	12.5	12.5	12.5	13.7	13.5	12.5	18.2	11.2	18.2	18.3	18.3	12.5	12.7	13.5	13.5	13.7	13.5		
236	12.5	19.6	13	14.7	12.4	19.8	20	12.8	13.1	18	25.5	16.7	12.6	15.5	13.9	21	14.2	14	20.1	17.9	17.7	13.4	25.8	22.8	13.1	11.1	12.3	21	15.6	15.6	18.1	14.3	14.8	12.2	11.8	14	12.2	12.2	12.2	12.2	12.2	14.1	14	12.2	18	11.8	18	18.2	18.2	12.2	12.4	14	14	14.1	14	
237	12.2	19.9	15.1	16.2	12.2	19.1	20	16.6	16.9	19.8	26.8	17.6	16	19.1	17.4	23.2	16.9	18.5	22.3	19.9	20.9	17	27.7	24.4	16.4	16.7	15.2	23.6	17.5	17.5	18.3	17.3	16.7	11.9	1.2	14.7	11.9	11.9	11.9	11.9	11.9	14.8	14.7	11.9	19.1	1.2	18.9	19.1	19.1	11.9	12.1	14.7	14.7	14.8	14.7	
238	12.2	19.9	15.1	16.2	12.2	19.1	20	16.6	16.9	19.8	26.8	17.6	16	19.1	17.4	23.2	16.9	18.5	22.3	19.9	20.9	17	27.7	24.4	16.4	16.7	15.2	23.6	17.5	17.5	18.3	17.3	16.7	11.9	1.2	14.7	11.9	11.9	11.9	11.9	11.9	14.8	14.7	11.9	19.1	1.2	18.9	19.1	19.1	11.9	12.1	14.7	14.7	14.8	14.7	
239	12.7	19.3	13.5	15.1	12.5	19.8	20.3	13	13.3	18.7	25.5	16.6	13.9	15.9	13.9	21.1	14.7	14.7	20.9	18.6	17.4	12.9	25.9	23.4	14.1	11.6	12.7	21.1	15.7	15.7	17	14.8	14.7	12.4	11.4	13.7	12.4	12.4	12.4	12.4	13.8	13.7	12.4	18.3	11.4	18.3	18.5	18.5	12.4	12.5	13.7	13.7	13.8	13.7		
240	12.4	19.5	12.8	14.6	12.2	19.7	19.8	12.7	13	17.9	25.3	16.6	12.5	15.3	13.7	20.9	14	13.9	20	17.8	17.9	13.2	25.7	22.6	12.9	11	12.2	20.8	15.4	15.4	18.1	14.1	14.7	12.1	11.6	13.8	12.1	12.1	12.1	12.1	12.1	14	13.8	12.1	17.9	11.6	17.9	18	18	12.1	12.2	13.8	13.8	14	13.8	
241	12.7	19.3	13.5	15.1	12.5	19.8	20.3	13	13.3	18.7	25.5	16.6	13.9	15.9	13.9	21.1	14.7	14.7	20.9	18.6	17.4	12.9	25.9	23.4	14.1	11.6	12.7	21.1	15.7	15.7	17	14.8	14.7	12.4	11.4	13.7	12.4	12.4	12.4	12.4	13.8	13.7	12.4	18.3	11.4	18.3	18.5	18.5	12.4	12.5	13.7	13.7	13.8	13.7		
242	12.8	19.3	13.7	15.3	12.7	20	20.4	13	13.3	18.9	25.5	16.7	14.1	15.9	13.9	21.1	14.7	14.7	20.9	18.6	17.6	13.1	25.9	23.4	14.2	11.6	12.7	21.1	15.6	15.6	17	15	14.8	12.5	11.5	13.8	12.5	12.5	12.5	12.5	14	13.8	12.5	18.5	11.5	18.5	18.6	18.6	12.5	12.7	13.8	13.8	14	13.8		
243	12.7	19.3	13.5	15.1	12.5	19.8	20.3	13	13.3	18.7	25.5	16.6	13.9	15.9	13.9	21.1	14.7	14.7	20.9	18.6	17.4	12.9	25.9	23.4	14.1	11.6	12.7	21.1	15.7	15.7	17	14.8	14.7	12.4	11.4	13.7	12.4	12.4	12.4	12.4	13.8	13.7	12.4	18.3	11.4	18.3	18.5	18.5	12.4	12.5	13.7	13.7	13.8	13.7		
244	12.5	19.6	13.6	15.3	12.5	19.4	20.3	16.6	16.9	19.9	26.9	18	16.3	19.4	17.4	23.6	17.1	18.5	22.5	20.1	21.1	17.1	27.7	24.5	16.4	16.7	15.4	23.3	17.8	17.8	18.4	17.6	17	12.2	0.3	14.8	12.2	12.2	12.2	12.2	12.2	15	14.8	12.2	19.5	0.3	19.4	19.5	19.5	12.2	12.4	14.8	14.8	15	14.8	
245	12.8	19.6	13.2	15	12.7	20.1	20.3	13.1	13.4	18.3	25.5	17	12.9	15.8	14.2	21.3	14.4	14.3	20.4	18.2	18	13.6	25.8	23.1	13.4	11.4	12.6	21.3	15.9	15.9	18.4	14.6	15.1	12.5	12.1	14.3	12.5	12.5	12.5	12.5	14.4	14.3	12.5	18.3	12.1	18.3	18.5	18.5	12.5	12.7	14.3	14.3	14.4	14.3		
246	12.5	19.6	13	14.7	12.4	19.8	20	12.8	13.1	18	25.5	16.7	12.6	15.5	13.9	21	14.2	14	20.1	17.9	17.7	13.4	25.8	22.8	13.1	11.1	12.3	21	15.6	15.6	18.1	14.3	14.8	12.2	11.8	14	12.2	12.2	12.2	12.2	12.2	14.1	14	12.2	18	11.8	18	18.2	18.2	12.2	12.4	14	14	14.1	14	
247	12.4	19.5	13.1	14.6	12.2	19.7	19.8	12.7	13	17.9	25.3	16.6	12.5	15.3	13.7	20.9	14	13.9	20	17.8	17.6	13.2	25.7	22.6	12.9	11	12.2	20.8	15.4	15.4	18.1	14.1	14.7	12.1	11.6	13.8	12.1	12.1	12.1	12.1	12.1	14	13.8	12.1	18.2	11.6	18.2	18.3	18.3	12.1	12.2	13.8	13.8	14	13.8	
248	12.5	19.6	13	14.7	12.4																																																			

297	12.7	19.3	13.5	15.1	12.5	19.8	20.3	13	13.3	18.7	25.5	16.6	13.9	15.9	13.9	21.1	14.7	14.7	20.9	18.6	17.4	12.9	25.9	23.4	14.1	11.6	12.7	21.1	15.7	15.7	17	14.8	14.7	12.4	11.4	13.7	12.4	12.4	12.4	12.4	12.4	13.8	13.7	12.4	18.3	11.4	18.3	18.5	18.5	12.4	12.5	13.7	13.7	13.8	13.7
298	1.5	19.6	16.2	15	1.5	20.9	21.3	16.2	16.5	18.4	26.2	17.1	15.8	17.6	16.6	24.9	16.6	17.5	20.9	18.6	20.2	16.1	28.4	25.5	15.2	14.9	15.1	23.6	17.9	17.9	18.6	17.3	17.3	0.6	12.7	14.1	0.6	0.6	0.6	0.6	0.6	14.3	14.1	0.6	18	12.7	18	18.2	18.2	0.6	0.7	14.1	14.1	14	14.1
299	1.5	19.6	16.2	15	1.5	20.9	21.3	16.2	16.5	18.4	26.2	17.1	15.8	17.6	16.6	24.9	16.6	17.5	20.9	18.6	20.2	16.1	28.4	25.5	15.2	14.9	15.1	23.6	17.9	17.9	18.6	17.3	17.3	0.6	12.7	14.1	0.6	0.6	0.6	0.6	0.6	14.3	14.1	0.6	18	12.7	18	18.2	18.2	0.6	0.7	14.1	14.1	14	14.1
300	12.4	19.5	13.1	14.6	12.2	19.7	19.8	12.7	13	17.9	25.3	16.6	12.5	15.3	13.7	20.9	14	13.9	20	17.8	17.6	13.2	25.7	22.6	12.9	11	12.2	20.8	15.4	15.4	18	14.1	14.7	12.1	11.6	13.8	12.1	12.1	12.1	12.1	12.1	14	13.8	12.1	18.2	11.6	18.2	18.3	18.3	12.1	12.2	13.8	13.8	14	13.8
301	12.4	19.5	13.1	14.6	12.2	19.7	19.8	12.7	13	17.9	25.3	16.6	12.5	15.3	13.7	20.9	14	13.9	20	17.8	17.6	13.2	25.7	22.6	12.9	11	12.2	20.8	15.4	15.4	18	14.1	14.7	12.1	11.6	13.8	12.1	12.1	12.1	12.1	12.1	14	13.8	12.1	18.2	11.6	18.2	18.3	18.3	12.1	12.2	13.8	13.8	14	13.8
302	12.5	19.6	13	14.7	12.4	19.8	20	12.8	13.1	18	25.5	16.7	12.6	15.5	13.9	21	14.2	14	20.1	17.9	17.7	13.4	25.8	22.8	13.1	11.1	12.3	21	15.6	15.6	18.1	14.3	14.8	12.2	11.8	14	12.2	12.2	12.2	12.2	12.2	14.1	14	12.2	18	11.8	18	18.2	18.2	12.2	12.4	14	14	14.1	
303	1.5	19.6	16.2	15	1.5	20.9	21.3	16.2	16.5	18.4	26.2	17.1	15.8	17.6	16.6	24.9	16.6	17.5	20.9	18.6	20.2	16.1	28.4	25.5	15.2	14.9	15.1	23.6	17.9	17.9	18.6	17.3	17.3	0.6	12.7	14.1	0.6	0.6	0.6	0.6	0.6	14.3	14.1	0.6	18	12.7	18	18.2	18.2	0.6	0.7	14.1	14.1	14	14.1
304	1.5	19.6	16.2	15	1.5	20.9	21.3	16.2	16.5	18.4	26.2	17.1	15.8	17.6	16.6	24.9	16.6	17.5	20.9	18.6	20.2	16.1	28.4	25.5	15.2	14.9	15.1	23.6	17.9	17.9	18.6	17.3	17.3	0.6	12.7	14.1	0.6	0.6	0.6	0.6	0.6	14.3	14.1	0.6	18	12.7	18	18.2	18.2	0.6	0.7	14.1	14.1	14	14.1
305	12.2	19.9	15.1	16.2	12.2	19.1	20	16.6	16.9	19.8	26.8	17.6	16	19.1	17.4	23.2	16.9	18.5	22.3	19.9	20.9	17	27.7	24.4	16.4	16.7	15.2	23.6	17.5	17.5	18.3	17.3	16.7	11.9	1.2	14.7	11.9	11.9	11.9	11.9	11.9	14.8	14.7	11.9	19.1	1.2	18.9	19.1	11.9	12.1	14.7	14.7	14.8	14.7	
306	12.4	19.5	13.1	14.6	12.2	19.7	19.8	12.7	13	17.9	25.3	16.6	12.5	15.3	13.7	20.9	14	13.9	20	17.8	17.6	13.2	25.7	22.6	12.9	11	12.2	20.8	15.4	15.4	18	14.1	14.7	12.1	11.6	13.8	12.1	12.1	12.1	12.1	12.1	14	13.8	12.1	18.2	11.6	18.2	18.3	18.3	12.1	12.2	13.8	13.8	14	13.8
307	12.4	19.5	13.1	14.6	12.2	19.7	19.8	12.7	13	17.9	25.3	16.6	12.5	15.3	13.7	20.9	14	13.9	20	17.8	17.6	13.2	25.7	22.6	12.9	11	12.2	20.8	15.4	15.4	18	14.1	14.7	12.1	11.6	13.8	12.1	12.1	12.1	12.1	12.1	14	13.8	12.1	18.2	11.6	18.2	18.3	18.3	12.1	12.2	13.8	13.8	14	13.8
308	12.4	19.5	13.1	14.6	12.2	19.7	19.8	12.7	13	17.9	25.3	16.6	12.5	15.3	13.7	20.9	14	13.9	20	17.8	17.6	13.2	25.7	22.6	12.9	11	12.2	20.8	15.4	15.4	18	14.1	14.7	12.1	11.6	13.8	12.1	12.1	12.1	12.1	12.1	14	13.8	12.1	18.2	11.6	18.2	18.3	18.3	12.1	12.2	13.8	13.8	14	13.8
309	12.5	19.6	13	14.7	12.4	19.8	20	12.8	13.1	18	25.5	16.7	12.6	15.5	13.9	21	14.2	14	20.1	17.9	17.7	13.4	25.8	22.8	13.1	11.1	12.3	21	15.6	15.6	18.1	14.3	14.8	12.2	11.8	14	12.2	12.2	12.2	12.2	12.2	14.1	14	12.2	18	11.8	18	18.2	18.2	12.2	12.4	14	14	14.1	
310	12.4	19.5	13.1	14.6	12.2	19.7	19.8	12.7	13	17.9	25.3	16.6	12.5	15.3	13.7	20.9	14	13.9	20	17.8	17.6	13.2	25.7	22.6	12.9	11	12.2	20.8	15.4	15.4	18	14.1	14.7	12.1	11.6	13.8	12.1	12.1	12.1	12.1	12.1	14	13.8	12.1	18.2	11.6	18.2	18.3	18.3	12.1	12.2	13.8	13.8	14	13.8
311	12.5	19.6	13.1	14.7	12.4	19.8	20	12.8	13.1	18	25.5	16.7	12.6	15.2	13.6	20.7	13.9	13.7	20.1	17.9	17.7	13.1	25.5	22.5	12.8	11.1	12	20.7	15.3	15.3	18.1	14	14.6	12.2	11.5	13.7	12.2	12.2	12.2	12.2	13.8	13.7	12.2	18	11.5	18	18.2	18.2	12.2	12.4	13.7	13.7	13.8	13.7	
312	1.5	19.6	16.2	15	1.5	20.9	21.3	16.2	16.5	18.4	26.2	17.1	15.8	17.6	16.6	24.9	16.6	17.5	20.9	18.6	20.2	16.1	28.4	25.5	15.2	14.9	15.1	23.6	17.9	17.9	18.6	17.3	17.3	0.6	12.7	14.1	0.6	0.6	0.6	0.6	0.6	14.3	14.1	0.6	18	12.7	18	18.2	18.2	0.6	0.7	14.1	14.1	14	14.1
313	12.4	19.5	13.1	14.6	12.2	19.7	19.8	12.7	13	17.9	25.3	16.6	12.5	15.3	13.7	20.9	14	13.9	20	17.8	17.6	13.2	25.7	22.6	12.9	11	12.2	20.8	15.4	15.4	18	14.1	14.7	12.1	11.6	13.8	12.1	12.1	12.1	12.1	12.1	14	13.8	12.1	18.2	11.6	18.2	18.3	18.3	12.1	12.2	13.8	13.8	14	13.8
314	12.5	19.6	13	14.7	12.4	19.8	20	12.8	13.1	18	25.5	16.7	12.6	15.5	13.9	21	14.2	14	20.1	17.9	17.7	13.4	25.8	22.8	13.1	11.1	12.3	21	15.6	15.6	18.1	14.3	14.8	12.2	11.8	14	12.2	12.2	12.2	12.2	12.2	14.1	14	12.2	18	11.8	18	18.2	18.2	12.2	12.4	14	14	14.1	
315	1.5	19.6	16.2	15	1.5	20.9	21.3	16.2	16.5	18.4	26.2	17.1	15.8	17.6	16.6	24.9	16.6	17.5	20.9	18.6	20.2	16.1	28.4	25.5	15.2	14.9	15.1	23.6	17.9	17.9	18.6	17.3	17.3	0.6	12.7	14.1	0.6	0.6	0.6	0.6	0.6	14.3	14.1	0.6	18	12.7	18	18.2	18.2	0.6	0.7	14.1	14.1	14	14.1
316	1.6	19.6	16.3	15.1	1.6	20.9	21.3	16.2	16.5	18.4	26.2	17.1	15.8	17.6	16.6	24.9	16.6	17.5	20.9	18.6	20.2	16.1	28.4	25.5	15.2	14.9	15.1	23.6	17.9	17.9	18.6	17.3	17.3	0.6	12.7	14.3	0.7	0.7	0.7	0.7	14.4	14.3	0.7	18.2	18.2	18.2	18.3	18.3	0.7	0.9	14.3	14.3	14.1	14.3	
317	1.5	19.6	16.2	15	1.5	20.9	21.3	16.2	16.5	18.4	26.2	17.1	15.8	17.6	16.6	24.9	16.6	17.5	20.9	18.6	20.2	16.1	28.4	25.5	15.2	14.9	15.1	23.6	17.9	17.9	18.6	17.3	17.3	0.6	12.7	14.1	0.6	0.6	0.6	0.6	0.6	14.3	14.1	0.6	18	12.7	18	18.2	18.2	0.6	0.7	14.1	14.1	14	14.1
318	1.5	19.6	16.2	15	1.5	20.9	21.3	16.2	16.5	18.4	26.2	17.1	15.8	17.6	16.6	24.9	16.6	17.5	20.9	18.6	20.2	16.1	28.4	25.5	15.2	14.9	15.1	23.6	17.9	17.9	18.6	17.3	17.3	0.6	12.7	14.1	0.6	0.6	0.6	0.6	0.6	14.3	14.1	0.6	18	12.7	18	18.2	18.2	0.6	0.7	14.1	14.1	14	14.1
319	1.5	19.6	16.2	15	1.5	20.9	21.3	16.2	16.5	18.4	26.2	17.1	15.8	17.6	16.6	24.9	16.6	17.5	20.9	18.6	20.2	16.1	28.4	25.5	15.2	14.9	15.1	23.6	17.9	17.9	18.6	17.3	17.3	0.6	12.7	14.1	0.6	0.6	0.6	0.6	0.6	14.3	14.1	0.6	18	12.7	18	18.2	18.2	0.6	0.7	14.1	14.1	14	14.1
320	12.8	19.2	13.4	15	12.7	19.7	20.1	12.8	13.1	18.6	25.3	16.4	13.8	16	13.7	21	14.6	14.6	20.7	18.5	17.6	13.1	25.8	23.2	13.9	11.4	12.6	21	15.6	15.6	17.1	14.7	14.6	12.5	11.2	13.5	12.5	12.5	12.5	12.5	13.7	13.5	12.5	18.2	11.2	18.2	18.3	18.3	12.5	12.7	13.5	13.5	13.7	13.5	
321	12.8	19.2	13.4	15	12.7	19.7	20.1	12.8	13.1	18.6	25.3	16.4	13.8	16	13.7	21	14.6	14.6	20.7	18.5	17.6	13.1	25.8	23.2	13.9	11.4	12.6	21	15.6	15.6	17.1	14.7	14.6	12.5	11.2	13.5	12.5	12.5	12.5	12.5	13.7	13.5	12.5	18.2	11.2	18.2	18.3	18.3	12.5	12.7	13.5	13.5	13.7	13.5	
322	12.8	19.2	13.4	15	12.7	19.7	20.1	12.8	13.1	18.6	25.3	16																																											

