UNIVERSIDADE FEDERAL DO RIO GRANDE DO SUL
FACULDADE DE AGRONOMIA
PROGRAMA DE PÓS-GRADUAÇÃO EM FITOTECNIA

DIVERSIDADE DE PARASITOIDES (HYMENOPTERA) EM ÁREAS ORIZÍCOLAS COM MANEJO ORGÂNICO E CONVENCIONAL E ANÁLISE FILOGENÉTICA DE POPULAÇÕES DE *Telenomus podisi*

Gisele De Souza Da Silva
Bióloga/UNILASALLE
Me. em Fitotecnia/Ênfase Entomologia

Tese apresentada como um dos requisitos
à obtenção do Grau de Doutor em Fitotecnia
Área de concentração Fitotecnia / Ênfase Entomologia

Porto Alegre (RS), Brasil
Janeiro de 2017

GISELE DE SOUZA DA SILVA
Bacharel em Ciência Biológicas - UNILASALLE
Mestre em Fitotecnia - UFRGS

TESE

Submetida como parte dos requisitos
para obtenção do Grau de

DOUTOR EM FITOTECNIA

Programa de Pós-Graduação em Fitotecnia
Faculdade de Agronomia
Universidade Federal do Rio Grande do Sul
Porto Alegre (RS), Brasil

Aprovado em: 18.01.2017 Pela Banca Examinadora	Homologado em: 25.04.2017 Por
SIMONE MUNDSTOCK JAHNKE Orientadora - PPG Fitotecnia	SIMONE MUNDSTOCK JAHNKE Coordenadora do Programa de Pós-Graduação em Fitotecnia
NORMAN F. JOHNSON Coorientador – Ohio State University	
LUIZA RODRIGUES REDAELLI PPG Fitotecnia/UFRGS	
RICARDO OTT Fundação Zoobotânica – POA/RS	
VALMIR ANTÔNIO DA COSTA Instituto Biológico Campinas/SP	CARLOS ALBERTO BISSANI Diretor da Faculdade de Agronomia

AGRADECIMENTOS

A minha mãe, Regina, que me acompanhou desde o início da trajetória, me deu força e incentivo em todos os momentos, obrigada pelo suporte e amor de sempre! Meu pai, Manoel, pelo apoio e carinho de sempre. Meus irmãos Marco e Felipe, que cada um a seu jeitinho, sempre me apoiaram e incentivaram. Minha cunhada Elisa que também esteve comigo durante essa caminhada me dando apoio e carinho. Agradeço muito vocês por estarem comigo durante esse processo, do início até a conquista. Amo vocês!

À minha orientadora, Dra. Simone Mundstock Jahnke por confiar na minha capacidade desde os tempos remotos da graduação até hoje. Esse tempo aprendi muito e serei eternamente grata por tudo! Se voltasse no tempo, faria tudo denovo contigo...Muito obrigada por ser mais que uma orientadora!

Ao meu coorientador Dr. Norman Johnson pela orientação, apoio, ensinamentos e receptividade desde o primeiro momento. Você e a Dr. Luciana Musetti foram e são muito importantes para mim!

Ao Huayan Chen, que me ajudou muito durante meu trabalho no doutorado sanduiche na The Ohio State University, com paciência e dedicação nos ensinamentos.

Aos professores do PPG Fitotecnia, Dra. Luiza Rodrigues Redaelli, Dr. Josué Sant’Ana e Ana Ott pelos ensinamentos, críticas, paciência e atenção dedicada durante esse período no laboratório.

À Marisa Carvalho Bello, secretária do Pós, por toda atenção, simpatia e disponibilidade de sempre.

Ao Professor Dr. Valmir Antonio Costa, do Instituto Biológico de Campinas, por além de tantos outros socorros, me apresentar para o NESH, curso de taxonomia de parasitoides, e assim eu adentrar um pouco mais no mundo desses seres vivos maravilhosos que sempre me fascinaram!

Aos amigos que fiz nesse período de convívio, parceria dentro e fora do laboratório, Joana Klein, Vivi Pretz, Leonardo Giraldo, Fatiane Borges, Leandro Menegon...Vocês fizeram e fazem meus dias mais felizes!

Ao pessoal que me ajudou arduamente nos tão famosos campos barrentos de arroz: Dani, Kadi, Fati, Leando e Leonardo. Vocês foram vitais nesse trabalho!

Ao pessoal dos laboratórios próximos e misturado as vezes (hehehe), Rita, Fernanda, Thais, Roberta, pelo carinho e risadas de sempre.

Ao pessoal do OSU C.A. Triplehorn Insect Collection pelo carinho e simpatia com que me receberam em Columbus.

As minhas amigas que sempre apoiaram essa amiga bióloga louca e que estuda coisas estranhas (para elas hehe): Lari, Cynthia, Carla, Aline, Ju, Ana Luisa, Fernanda, Luana.

Ao Programa de Pós-Graduação em Fitotecnia pela indicação e auxílio concedido para participar do Programa de Missão Científica de Curta Duração (MCCD).

Ao Conselho Nacional de Pesquisa e Desenvolvimento Tecnológico (CNPq) pela concessão de bolsa de estudos.

Ao Conselho de Aprimoramento Profissional em Ensino Superior (CAPES) pela bolsa de doutorado sanduiche no exterior (PDSE).

Aos motoristas da garagem da UFRGS por me acompanharem nas atividades de campo com boa vontade, energia e simpatia.

A todos que de alguma forma contribuíram para com a realização deste trabalho, muito obrigada!

DIVERSIDADE DE PARASITOIDES (HYMENOPTERA) EM ÁREAS ORIZÍCOLAS COM MANEJO ORGÂNICO E CONVENCIONAL E ANÁLISE FILOGENÉTICA DE POPULAÇÕES DE *Telenomus podisi*[1]

Autora: Gisele De Souza Da Silva
Orientadora: Drª. Simone Mundstock Jahnke
Coorientador: Dr. Norman Johnson

RESUMO

Parasitoides são importantes agentes de controle biológico em agroecossistemas e sua diversidade pode aumentar com a heterogeneidade do habitat. O conhecimento sobre as espécies associadas em cada sistema é importante para entender sua dinâmica e ajudar no manejo de diversas culturas, entre elas o arroz, que incluem ambientes naturais e com interferência antrópica. Espécies de Scelioninae, Telenominae e Teleasinae (Hymenoptera: Platygastridae) destacam-se no controle biológico de várias pragas agrícolas, especialmente *Telenomus podisi*, embora haja alguma discordância sobre a monofilia do grupo. Assim, esta pesquisa tem dois objetivos. Primeiro, avaliar a contribuição da presença de vegetação natural próxima às áreas de cultivo do arroz e a influência de diferentes manejos da cultura (orgânica e convencional) na diversidade de himenópteros parasitoides e dentro das três subfamílias de Platygastridae através dos gradientes de distância e nos estádios fenológicos da cultura. Segundo, através do uso dos marcadores moleculares COI e ITS2, analisar as relações entre populações de *T. podisi* de diferentes regiões biogeográficas. Para o primeiro objetivo, o trabalho foi realizado em duas áreas de arroz, uma com manejo orgânico (MO) e outra com convencional (MC), em Nova Santa Rita, RS, durante as safras 2013/2014 e 2014/2015. As coletas foram quinzenais durante o ciclo do arroz com armadilhas Malaise dispostas a diferentes distâncias em relação à vegetação nativa próxima da cultura do arroz. Para o segundo objetivo, 149 exemplares de *T. podisi* provenientes de 18 localidades em sete países foram amostrados, extraídos um fragmento de COI e todo ITS2 e amplificados através de primers específicos. Na primeira safra, foram 1104 indivíduos de parasitoides no MO (21 famílias) e 860 no MC (18 famílias). Na segunda safra, foram 1064 parasitoides no MO (19 famílias) e 389 no MC (16 famílias). Houve uma correlação negativa entre a distância da vegetação nativa e a abundância de parasitoides em áreas de MC. Os estágios fenológicos do arroz afetaram a composição de parasitoides no local. Dentro das três subfamílias, o total de indivíduos na primeira safra foram 268 no MO (31 morfoespécies) e 172 no MC (24 morfoespécies). Na segunda safra foram 151 indivíduos no MO (34 morfoespécies) e 93 no MC (21 morfoespécies). Os gêneros mais abundantes foram *Idris*, *Telenomus* e *Baeus*. *Telenomus podisi*, *Telenomus* sp.3, *Telenomus* sp.2 e *Telenomus* sp.1, foram as morfoespécies mais abundantes, respectivamente. Foram identificados 73 haplótipos de COI e ITS2. Mais de 70% dos haplótipos foram singletons e 89% foram exclusivos de uma área geográfica. Alguns haplótipos parecem estar evoluindo através de caminhos diferentes. Outros fatores podem estar exercendo pressão sobre esses haplótipos, como barreiras climáticas, deslocamento do hospedeiro e da flora associada.

---

[1] Tese de Doutorado em Fitotecnia, Faculdade de Agronomia, Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, Brasil. (134f.) Janeiro, 2017.

PARASITOIDS DIVERSITY (HYMENOPTERA) IN RICE FIELDS WITH ORGANIC AND CONVENTIONAL MANAGEMENT AND PHYLOGENETIC ANALYSIS OF *Telenomus podisi* POPULATION[1]

Author: Gisele De Souza Da Silva
Adviser: Dr$^{a.}$Simone Mundstock Jahnke
Co-adviser: Dr. Norman Johnson

ABSTRACT

Hymenopteran parasitoids are important biological control agents in agroecosystems, and their diversity can be increased with habitat heterogeneity. Knowledge about associate's species in every system is important to understand the dynamic and to help the management of several crops, between them the rice crop, which include natural and anthropic environmental. Species of Scelioninae, Telenominae and Teleasinae (Hymenoptera: Platygastridae) stand out in the biological control of several crop pests, especially *Telenomus podisi* although there is some disagreement about monophyly in *podisi* group. Thus, this research has two objectives. First, it was to evaluate the contribution of the presence of natural vegetation near rice-growing areas and the influence of different management of the crop (organic and conventional) on the diversity of parasitoids and within the three subfamilies of Platygastridae (richness), through distance gradients, and on the phenological stages of the crop. Second, it was to use population genetic methods in conjunction with two molecular markers: COI and ITS2, to address relationships between *T. podisi* specimens from different biogeography regions. For the first aim, the work took place in two rice crops, one with organic management (O.M.) and another one with conventional (C.M.), in Nova Santa Rita, RS, Brazil, during the 2013/2014 and 2014/2015 seasons. The parasitoids were collected twice a month in the crop cycle with Malaise trap at different distances in relation to the native vegetation surrounding the rice crop. For the second aim, one hundred and forty-nine specimens of *T. podisi* were sampled from 18 localities in seven countries and a fragment extraction of COI and the entire ITS2 region was amplified trough specific primers. In the first season, 1104 individuals of parasitoids were sampled in O.M. (21 families) and 860 in C.M. (18 families). In the second season, 1064 parasitoids in O.M. (19 families) and 389 in C.M. (16 families) were sampled. There was a negative correlation between distance from native vegetation and parasitoid abundance in CM areas. The phenological stages of rice affect the parasitoid assemblage on site. Within the three subfamilies, 268 individuals were sampled in the first season in O.M. (31 morphospecies) and 172 in C.M. (24 morphospecies). In the second season, 151 individuals in O.M. (34 morphospecies) and 93 in C.M. (21 morphspecies) were smapled. The most abundant genera were *Idris*, *Telenomus* and *Baeus*. *Telenomus podisi*, *Telenomus* sp.3, *Telenomus* sp.2 and *Telenomus* sp.1, were the most abundant morphospecies, respectively. Seventy-three COI and ITS2 haplotypes were identified. More than 70% of haplotypes were singletons and 89% unique to a geographic area. Some haplotypes seem to be evolving through different pathways. Others features may be putting pressure on these haplotypes, such as climatic barriers, shift of host and flora associate.

---

[1] Doctoral thesis in Plant Science, Faculdade de Agronomia, Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, Brazil. (134p.) January, 2017.

SUMÁRIO

RELAÇÃO DE TABELAS

RELAÇÃO DE FIGURAS

Página

ARTIGO 1

ARTIGO 2

ARTIGO 3

1 INTRODUÇÃO

A maioria dos organismos considerados pragas na cultura do arroz tem registro de ocorrência de parasitismo por himenópteros parasitoides (Islam *et al*., 2012). O estudo da taxonomia, diversidade e ecologia populacional desses inimigos naturais proporciona subsídios para um maior conhecimento desse grupo e para sua utilização eficaz no controle das pragas.

O controle biológico se baseia em um processo ecológico natural da rede alimentar em que os parasitoides são animais topo de cadeia e, consequentemente, controladores das populações de hospedeiros que, frequentemente, são insetos fitófagos (Pywell *et al.*, 2011).

Áreas de vegetação nativa preservadas dentro de propriedades rurais contribuem para a conservação de processos ecológicos e da biodiversidade do local ou, ao menos, minimizam as perdas (Altieri *et al.*, 2003). Estudos sobre comunidades de insetos, como levantamentos de diversidade taxonômica e funcional e a relação com a paisagem agrícola, possibilitam o entendimento dos papeis destes organismos no agroecossistema. Tendo como base este conhecimento, pode-se trabalhar na manutenção de áreas que sirvam de reservatório de inimigos naturais que possam atuar no controle biológico de pragas existentes nas culturas, visto que são um meio para se construirem alternativas sustentáveis em agroecossistemas.

As práticas relacionadas aos conceitos da agricultura sustentável e da biologia da conservação visam manter a produtividade dos ecossistemas, preservando a biodiversidade e limitando as práticas ambientalmente destrutivas. Estes conceitos partem do princípio de que os ecossistemas agrícolas e os naturais são geridos por processos ecológicos semelhantes e que os mesmos fatores determinam sua sustentabilidade (Altieri *et al.*, 2003).

Entretanto, os sistemas agrícolas de modo geral são simplificados, constituindo-se de grandes extensões de monoculturas com reduzida diversidade biológica (Jonsson *et al.*, 2015). A diversificação do ambiente agrícola possibilita um aumento das comunidades de organismos associados a este, através da implementação de arquiteturas vegetais que suportem populações de inimigos naturais ou que causem efeito direto sobre fitófagos pragas (Gliessman, 2001). Em algumas culturas, por outro lado, isso não se torna viável, como é o caso do arroz irrigado que exige uma área inundável que possa ser, em algumas ocasiões, drenada, dificultando a associação com outras espécies vegetais, além de outras constantes intervenções de manejo. Sistemas agrícolas deste tipo têm evoluído para habitats que são muito mais simples em estrutura e mais pobres em espécies que os outros. Assim, a implantação ou conservação de uma vegetação diversificada no entorno, ou próxima da cultura, torna-se uma alternativa para a manutenção da diversidade desses agroecossistemas. Além disso, o conhecimento da variação na abundância e composição de diferentes grupos de parasitoides em relação à cultura serve como base para o desenvolvimento de planos de manejo adequados para diminuição de pragas específicas.

Platygastridae é uma família de himenópteros parasitoides que utiliza como hospedeiros principalmente os pentatomídeos. Esses hemípteros incluem espécies registradas como pragas da cultura do arroz (SOSBAI, 2014). Os platigastrídeos ovipositam nos ovos do hospedeiro, atacando-os no início de seu desenvolvimento. Possuem alta especificidade em relação aos mesmos (Hanson & Gauld, 2006), sendo estas características importantes para um controle biológico eficaz (Van Driesche & Bellows, 1996). Entretanto, para o sucesso no controle biológico, é necessária a correta identificação da espécie objeto de trabalho. As potenciais consequências de uma taxonomia falha conduz a cascatas de erros que afetam hipóteses e ideias científicas, sendo comumente subestimadas ou ignoradas, mas podendo ter graves implicações ecológicas e econômicas (Wägele *et al*., 2011). A taxonomia em nível específico dessas vespas parasitoides, requer trabalho exaustivo em função da alta similaridade morfológica. Mais recentemente, diversos trabalhos com himenópteros parasitoides têm recomendado a adição de técnicas moleculares para confirmação de variações intraespecíficas em espécies crípticas, ou seja, similares morfologicamente (Johnson, 2011; Derocles *et al*., 2016).

Ferramentas de diagnóstico molecular proporcionam um meio rápido e preciso de identificação quando caracteres morfológicos não são suficientes. Em contraste com as características morfológicas, dados moleculares são expressões de modificações em nível de gene e são menos influenciados pelo meio.

Os objetivos do trabalho foram avaliar a contribuição da presença de fragmentos de vegetação natural através de gradientes de distância sobre a riqueza e abundância de himenópteros parasitoides em sistemas orizícolas com diferentes manejos da cultura e sob os diferentes estágios de desenvolvimento da planta e analisar as variações de populações de *Telenomus podisi* (Ashmead) (Hymenoptera: Platygastridae) através de dois marcadores moleculares.

2 REVISÃO BIBLIOGRÁFICA

2.1 A cultura orizícola

O arroz (*Oryza sativa* L.) é uma gramínea anual originária da Ásia e sua domesticação ocorreu há cerca de 10 mil anos (Islam *et al*., 2012). Foi trazido pelos colonizadores portugueses ao Brasil, tendo os espanhóis o introduzido na América Central e em partes da América do Sul (Pereira *et al*., 1999). No Rio Grande do Sul (RS), acredita-se que, em meados do século XVIII, os açorianos já cultivavam o arroz na região dos Sete Povos das Missões (Pereira *et al*., 1999; Zilli & Barcellos, 2006).

As áreas próprias para o cultivo do arroz irrigado caracterizam-se por apresentar uma topografia plana e de difícil drenagem, onde os solos permanecem saturados em períodos de maior precipitação pluvial. Essas características, normalmente desfavoráveis para outras culturas, tornam-se adequadas para o cultivo do arroz, facilitando a manutenção de uma lâmina d'água sobre a superfície e dificultando a lixiviação de nutrientes (SOSBAI, 2014). Para um aproveitamento eficiente desses solos, é necessário um processo de sistematização, de modo que se adotam quadros fixos, regulares e, em geral, de pequenas dimensões, separados por taipas permanentes (EMBRAPA CLIMA TEMPERADO, 2005). As taipas são pequenos taludes de terra delimitando quadros com irrigação de água, tendo altura variável de acordo com o nível de água dentro da lavoura (Brouwer, 1988). Em algumas situações de topografia, é viável utilizar as áreas entre taipas em curvas de nível (EMBRAPA CLIMA TEMPERADO, 2005).

Para uma melhor comunicação entre técnicos e produtores e a adoção de tecnologias e práticas de manejo eficientes no desenvolvimento do cultivo do arroz, faz-se necessário o uso de uma escala apropriada para expressar o desenvolvimento da planta (SOSBAI, 2014). De acordo com Counce *et al*. (2000), o ciclo de desenvolvimento do arroz pode ser dividido em três fases principais, a saber: plântula, vegetativa e reprodutiva. A duração de cada fase varia em função do cultivar, época da semeadura, região de cultivo e condições de fertilidade do solo, por exemplo. Para a maioria das cultivares utilizadas no Rio Grande do Sul, as quais necessitam temperatura ao redor de 24 a 30 °C e radiação solar elevada, o ciclo é entre 100 e 140 dias (EMBRAPA CLIMA TEMPERADO, 2005).

O Brasil apresentou uma produção anual entre 11 e 13 milhões de toneladas de arroz nas últimas safras (IBGE, 2016), sendo responsável por cerca de 79,3% da produção do Mercosul (SOSBAI, 2014). O Rio Grande do Sul se destaca, sendo responsável por cerca de 69% do total produzido no Brasil, com uma produção de mais 8,6 milhões de toneladas em 2016 e um rendimento médio de 7.700 kg/ha (CONAB, 2016).

Quanto ao aspecto social, a importância do arroz é representada pela possibilidade de ser cultivado tanto em pequenas como em médias e grandes áreas. Esta flexibilidade da cultura permite que a agricultura familiar e a empresarial se desenvolvam e utilizem o arroz como alternativa para geração de renda e de empregos (SOSBAI, 2014). No último Censo Agropecuário, foram registrados para o RS 354.677 estabelecimentos de agricultura familiar que produziram 3,2 ton de arroz (base casca) em uma área colhida de 1.167 ha (IBGE, 2006). Atualmente, este número deve ter crescido, tendo em vista o aumento registrado de produção geral (IBGE, 2016).

2.2 Manejo de pragas em agroecossistemas

As atividades agrícolas têm contribuído muito para redução dos recursos naturais e da qualidade ambiental no Brasil, tanto na Região Centro-Oeste, Oeste da Bahia e na Região Sul (Barrigossi *et al*., 2004). Com a modernização da agricultura, a produção em grandes áreas de monocultura passou a predominar, em detrimento dos princípios ecológicos e da preocupação com o ambiente (Altieri *et al*., 2003). Os cultivos em grande escala promovem a simplificação da biodiversidade e a formação de um sistema artificial, que requer constante intervenção humana com utilização de agroquímicos que, apesar de contribuir para elevar a produtividade temporariamente, apresenta diversas desvantagens sob o ponto de vista ambiental e econômico (Barrigossi *et al*., 2004).

As áreas cultivadas de arroz são circundadas por habitats aquáticos e terrestres, compreendendo um mosaico de ambientes em transformação. Comparados com outras culturas agrícolas, estes podem abrigar grande diversidade biológica, mantida pela rápida colonização, assim como pela rápida reprodução e crescimento dos organismos (Fritz, 2009). A fauna associada a estes sistemas compreende vertebrados e invertebrados que habitam a vegetação, a água e o solo dos campos orizícolas (Hook, 1994).

O manejo de pragas e doenças é um dos principais pontos que deve ser considerado em relação à competitividade e sustentabilidade da agricultura (Altieri *et al*., 2003). Este tem sido focado mais no aspecto econômico que no ambiental (Waquil *et al.*, 2006). O ideal seria a escolha de um método a ser empregado pautado em avaliações socioeconômica e ambiental, utilizando-se da associação de várias técnicas como resistência varietal, controle biológico, químico, cultural, dentre outros (Barrigossi *et al*., 2004). Segundo os mesmos autores, pesquisadores concordam que a agricultura moderna tem confrontado muitos dos princípios ecológicos básicos e que as perdas de produção devido às pragas ainda são elevadas, apesar do consumo de agrotóxicos ter aumentado em escala mundial. Uma alternativa tem sido resgatar os princípios ecológicos na forma de produzir. Assim, além da inovação tecnológica, deve ser considerada a complexidade das interações entre os recursos, pessoas e o ambiente (Rodrigues *et al.,* 2003).

A compreensão de como as práticas de manejo agrícola interferem negativamente na biodiversidade dos ecossistemas agrícolas, neste caso, da cultura do arroz, permitirá aos produtores a incorporação de estratégias de conservação das espécies e restauração de áreas degradadas (Fritz *et al.*, 2008).

Na busca de práticas agrícolas com menos impactos ambientais, surgem alternativas orientadas pelo conhecimento dos processos ecológicos que ocorrem em agroecossistemas (Gliessman, 2001). No Brasil, a Lei 10.831/2003 e o Decreto 6.323/2007 (BRASIL, 2003; BRASIL, 2007) deram início à regulamentação da agricultura orgânica. Nesses instrumentos, o termo institucionalizado foi o “orgânico”, que engloba todos os outros: biodinâmico, natural, biológico, agroecológico e permacultura.

A produção orgânica de arroz irrigado está baseada na eliminação do uso de insumos químicos sintéticos, como fertilizantes, agrotóxicos e reguladores de crescimento, sendo privilegiadas tecnologias alternativas como mecanização, preparo do solo, adubação e controle de pragas, incluindo plantas daninhas, doenças e insetos (EMBRAPA CLIMA TEMPERADO, 2009). Neste sistema, a diversidade na produção vegetal é assegurada, no mínimo, pela prática de associação de culturas a partir das técnicas de rotação e consórcios (EMBRAPA CLIMA TEMPERADO, 2009). Além disso, a manutenção das áreas de preservação permanente e a atenuação da pressão antrópica sobre os ecossistemas naturais e modificados são aspectos ambientais que os sistemas de produção orgânica de arroz devem buscar para obtenção da certificação (EMBRAPA CLIMA TEMPERADO, 2009).

2.3 Pragas associadas ao arroz

Algumas espécies de insetos e outros fitófagos que ocorrem na cultura do arroz irrigado podem atingir níveis populacionais de dano econômico e causar perdas de produtividade da ordem de 10 a 35 % (Martins *et al*., 2009).

De maneira geral, a planta de arroz pode sofrer danos em diferentes partes por diversos grupos de fitófagos (EMBRAPA CLIMA TEMPERADO, 2005). As sementes, plântulas e raízes são atacadas, principalmente, por larvas e adultos de coleópteros, por pássaros e moluscos (SOSBAI, 2014). Os colmos e folhas são alvos de insetos mastigadores, sugadores e raspadores, sendo os dois primeiros grupos os mais importantes. Os grãos, por sua vez, sofrem ataques de um conjunto de insetos sugadores que afetam diretamente a quantidade e a qualidade do arroz (SOSBAI, 2014).

As pragas da orizicultura podem ser divididas em primárias e secundárias, causando danos diretos ou indiretos (Domiciano, 2001). Entre as consideradas primárias, estão os lepidópteros da família Noctuidae, como as lagartas-dos-milharais e capinzais (*Pseudaletia sequax* Franclemonte e *Pseudaletia adultera* Schaus), a lagarta-militar [*Spodoptera frugiperda* (Smith)], coleópteros Curculionidae, como a bicheira-da-raiz-do-arroz [*Oryzophagus oryzae* (Costa Lima)], e os hemípteros Pentatomidae, o percevejo-do-colmo (*Tibraca limbativentris* Stål) e o percevejo-do-grão-do-arroz [*Oebalus poecilus* (Dallas)]. As pragas de importância secundária são os coleópteros pulga-do-arroz (*Chaetocnema* sp., Chrysomelidae) e cascudo-preto (*Euetheola humilis* Burmeister, Scarabaeidae), os hemípteros pulgão-da-raiz [*Rhopalosiphum rufiabdominalis* (Sasaki), Aphididae] e o percevejo-do-capim [*Collaria scenica* (Stål), Miridae], os lepidópteros broca-da-cana [*Diatraea saccharalis* (Fabricius), Pyralidae], lagarta-boiadeira (*Nymphula indomitalis* Berg, Pyralidae) e o coleóptero broca-do-colo [*Ochetina uniformis* (Pascoe), Curculionidae] (Gomes & Magalhães-Junior, 2004).

Embora haja registros de muitas espécies de insetos danificando o arroz, a maioria destas pode apresentar outras funções no agroecossistema orizícola. Settle *et al.* (1996) em levantamento realizado em cultura de arroz irrigado na Indonésia, por exemplo, registraram a maioria dos indivíduos como inimigos naturais de pragas, sendo 40% predadores, 24% parasitoides, 19% detritívoros e somente 17% fitófagos.

2.4 Controle de insetos na cultura do arroz

Para o controle de fitófagos, o manejo convencional utiliza principalmente inseticidas dos grupos químicos neonicotinoide, diamida, piretroide e carbamato (AGROFIT, 2016), cujos sítios de ação primária são agonistas de receptores nicotínicos da acetilcolina, moduladores de receptores de rianodina, moduladores de canais de sódio e inibidores de acetilcolinesterase (Salazar Cavero, 1998). Esses inseticidas, portanto, são classificados como neurotóxicos e não seletivos, podendo atingir tanto fitófagos como inimigos naturais e polinizadores (Omoto & Guedes, 2000).

Por outro lado, as recomendações técnicas para o controle de insetos e outros fitófagos no arroz irrigado no Rio Grande do Sul preconizam o emprego de medidas integradas de manejo que reduzam os danos causados à cultura (SOSBAI, 2014).

Em sistemas orgânicos, como o do arroz, a restrição ao uso de inseticidas é ainda maior do que no Manejo Integrado de Pragas (MIP), no qual é previsto um sistema de manejo sustentável da unidade de produção com enfoque sistêmico que privilegia a preservação ambiental, a agrobiodiversidade, os ciclos biogeoquímicos e a qualidade de vida humana (EMBRAPA AGROBIOLOGIA, 2004).

O controle biológico conservativo, uma das importantes técnicas de manejo, atua com outros fatores do meio e contribui decisivamente para diminuir a importância dos fitófagos do arroz, devendo os inimigos naturais serem preservados pela utilização adequada das práticas de manejo (Fritz *et al.*, 2008).

2.5 Importância dos fragmentos vegetais naturais próximos às áreas de cultivo

A intensificação da agricultura frequentemente prejudica os serviços ecológicos que poderiam beneficiar a produção (Jonsson *et al.,* 2015), como por exemplo a preparação do solo e aplicação de pesticidas, além de outros fatores (Tscharntke *et al.,* 2005). O aumento da perturbação pode ser mais prejudicial aos inimigos naturais do que para os insetos pragas, podendo enfraquecer a supressão dos mesmos (Krauss *et al.*, 2011; Jonsson *et al.,* 2012), resultando em uma necessidade ainda maior de agroquímicos para resolver os problemas locais com os ataques aos cultivos (Jonsson *et al.,* 2015). Além disso, o aumento dos campos de cultivo, contínuos em extensão e dominados por poucas espécies vegetais, leva a homogeneização do local, tornando-os simples em estrutura e composição de espécies (Margosian *et al.,* 2009). Essa simplificação aumenta a concentração de recursos que estão disponíveis para as pragas (Margosian *et al*., 2009; Tscharntke *et al.,* 2012) e reduz os habitats não agriculturáveis que suportam os inimigos naturais (Chaplin-Kramer *et al*., 2011).

Buscando entender e organizar as interações ecológicas, surge a abordagem do sistema “bottom-up”. Em uma comunidade, este sistema prediz que o equilíbrio ecológico é ditado de baixo para cima, ou seja, em que uma comunidade de vegetação mais diversa é associada com alta abundância e riqueza de predadores e parasitoides que se alimentariam de herbívoros em épocas específicas, realizando um controle biológico destes (Root, 1973; Haddad *et al.,* 2001; Pywell *et al*., 2011; Nemec *et al.,* 2014). Em um agroecossistema o controle “bottom-up” se refere a quanto um predador (ou grupo de predadores ou parasitoides) influencia a estrutura ou a dinâmica populacional do ecossistema (Pywell *et al*, 2011).

Para um uso efetivo no controle biológico conservativo é necessário saber se esse equilíbrio do sistema favorece um aumento nas taxas de parasitismo. Fenoglio *et al*. (2013) analisaram a taxa de parasitismo associado a áreas com diferentes gradientes de isolamento e a associação dos mesmos com o aumento da riqueza de parasitoides. Apesar de o trabalho ser conduzido em ambientes urbanos, o mesmo mostra como a fragmentação de habitats e as áreas em mosaico afetam a taxa de parasitismo e a relação dos mesmos com a riqueza de parasitoides, podendo ser usado como base para agroecossistemas. Neste trabalho os autores encontraram que a taxa de parasitismo foi maior com o aumento no tamanho da área e diminuiu com o aumento no grau de isolamento. Além disso, os efeitos, tanto no tamanho quanto na isolação do habitat na taxa de parasitismo, foram indiretos, mediados pelas mudanças na abundância dos hospedeiros e da riqueza de espécies parasitoides. Conforme os autores, a riqueza de parasitoides foi significativamente correlacionada às taxas de parasitismo, indicando que o número de espécies parasitoides, independentemente da abundância de hospedeiros, influenciou a proporção de larvas parasitadas.

As mudanças nas paisagens dos agroecossistemas podem alterar a composição vegetal assim como os recursos disponíveis e os habitats, modificando o acesso dos insetos a alimentação e refúgios, afetando assim, sua estabilidade populacional (Tscharntke *et al*., 2012). A alta estabilidade de insetos poderia então ser benéfica para o controle biológico de pragas nos agroecossistemas (Haddad *et al.*, 2011). De acordo com Zaho *et al*. (2015), o alto nível de heterogeneidade de habitat em áreas de cultivo de trigo é um importante estabilizador da distribuição espacial de afídeos, parasitoides primários e secundários. Segundos os autores, a relação entre esta estabilidade e heterogeneidade de habitat pôde ser descrita por uma regressão linear, que indicou que os níveis tróficos mais altos (parasitoides) foram os mais sensitivos para as mudanças na vegetação da paisagem do que o nível trófico mais baixo (afídeos), levando a conclusão de que o aumento na heterogeneidade de habitat pode afetar ambos, afídeos e parasitoides, mas com os últimos sendo mais sensitivos a esse aumento.

Letourneau *et al*. (2012) analisaram a riqueza e abundância de parasitoides da família Tachinidae (Diptera) em cultivos vegetais (brócolis, couve, cenoura, repolho, alface, entre outras) com áreas adjacentes variando desde complexos mosaicos de vegetação até áreas homogêneas de produção agrícola na Califórnia. Os autores constataram associação positiva da riqueza e abundância de Tachinidae com áreas permanentes de vegetação e a negativa relação com áreas de cultivo o que suporta a conclusão de que a efetiva conservação de parasitoides nativos acontecera pela preservação e/ou restauração de um habitat com estágio sucessional avançado dentro da paisagem agrícola. Esta conclusão também foi feita por Marino *et al*. (2006), estudando os parasitoides de lepidópteros pragas de diferentes culturas na América do Norte. Segundo os autores, os lepidópteros analisados eram atacados principalmente por parasitoides que tinham hospedeiros alternativos que se alimentam exclusivamente em vegetação com estágio sucessional avançado.

A discussão a respeito do uso de controle biológico conservativo ser aplicável somente em pequenas áreas tem sido discutida por pesquisadores como Merck & Pereira (2015), que defendem a remodelação da agricultura em larga escala, buscado a produtividade e, ao mesmo tempo, tornando-a integrada ao sistema natural. Assim, o controle biológico através da conservação, restauração ou estabelecimento de vegetação nos cultivos ou ao redor deles apresenta-se como uma estratégia promissora (Thies *et al.*, 2011).

2.6 Parasitoides: inimigos naturais de pragas agrícolas

Os inimigos naturais que desempenham um papel fundamental no manejo das culturas incluem predadores, parasitoides e microrganismos patogênicos capazes de reduzir a densidade populacional das pragas e, consequentemente, o dano das mesmas (Heinrichs & Barrion, 2004).

Os parasitoides são insetos cujas larvas alimentam-se de outros artrópodes, geralmente insetos, levando à morte o hospedeiro (Godfray, 1994). Os adultos são de vida livre, mas ovipositam próximo, sobre ou no interior de outros insetos, em aranhas ou isópodes, com a larva se desenvolvendo no interior ou na superfície do hospedeiro (Jervis & Kidd, 1991). No início do seu desenvolvimento, a larva causa um dano pouco aparente ao hospedeiro, mas acaba consumindo-o quase totalmente e, portanto, matando-o (Godfray, 1994). Quando está totalmente desenvolvido, o parasitoide emerge de onde aparentemente deveria emergir seu hospedeiro. Geralmente, apenas um parasitoide se desenvolve em cada hospedeiro, mas, muitas vezes, vários indivíduos podem compartilhar o mesmo (Begon *et al*., 2007). Segundo os mesmos autores, a grande maioria dos insetos é atacada por, pelo menos, uma espécie de parasitoide e este, por sua vez, pode ser atacado por outros.

Os parasitoides constituem um dos grupos de agentes de controle biológico mais importante no controle de populações de pragas de sistemas agrícolas, tanto pela ocorrência natural das espécies no ambiente, quanto pela sua utilização em programas de controle biológico aplicado (Hanson & Gauld, 2006). Sua diversidade, associada a diferentes sistemas de cultivos, é determinada por fatores ambientais, biológicos e de manejo (Chay-Hernandez *et al*., 2006). Em grandes monoculturas, a diversidade de parasitoides pode ser suprimida por pesticidas, simplificação de vegetação e outros distúrbios ambientais (Altieri, 2002). Em agroecossistemas menos perturbados, a diversidade mostra-se relacionada à diversidade de cultivos, plantas invasoras, cobertura do solo e vegetação nativa próxima aos cultivos (Onody, 2009; Liere *et al*., 2015). A ocorrência natural dos parasitoides nos agroecossistemas é um fator de grande importância para a redução da infestação de pragas, portanto, o conhecimento desta fauna e a conservação do meio ambiente tornam-se imprescindíveis para o sucesso de sua conservação nos locais em que ocorre (Hanson & Gauld, 2006).

As ordens Hymenoptera e Diptera são as que apresentam maior representatividade dentre os grupos de parasitoides (Gullan & Cranston, 2008). Em relação aos himenópteros parasitoides, vários são os trabalhos que afirmam a importância destes como reguladores naturais das populações de vários hospedeiros, o que os torna essenciais para a manutenção do equilíbrio ecológico (Thies *et al*., 2011; Purnomo & Wright, 2016). Esses organismos são abundantes na natureza e ocupam os mais diversos tipos de ambientes disponíveis (Gallo *et al.*, 2002). Para a ordem Hymenoptera, um total de 153.088 espécies existentes foram descritas, além de 2.429 espécies extintas, sendo considerada uma das mais ricas, atrás apenas de Coleoptera e Lepidoptera (Aguiar *et al*., 2013).

No MIP, os parasitoides de ovos são considerados, em vários países, como os principais inimigos naturais de Pentatomidae (Pacheco & Corrêa-Ferreira, 2000). Além disso, existem várias espécies de himenópteros parasitoides importantes no controle de ovos e lagartas de Lepidoptera (Gondim *et al*., 2011; Gates *et al*., 2012; Luna *et al*., 2015).

Vários são os estudos relacionando parasitoides a diferentes pragas da cultura do arroz. Em um trabalho realizado no Maranhão, foi registrado um parasitismo de 23,4% em ovos de *T. limbativentris*. As espécies encontradas foram *Telenomus podisi* Ashmead, *Trissolcus urichi* (Crawford) (Hymenoptera: Platygastridae) e *Ooencyrtus submetallicus* (Howard) (Hymenoptera: Encyrtidae) (Maciel *et al.*, 2007). Em lavouras arrozeiras, em Santa Catarina, as mesmas espécies foram encontradas em ovos do percevejo-do-colmo, apresentando, entretanto, um índice superior a 70% (Riffel, 2007). Em lavouras do Rio Grande do Sul, no município de

Eldorado do Sul, *T. podisi* teve um índice de parasitismo de 75% sobre *T. limbativentris* (Idalgo *et al*., 2013). Ainda no RS, em lavouras de manejo orgânico em Águas Claras, Viamão, os parasitoides mais frequentes em lavouras de arroz foram os das famílias Mymaridae e Platygastridae (Simões-Pires *et al*., 2016).

São relacionadas também 17 espécies de himenópteros parasitoides, pertencentes às famílias Braconidae, Eulophidae, Ichneumonidae, Trichogrammatidae, parasitando *S. frugiperda* na cultura do arroz (EMBRAPA ARROZ E FEIJÃO, 2008). Para *Elasmopalpus lignosellus* (Zeller) (Lepidoptera: Pyralidae), são citadas espécies de parasitoides de lagartas das famílias: Platygastridae, Braconidae, Ichneumonidae, Chalcididae, Eulophidae e Perilampidae (EMBRAPA ARROZ E FEIJÃO, 2008). No que se refere à broca-do-colmo, *D. saccharalis*, os himenópteros parasitoides de ovos, *Telenomus* spp. e *Trichogramma* spp. são destaque e, para lagartas, o principal é *Cotesia flavipes* Cameron [= *Apanteles flavipes* (Cameron)] (Braconidae) (EMBRAPA ARROZ E FEIJÃO, 2008).

Em relação ao gorgulho-aquático *O. oryzae*, entretanto, não há referência de parasitoides. Os percevejos-das-panículas, *O. poecilus* e *Oebalus ypsilongriseu*s (De Geer) (Hemiptera: Pentatomidae) possuem como parasitoides de ovos *Trissolcus* (=*Microphanurus*) *mormideae* Lima e *Telenomus mormideae* Lima (Hymenoptera: Platygastridae) (EMBRAPA ARROZ E FEIJÃO, 2008). Fritz *et al.* (2008) realizaram um levantamento bibliográfico a respeito de registros de ocorrência de insetos pragas e inimigos naturais em agrossistemas orizícolas irrigados no Brasil. Entretanto, embora existam estes registros, poucos são os trabalhos que avaliam as populações de inimigos naturais ou realizam análises de diversidade destes.

Através do estudo de similaridade na composição das famílias e espécies mais abundantes nas áreas preservadas próximas aos cultivos, infere-se que estes refúgios de vegetação natural podem servir de repositório de inimigos naturais de insetos pragas das culturas (Bambaradeniya & Edirisinghe, 2008; Ferreira *et al.*, 2014; Da Silva *et al*., 2016).

Apesar das evidências da importância dos fatores ambientais como condições climáticas, solo e feições fitogeográficas, afetando os parasitoides de pragas do arroz, o uso da manipulação do habitat para aumentar o controle biológico da segunda maior cultura de cereal do mundo (SOSBAI, 2014) é surpreendentemente sub-representada na literatura (Way & Javier, 2001; Gurr *et al*., 2011), o que ressalta a relevância do trabalho aqui desenvolvido.

2.7 Importância da família Platygastridae em culturas agrícolas

Dentro da família Platygastridae, os integrantes das subfamílias Teleasinae, Scelioninae e Telenominae são parasitoides de ovos e possuem ampla gama de hospedeiros entre lepidópteros, hemípteros e dípteros (Hanson & Gauld, 2006). Segundo os mesmos autores, a maioria das espécies mostra alto grau de especificidade, algumas restritas somente a uma espécie hospedeira e, a maior parte, a uma só família (Hanson & Gauld, 2006).

A composição das famílias e espécies de parasitoides em diferentes locais e cultivos também pode ser alterada em decorrência das pragas que lhes servem de hospedeiros. A maior abundância de parasitoides, encontrados no trabalho de Bambaradeniya & Edirisinghe (2008) em arroz no Sri Lanka, por exemplo, foi da família Mymaridae, (39%), que atacam os insetos *Nilaparvata lugens* (Stål) e *Sogatella furcifera* (Horváth) (Hemiptera: Delphacidae), importantes pragas naquela região. Entretanto, Gurr *et al*., (2011) alertaram que o fato de Platygastridae não aparecer como uma família representativa parasitando Delphacidae na região, pode ser em razão da identificação errada ou escassez de pesquisa na região.

Trabalhos anteriores já mostram a importância de Platygastridae em áreas orizícolas, atuando como controlador da abundância de pragas desta cultura (Fritz *et al*., 2008 e 2011; Da Silva *et al*., 2016).

Em outras regiões do mundo, como a Ásia e África, Platygastridae também é uma família importante para a cultura do arroz. No continente asiático, *Platygaster oryzae* Cameron é um parasitoide do galhador *Orseolia oryzae* Wood Mason (Diptera: Cecidomyiidae) encontrado em áreas orizícolas da Índia, China, Nepal, Sri Lanka e Laos (Katiyar *et al*., 2000). O percevejo-preto-do-arroz, *Scotinophara* sp. (Hemiptera: Pentatomidae), da Índia, é parasitado por várias espécies de platigastrídeos como *Telenomus triptus* Nixon, *Telenomus cyrus* Nixon, *Telenomus chloropus* (Thomson), *Telenomus gifuensis* Ashmead (Polaszek & Rajmohana, 2007) e *Telenomus oryzae* Rajmohana & Nisha. Em levantamentos de diversidade na cultura do arroz, é grande o número de representantes desta família, como por exemplo, no trabalho de Gnanakumar *et al*. (2012), na Índia, onde foram encontradas 40 espécies de parasitoides, sendo 29 pertencentes a Platygastridae. No continente africano, tem sido registrado o parasitismo por *Platygaster diplosisae* Risbec sobre o galhador *Orseolia oryzivora* Harris & Gagné (Diptera: Cecidomyiidae), praga das áreas de arroz irrigado e de terras baixas na África Subsaariana, na Nigéria (Ogah *et al*., 2012).

Platygastridae parasitoides de ovos são importantes inimigos naturais de Pentatomidae, sendo que algumas espécies dessa família, especialmente os cosmopolitas *Trissolcus basalis* (Wollaston) e *T. podisi*, estão sendo usadas em muitos países no controle biológico (Clarke & Walter, 1995; Corrêa-Ferreira & Moscardi, 1996; Corrêa-Ferreira, 2002; Ehler, 2002). Estes parasitoides têm atributos biológicos e comportamentais que levam a um parasitismo densidade-dependente e regulação local das populações de pentatomídeos (Laumann *et al*., 2008). No

Brasil, Corrêa-Ferreira & Moscardi (1996) mostraram que a liberação inoculativa de *T. basalis* pode controlar a população de percevejos.

Trissolcus spp. são parasitoides solitários que se desenvolvem dentro dos ovos dos hospedeiros. O ciclo de vida de *T. basalis* requer, em média, 17 horas para o desenvolvimento dos ovos, quatro dias para as larvas e seis dias para as pupas (Corrêa-Ferreira, 1993).

Um trabalho de Cingolani *et al.* (2012), em que é analisado em laboratório o multiparasitismo de ovos de *Piezodorus guildinii* (Westwood) (Hemiptera: Pentatomidae) por *T. podisi* e *T. urichi,* indica esta última espécie como um melhor competidor intrínseco e que, apesar de *T. podisi* ser dominante em campo, *T. urichi* poderia estar usando outros ovos de pentatomídeos como recurso, mostrando seu potencial como controlador de vários Pentatomidae. Corrêa-Ferreira (2003) observou no Paraná, em duas safras consecutivas de soja orgânica, que a incidência de parasitismo em áreas sem liberação de parasitoides foi de 41,3% na primeira e 40,7% na segunda. Em áreas onde foram liberados os parasitoides *T. basalis* e *T. podisi,* os índices atingiram 44,3% no primeiro ano e 54,4% no segundo. Corrêa-Ferreira (2003) relatou que, geralmente, *T. basalis* e *T. podisi* são os parasitoides que apresentam maior eficiência de parasitismo. A primeira, preferencialmente, em ovos de *Nezara viridula* (Linnaeus) (Hemiptera: Pentatomidae) e a segunda em ovos de *Euschistus heros* (Fabricius) (Hemiptera: Pentatomidae).

Estes gêneros de parasitoides também são registrados em outras culturas, tais como no trabalho de Favetti *et al*. (2013), no qual, em um levantamento de parasitismo de ovos de *Edessa meditabunda* (Fabricius) (Hemiptera: Pentatomidae), em alface, foram encontrados 578 ovos, sendo 38,2% parasitados por *T. urichi.* Foi o primeiro registro de ocorrência em alface. Em um trabalho realizado por Santos (2008) em cultura de soja orgânica no Rio Grande do Sul, também foram encontrados parasitoides do gênero *Telenomus,* preferencialmente, em ovos de *Dichelops* *furcatus* (Fabricius) (Hemiptera: Pentatomidae), enquanto que em ovos de *Chinavia* (=*Acrosternum*) *impicticorne* (Stal) (Hemiptera: Pentatomidae) e de *N. viridula* os parasitoides encontrados foram do gênero *Trissolcus.*

2.8 Problemática taxonômica e filogenética

Platygastridae pertence a superfamília Platygastroidea com 6011 espécies descritas (Hymenoptera online, 2016). As relações filogenéticas dos elementos deste grupo não são claras, sendo que, através de dados moleculares, suportam uma relação com Chalcidoidea como grupo irmão, e com dados morfológicos, indicam uma relação com Ceraphronoidea (Austin *et al*., 2005). Apesar da relação com o grupo irmão da superfamília Platygastroidea ser ainda discutida, a sua monofilia é indiscutível (Austin *et al.*, 2005). Masner (1976), Johnson (1992) e Vlug (1995) compilaram literaturas registradas desde 1758 com espécies de Platygastroidea ocorrentes em várias partes do mundo.

Em Platygastridae, existe muita discordância a respeito da classificação na subfamília Telenominae (Kozlov,1970; Masner, 1972; 1976; Masner & Huggert, 1979; Kozlov & Kononova,1983). A maior parte das espécies é descrita em um dos dois gêneros, seja *Trissolcus* Ashmead (179 espécies válidas) ou *Telenomus* Haliday (652 espécies válidas), sendo, ambos, cosmopolitas. Dos gêneros restantes, 14 têm apenas uma ou duas espécies descritas (Taekul *et al*., 2014). Alguns trabalhos apontam que não foi encontrada monofilia entre certos gêneros, entre eles *Telenomus* (Murphy *et al*., 2007; Taekful *et al*., 2014), no qual não foi encontrada monofilia inclusive no grupo *podisi* (Taekful *et al*., 2014).

Estudos referentes à localização e preferência de hospedeiros têm começado a questionar se os indivíduos identificados como *T. podisi* pertencem efetivamente a uma única espécie. Em um estudo com *T. podisi* do Brasil e Estados Unidos, por exemplo, Borges *et al*. (2003)

encontraram diferenças nas respostas em relação às pistas deixadas pelos hospedeiros, tolerância ao frio, composição de hidrocarbonetos cuticulares e acasalamento entre as duas populações.

A elucidação de tais questionamentos poderá ser realizada com estudos a respeito da variação morfológica e biológica entre grupos de indivíduos e, segundo (Godfray, 1994), as técnicas moleculares ajudarão a construir relações filogenéticas entre eles. Buscando esclarecer estas questões, a sistemática filogenética pode servir a dois objetivos principais. Um deles é fornecer subsídios para uma compreensão geral da diversidade biológica, da evolução dos táxons e da modificação de caracteres. O outro é desenvolver a habilidade de propor hipóteses sobre a evolução de caracteres ou sobre as relações de parentesco entre membros de um grupo (Amorim, 2011). Segundo o mesmo autor, esta área de conhecimento deveria ser dominada por qualquer pesquisador que lide direta ou indiretamente com problemas ligados à comparação entre estruturas biológicas – de moléculas ao comportamento – de grupos diferentes de organismos.

A identificação taxonômica de fauna e flora é essencial para qualquer estudo envolvendo biodiversidade (Wägele *et al*., 2011) e, atualmente, a falta de taxonomistas é aguda nas regiões com maiores produções de arroz, incluindo os Platygastridae (Islam *et al.*, 2012). Antigamente, alguns países desenvolvidos e organizações internacionais proviam serviços taxonômicos à uma taxa mínima, mas a crise de financiamento cortou a atividade da maioria destes serviços, sendo este o maior empecilho para pesquisas de diversidade no arroz (Islam *et al*., 2012). Para os autores, há uma necessidade urgente de desenvolvimento de mão de obra e instalações para o serviço de taxonomia para países em desenvolvimento que cultivam arroz.

Extrapolando as dificuldades dentro do grupo Platygastridae para insetos em geral, entomologistas estão sendo cada vez mais solicitados em áreas de quarentena, biossegurança, agricultura e na saúde humana e animal para reconhecimento de espécies pragas, com potencial de controle biológico e que causam doenças em humanos e animais para deliberar a respeito das filogenias e de como estas se relacionam com aspectos práticos (Gullan & Cranston, 2010). Consequentemente, para os autores, há um aumento na demanda por estudos de sistemática, através de caracteres morfológicos, comportamentais e técnicas moleculares para o efetivo reconhecimento das espécies.

2.9 Identificação de espécies com o uso de marcadores moleculares

A existência de um número de entidades ou táxons, que, de alguma maneira podem ser distinguidos uns dos outros, caracteriza a diversidade biológica (Amorim, 2011). Essa diversidade pode ser identificada de diferentes maneiras, podendo ser através da análise comportamental, morfológica e através da diversidade genética (Amorim, 2011).

Na diversidade genética, caracteres não aparentes podem interferir no organismo, sendo que estes cobrem os genes encontrados dentro de uma dada população de uma única espécie e o padrão de variação através de diferentes populações daquelas espécies, sendo necessária para as populações serem capazes de lidar com mudanças ambientais (Gurr *et al*., 2012). A perda da diversidade genética é, muitas vezes, associada com a redução do valor adaptativo reprodutivo, sendo então, a matéria-prima para as mudanças adaptativas evolucionárias (Futuyma, 2002).

O estudo da diversidade genética tem sido importante em diversas linhas de pesquisas científicas na área agronômica como: resistência de organismos a inseticidas (Xie *et al*., 2012), estudos de cadeia alimentar (Gurr *et al.*, 2012), dispersão geográfica de espécies (Chen *et al.*, 2013; Justi *et al*., 2016) e diferenciação de espécies crípticas (Mapondera *et al.*, 2012; Derocles *et al*., 2016). A respeito deste último item, diversos autores vêm usando a técnica molecular para a diferenciação de espécies idênticas ou muito similares morfologicamente, tanto de pragas como de inimigos naturais (Gariepy *et al*., 2014; Uesugi *et al*., 2016). Para o desenvolvimento de estudos nestas áreas, são utilizados marcadores moleculares encontrados nos genes (Gariepy *et al*., 2007; Derocles *et al*., 2014; Ronque *et al*., 2015).

Dentre os genes utilizados como marcadores para identificação de espécies e genética de populações, encontramos o gene mitocondrial COI (citocromo oxidase I) e o ITS2 (espaço transcrito interno2 do DNA ribossomal). Ambos são marcadores com alta taxa evolutiva e o COI possui muitas variações no 3º códon de bases nitrogenadas.

Sequências do gene COI têm sido usadas para identificação de muitas espécies de insetos como *Torymus* spp. (Hymenoptera: Torymidae) (Yara, 2004), *Encarsia* spp. (Hymenoptera: Aphelinidae) (Monti *et al*., 2005), *Calliphora vicina* Robineau-Desvoidy e *C. vomitoria* (L.) (Diptera: Calliphoridae) (Ames *et al*., 2006), *Elachista* spp. (Lepidoptera: Elachistidae) (Kaila & Stahls, 2006), cochonilhas (Hemiptera: Pseudococcidae) (Saccaggi *et al*., 2008), *Baetis vernus* Curtis e *B. macani* Kimmin (Ephemeroptera: Baetidae) (Stahls & Savolainen, 2008), quironomídeos (Diptera: Chironomidae) (Failla *et al*., 2016), moscas varejeiras (Diptera: Calliphoridae) (Khullar *et al*., 2016), *Eumerus* sp. (Diptera: Syrphidae) (Chroni *et al*., 2016), entre outras.

Em rDNA, o ITS2 é uma escolha adequada para a identificação de espécies estreitamente relacionadas ou populações simpátricas e utilizado em espécies barcoding e tecnologias de matriz de DNA (Heraty, 2004). Apresenta a mesma funcionalidade do COI, com muitos estudos mostrando a utilidade de ITS2 na identificação de espécies (Young & Coleman, 2004), incluindo himenópteros parasitoides como *Lysiphlebus* spp. (Braconidae) (Rahimi *et al*., 2012), *Horismenus* spp. (Eulophidae) (Kenyon *et al*., 2015), Trichogrammatidae (Almeida & Stouthamer, 2015; Venkatesan, 2016).

Além disso, como citado anteriormente, através dos marcadores moleculares, pode-se estudar a genética de populações. A mesma investiga a conexão entre características demográficas e a distribuição de variações moleculares e genéticas. Medindo a variação genética pode ser feita inferência a respeito da biologia de organismos (Sunnucks, 2000). No trabalho de Zepeda-Paulo *et al*. (2015), os autores avaliaram populações do parasitoide *Aphidius ervi* Haliday (Hymenoptera: Braconidae) introduzido no Chile como agente de controle de afídeos pragas. Os autores verificaram que as populações desses parasitoides sofreram o efeito gargalo moderado durante a introdução, mostrando ainda uma forte diferenciação genética entre as populações da região de origem e as de ambientes novos. Assim, processos que afetam indivíduos podem acumular efeitos nas populações podendo influenciar a especiação e, consequentemente, categorias taxonômicas (Sunnucks, 2000). Por isso, a maioria dos taxonomistas, além das características morfológicas, incorporam análises filogenéticas em seus trabalhos, buscando uma taxonomia integrativa a fim de elucidar questões referentes às espécies estudadas (Schlick-Steiner *et al*., 2010; Johnson, 2011). Dessa maneira, essa ferramenta poderá auxiliar a esclarecer as dúvidas a respeito da filogenia assim como a delimitação de espécies do grupo em questão.

3.0 Referências bibliográficas

AGUIAR, A. P. et al. Order Hymenoptera. **Zootaxa**, Auckland, v. 3703, n. 1, p. 051–062, 2013.

AGROFIT. Ministério da Agricultura, Pecuária e Abastecimento. Coordenação Geral de Agrotóxicos e Afins/DFIA/DAS. **Agrofit.** Disponível em: <http://agrofit.agricultura.gov.br/agrofit_cons/principal_agrofit_cons> Acesso em: 07 Ago 2016.

ALMEIDA, R. P.; STOUTHAMER, R. ITS-2 sequences-based identification of *Trichogramma* species in South America. **Brazilian Journal of Biology**, São Carlos, v. 75 n. 4, p. 974-982, 2015.

ALTIERI, M. A. **Agroecologia**: bases científicas para uma agricultura sustentável. Guaíba: Agropecuária, 2002. 592 p.

ALTIERI, M. A.; SILVA, E. N.; NICHOLLS, C. I. **O papel da biodiversidade no manejo de pragas**. Ribeirão Preto: Holos, 2003. 223 p.

AMES, C.; TURNER, B.; DANIEL, B. The use of mitochondrial cytochrome oxidase I gene (COI) to differentiate two UK blowfly species *Calliphora vicina* and *Calliphora vomitoria*. **Forensic Science International,** Lausanne, v. 164, n. 2-3, p. 179-182, 2006.

AMORIM, D. de S. **Fundamentos de Sistemática Filogenética**. 4. ed. Ribeirão Preto: Holos, 2011. 156 p.

AUSTIN, A. D.; JOHNSON, N. F.; DOWTON. M. Systematics, Evolution, and Biology of Scelionid and Platygastrid wasps. **Annual Review of Entomology**, Palo Alto, v. 50, p. 553–582. 2005.

BAMBARADENIYA, C. N. B.; EDIRISINGHE, J. P. Composition, structure and dynamics of arthropod communities in a rice agro-ecosystem. **Ceylon Journal of Science (Biological Science.)** Colombo, Sri Lanka, v. 37, n. 1, p. 23-48, 2008.

BARRIGOSSI, J. A. F.; LANNA, A. C.; FERREIRA, E. **Agrotóxicos no Cultivo do Arroz no Brasil:** análise do consumo e medidas para reduzir o impacto ambiental negativo. Santo Antônio de Goiás: Dezembro, 2004. (Circular Técnica, 67).

BEGON, M.; TOWNSEND, C. R.; HARPER, J. L. **Ecologia de indivíduos e ecossistemas.** Tradução Adriano Sanches. 4. ed. Porto Alegre: Artmed, 2007. 740 p.

BORGES, M. et al. Kairomonal effect of walking traces from *Euschistus heros* (Heteroptera: Pentatomidae) on two strains of *Telenomus podisi* (Hymenoptera: Scelionidae). **Physiological Entomology**, Oxford, v. 28, n. 4, p. 349–355, 2003.

BRASIL. Lei nº10831, de 23 de dezembro de 2003. Dispõe sobre a agricultura orgânica e dá outras providências. **Diário Oficial da União**, Brasília, 24 dez. 2003. Disponível em: <http://www.planalto.gov.br/ccivil_03/leis/2003/L10.831.htm>. Acesso em: 26 Dez. 2012.

BRASIL. Decreto nº 6.323, de 27 de dezembro de 2007. Regulamenta a Lei nº 10.831, de 23 de dezembro de 2003, que dispõe sobre a agricultura orgânica, e dá outras providências.

Presidência da República, Casa Civil, Subchefia para Assuntos Jurídicos, **Diário Oficial da União**, Brasília, 27 dez. 2007. Disponível em: <http://www.planalto.gov.br/ccivil_03/_ato2007-2010/2007/Decreto/D6323.htm>. Acesso em: 26 dez. 2012.

BRASIL. Lei nº 11.947, de 16 de junho de 2009. Dispõe sobre o atendimento da alimentação escolar e do Programa Dinheiro Direto na Escola aos alunos da educação básica; altera as Leis n$^{\underline{os}}$ 10.880, de 9 de junho de 2004, 11.273, de 6 de fevereiro de 2006, 11.507, de 20 de julho de 2007; revoga dispositivos da Medida Provisória n$^{\underline{o}}$ 2.178-36, de 24 de agosto de 2001, e a Lei n$^{\underline{o}}$ 8.913, de 12 de julho de 1994; e dá outras providências. Presidência da República, Casa Civil, Subchefia para Assuntos Jurídicos, **Diário Oficial da União,** Brasília, 16 jun. 2009. Seção 1. Disponível em: <http://www.planalto.gov.br/ccivil_03/_ato2007 2010/2009/lei/l11947.htm>. Acesso em: 26 Dez. 2012.

BROUWER, C. **Irrigation Water Management**: Irrigation Methods. International Institute for Land Reclamation and Improvement. Wageningen: FAO Land and Water Development Division, 1988. 140 p.

CHAPLIN-KRAMER, R. et al. A meta-analysis of crop pest and natural enemy response to landscape complexity. **Ecology Letters**, Oxford, v. 14, n. 9, p. 922–932, 2011.

CHAY-HERNANDEZ, D. A. et al. Ichneumonoidea (Hymenoptera) Community Diversity in an Agricultural Environment in the State of Yucatan, Mexico. **Environmental Entomology**, College Park, v. 35, n. 5, p. 1286-1297, 2006.

CHEN, H. et al. Molecular phylogeny and biogeography of lac insects (Hemiptera: Kerriidae) inferred from nuclear and mitochondrial gene sequences. **Molecular Biology Reports**, Dordrecht, v. 40, n. 10, p. 5943–5952, 2013.

CHRONI, A. et al. Molecular species delimitation in the genus *Eumerus* (Diptera: Syrphidae). **Bulletin of Entomological Research**, London, v. 107, n. 1, p. 126-138, 2016.

CINGOLANI, M. F. et al. Multiparasitism of *Piezodorus guildinii* eggs by *Telenomus podisi* and *Trissolcus urichi.* **BioControl,** Dordrecht, v. 58, n. 1, p. 37–44, 2013.

CLARKE, A. R.; WALTER, G. H. “Strains” and the classical biological control of insect pests. **Canadian Journal of Zoology**, Ottawa, v. 73, n. 10, p. 1777-1790, 1995.

CONAB. Companhia Nacional de Abastecimento. **Levantamento das Safras**. 2016. Disponível em: <http://www.conab.gov.br/>. Acesso em: 10 out. 2016.

CORRÊA-FERREIRA, B. S.; MOSCARDI, F. Biological control of soybean stinkbugs by inoculative releases of *Trissolcus basalis*. **Entomologia Experimentalis et Applicata**, Dordrecht, v. 79, n. 1, p. 1- 7. 1996**.**

CORRÊA-FERREIRA, B. S. *Trissolcus basalis* para o controle de percevejos da soja. In: PARRA, J.R.P.; et al. (Ed.). **Controle biológico no Brasil**: parasitoides e predadores. São Paulo: Manole,2002. p. 449- 476.

CORRÊA-FERREIRA, B. S. **Soja Orgânica**: Alternativas para o Manejo dos Insetos-Pragas. Londrina: Embrapa-CNPSo, 2003. 83 p.

COUNCE, P. A. et al. A Unform, Objective, and Adaptive System for Expressing Rice Development. **Crop Science**, Madison, v. 40, p. 436-443, 2000.

DA SILVA, G. DE S. **Diversidade de himenópteros parasitoides em uma área de arroz com produção orgânica e em uma unidade de conservação, na Área de Proteção Ambiental Banhado Grande, Viamão, RS**. 2013. 86 f. Dissertação (Mestrado) - Programa de Pós-Graduação em Fitotecnia, Faculdade de Agronomia, Universidade Federal de Rio Grande do Sul, Porto Alegre, 2013.

DA SILVA, G. DE S.; JAHNKE, S. M.; FERREIRA, M. L. G. Hymenoptera parasitoids in protected area of Atlantic Forest biomes and organic rice field: 2 compared assemblages. **Revista Colombiana de Entomologia,** Bogotá, v. 42, n. 2, p. 110-117, 2016.

DEROCLES, S. A. P. et al. Molecular analysis reveals high compartmentalization in aphid–primary parasitoid networks and low parasitoid sharing between crop and noncrop habitats. **Molecular Ecology**, Oxford, v. 23, n. 15, p. 3900–3911, 2014.

DEROCLES, S. A. P. et al. Are generalist Aphidiinae (Hym. Braconidae) mostly cryptic species complexes? **Systematic Entomology**, Oxford, v. 41, n. 2, p. 379–391, 2016.

DOMICIANO, N. L. **Arroz Irrigado**: práticas de cultivo. Londrina: Instituto Agronômico do Paraná, 2001. 197 p.

EHLER, L. E. An evaluation of some natural enemies of *Nezara viridula* in northern California. **Biocontrol**, Dordrecht, v. 47, n. 3, p. 309-325, 2002.

EMBRAPA CLIMA TEMPERADO. **Cultivo do Arroz irrigado no Brasil.** Importância Econômica, Agrícola e Alimentar do Arroz. Nov. 2005. (Sistemas de Produção nº 3, versão eletrônica). Disponível em: <http://sistemasdeproducao.cnptia.embrapa.br/FontesHTML/Arroz/ArrozIrrigadoBrasil/cap01.htm#mundo>. Acesso em: 29 ago. 2011.

EMBRAPA AGROBIOLOGIA. **Cultivo do Café Orgânico**. Fundamentos da agricultura orgânica. Seropédica: Embrapa Agrobiologia, 2004. 95 p. (Embrapa Agrobiologia. Sistemas de Produção, 2). Disponível em: <https://docsagencia.cnptia.embrapa.br/agriculturaOrganica/SDP02_04.pdf >. Acesso em: 26 dez. 2014.

EMBRAPA ARROZ E FEIJÃO. **Informações Técnicas para a Cultura do Arroz Irrigado no Estado do Tocantins. Manejo dos principais insetos fitófagos**. 136 p. (Documentos / Embrapa Arroz e Feijão, 218). Disponível em: <https://www.agencia.cnptia.embrapa.br/Repositorio/doc_218_000g0qz6ick02wx5ok026zxpg0lrxr0k.pdf>. Acesso em: 05 set. 2016.

EMBRAPA CLIMA TEMPERADO. **Cultivo de arroz irrigado orgânico no Rio Grande do Sul.** 161 p. (Sistemas de produção / Embrapa Clima Temperado, 17). Disponível em: <http://ainfo.cnptia.embrapa.br/digital/bitstream/item/46576/1/sistema-17.pdf >. Acesso em: 01 set. 2016.

FAILLA, A. J. Morphological identification and COI barcodes of adult flies help determine species identities of chironomid larvae (Diptera, Chironomidae). **Bulletin of Entomological Research**, London, v. 106, n. 1, p. 34–46, 2016.

FAVETTI, B. M. et al. Egg parasitoids of *Edessa meditabunda* (Fabricius) (Pentatomidae) in lettuce crop. **Revista Brasileira de Entomologia, São** Paulo, v. 57, n. 2, p. 236–237, 2013.

FENOGLIO, M. S. et al. Beneficial insects in urban environments: Parasitism rates increase in large and less isolated plant patches via enhanced parasitoid species richness. **Biological Conservation**, Barking, v. 164, p. 82–89, 2013.

FERREIRA, M. L. G. et al. Diversidad de insectos depredadores en área orizícola orgánica y de conservación, en Viamão, RS. Brasil. **Revista Colombiana de Entomologia, Bogotá**, v. 40, n. 1, p. 120-128, 2014.

FRITZ, L.L. et al. Agroecossistemas orizícolas irrigados: insetos-praga, inimigos naturais e manejo integrado. **Oecologia brasiliensis**, Rio de Janeiro, v. 12, n. 4, p. 720-732, 2008.

FRITZ, L. L. **Biodiversidade de artrópodes em agroecossistemas orizícolas do Rio Grande do Sul, Brasil**. 2009. 119 f. Dissertação (Mestrado) - Programa de Pós-Graduação em Biologia: Diversidade e Manejo de Vida Silvestre, Universidade do Vale do Rio dos Sinos, São Leopoldo, 2009.

FUTUYMA, D. J. **Evolução, Ciência e Sociedade**. [São Paulo]: Sociedade Brasileira de Genética, 2002.

GALLO, D. et al. **Entomologia Agrícola**. Piracicaba: FEALQ, 2002. 920 p.

GARIEPY, T. D. et al. Parasitoids, predators and PCR: the use of diagnostic molecular markers in biological control of Arthropods. **Journal of Applied Entomology**, Berlin, v. 131, n. 4, p. 225–240, 2007.

GARIEPY, T. D.; HAYE, T.; ZHANG, J. A molecular diagnostic tool for the preliminary assessment of host–parasitoid associations in biological control programmes for a new invasive pest. **Molecular Ecology**, Oxford, v. 23, n. 15, p. 3912-24, 2014.

GATES, M. W. et al. Review of parasitoid wasps and flies (Hymenoptera, Diptera) associated with Limacodidae (Lepidoptera) in North America, with a key to genera. **Proceedings of the Entomological Society of Washington**, Washington, v. 114, n. 1, p. 24–110, 2012.

GLIESSMAN, S. R. **Agroecologia**: processos ecológicos em agricultura sustentável. 2. ed. Porto Alegre: Editora da UFRGS, 2001. 653 p.

GNANAKUMAR, M. et al. Diversity of Hymenopteran Egg Parasitoids in Organic and Conventional Paddy Ecosystems. **Tropical Agricultural Research**, Peradeniya, v. 23, n. 4, p. 300–308, 2012.

GODFRAY, H. C. J. **Parasitoids**: behavioral and evolutionary ecology. Princeton: Princeton University Press, 1994. 463 p.

GOMES, A. S.; MAGALHÃES-JUNIOR, A. M. **Arroz irrigado no Sul do Brasil**. Brasília: Embrapa Informações Tecnológica, 2004. 900 p.

GONDIM, D. M. C. et al. **Manual de identificação das pragas, doenças, deficiências minerais e injúrias do algodoeiro do Brasil**. 3. ed. Cascavel: Codetec/CIRAD, 2011. 120 p. (Boletim Técnico, 33).

GULLAN, P. J.; CRANSTON, P. S. **Os Insetos:** um resumo de entomologia. 3. ed. São Paulo: Roca Ltda, 2008. 440 p.

GULLAN, P. J.; CRANSTON, P. S. **The insects**: An outline of entomology. 4th ed. Oxford: Wiley- Blackwell, 2010. 565 p.

GURR, G. M. et al. Parasitoids f Asian rice planthopper (Hemiptera: Delphacidae) pests and prospects for enhancing biological control by ecological engineering. **Annals of Applied Biology,** Warwick, v. 158, n. 2, p. 149-176, 2011.

GURR, G. M.; WRATTEN, S. D.; SNYDER, W. E. **Biodiversity and Insect Pests**: Key Issue for Sustainable Management. Oxford: John Wiley & Sons Ltda, 2012.

HADDAD, N. M. et al. Contrasting effects of plant richness and composition on insect communities: a field experiment. **The American Naturalist**, Chicago, v. 158, n. 1, p. 17–35, 2001

HADDAD, N. M. et al. Plant diversity and the stability of foodwebs. **Ecology Letters**, Oxford, v. 14, n. 1, p. 42–46, 2011.

HANSON, P. E.; GAULD, I. D. **Hymenoptera de la Región Neotropical.** Gainesville: The American Entomological Institute, 2006. 994 p. v. 77.

HEINRICHS, E. A.; BARRION, A. T. **Rice-Feeding Insects and Selected Natural Enemies in West Africa**: biology, ecology, identification. Manila: International Rice Research Institute, 2004. 242 p.

HERATY, J. M. Molecular systematics, Chalcidoidea and biological control. In: EHLER, L.E.; SIORZA, R.; MATEILLE, T. (Ed.). **Genetics, Evolution and Biological Control**. London: CAB International, 2004. p. 39–71.

HOOK, T. V. The conservation challenge in agriculture and the role of entomologists. **Florida Entomologist**, Gainsville, v. 77, n. 1, p. 42-73, 1994.

HYMENOPTERA ONLINE (HOL). Disponível em: <http://hol.osu.edu.>. Acesso em: 19 nov. 2016.

IBGE. **Censo Agropecuário**. Rio de Janeiro: IBGE, 2006. 146 p. Disponível em: <http://www.ibge.gov.br/home/estatística/economia/agropecuária/censoagro/2006/agropecuário.pdf>. Acesso em: 27 nov. 2009.

IBGE. **Sidra.** Levantamento Sistemático da Produção Agrícola (LSPA). 2016. Disponível em: <http://www.sidra.ibge.gov.br/bda/prevsaf/default.asp?t=2&z=t&o=26&u1=1&u2=1&u3=34&u4=34>. Acesso em: 10 out. 2016.

IDALGO, T. D. N. et al. Parasitismo de ovos de *Tibraca limbativentris* Stål (Hemiptera: Pentatomidae) em lavoura de arroz irrigado, Eldorado do Sul, RS **Arquivos do Instituto Biológico**, São Paulo, v. 80, n. 4, p. 453-456, 2013.

ISLAM, Z. et al. **Invertebrates in rice production systems**: status and trends. Commission on Genetics Resources for food and agriculture. [S.l.: s.n.], 2012. (Background study paper, 62).

JERVIS, A.; KIDD, N. A. C. The Dynamic Significance of Host-Feeding by Insect Parasitoids: What Modellers ought to Consider Mark. **Oikos,** Copenhagen, v. 62, n. 1, p. 97-99, 1991.

JOHNSON, N. F. Catalog of world Proctotrupoidea excluding Platygastridae. **Memoirs of the American Entomological Institute,** Gainesville, v. 51, n. 1p. 825, 1992.

JOHNSON, N. F. A collaborative, integrated and electronic future for taxonomy. **Invertebrate Systematics**, Melbourne, v. 25, n. 5, p. 471-475, 2011.

JONSSON, M. et al. Agricultural intensification drives landscapecontext effects on host-parasitoid interactions in agroecosystems. **Journal of Applied Ecology**, Oxford, v. 49, n. 3, p. 706–714, 2012.

JONSSON, M. et al. Experimental evidence that the effectiveness of conservation biological control depends on landscape complexity. **Journal of Applied Ecology**, Oxford, v. 52, n. 5, p. 1274–1282, 2015.

JUSTI, S. A.; GALVÃO, C.; SCHRAGO, C. G. Geological Changes of the Americas and their Influence on the Diversification of the Neotropical Kissing Bugs (Hemiptera: Reduviidae: Triatominae). **PLOS Neglected Tropical Diseases**, San Francisco, v. 10, n. 4, 2016.

KAILA, L.; STAHLS, G. DNA barcodes: evaluating the potential of COI to differentiate closely related species of *Elachista* (Lepidoptera: Gelechioidea: Elachistidae) from Australia. **Zootaxa**, Auckland, v. 1170, p. 1-26, 2006.

KATIYAR, S. K. et al. Biodiversity of Asian rice gall midge (*Orseolia oryzae* Wood Mason) from five countries examined by AFLP analysis. **Genome,** Ottawa, v. 43, n. 2, p. 322–332, 2000.

KENYON, S. G. et al. Uncovering Cryptic Parasitoid Diversity in *Horismenus* (Chalcidoidea, Eulophidae). **PLoS ONE**, San Francisco, v. 10, n. 9, 2015.

KHULLAR, N.; SINGH, D.; JHA, C. K. Short *COI* marker: A valuable tool for identification and phylogenetic analysis of 6 forensically important blow fly species from India. **Journal of Entomology and Zoology Studies**, Delhi, v. 4, n. 3, p. 27-31, 2016.

KOZLOV, M. A. Supergeneric groupings of Proctotrupoidea (Hymenoptera). **Entomologicheskoye Obozreniye**, Moscow, v. 49, p. 203–226, 1970.

KOZLOV, M. A.; KONONOVA, S. V. **Telenominae of the Fauna of the USSR.** Nauka: Leningrad, 1983.

KRAUSS, J.; GALLENBERGER, I.; STEFFAN-DEWENTER, I. Decreased functional diversity and biological pest control in conventional compared to organic crop fields. **PLoS One**, San Francisco, v. 6, n. e19520, 2011.

LAUMANN, R. A. et al. Comparative biology and functional response of *Trissolcus* spp. (Hymenoptera: Scelionidae) and implications for stink bugs (Hemiptera: Pentatomidae) biological control. **Biological Control**, Orlando, v. 44, p. 32- 41, 2008.

LETOURNEAU, D. K.; ALLEN, S. G. B.; STIREMAN III, J. O. Perennial habitat fragments, parasitoid diversity and parasitism in ephemeral crops. **Journal of Applied Ecology**, Berlin, v. 49, n. 6, p. 1405–1416, 2012.

LIERE, H. et al. Trophic cascades in agricultural landscapes: indirect effects of landscape composition on crop yield. **Ecological Applications**, Tempe, Ariz., v. 25, n. 3, p. 652–661, 2015**.**

LUNA, M. G.; DESNEUX, N.; SCHNEIDER, M. Encapsulation and Self Superparasitism of *Pseudapanteles dignus* (Muesebeck) (Hymenoptera: Braconidae), a Parasitoid of *Tuta absoluta* (Meyrick) (Lepidoptera: Gelechiidae). **PLoS ONE**, San Francisco, v. 11, n. 10, p. 1-10, 2016.

MACIEL, A. A. S. et al. Parasitismo de Ovos de *Tibraca limbativentris* Stal (Hemiptera: Pentatomidae) na Cultura do Arroz no Maranhão. **Neotropical Entomology**, Londrina, v. 36, n. 4, p. 616-618, 2007.

MAPONDERA, T. S. et al. Identification and molecular phylogenetics of the cryptic species of the *Gonipterus scutellatus* complex (Coleoptera: Curculionidae: Gonipterini). **Australian Journal of Entomology**, Canberra, v. 51, v. 3, p. 175-188, 2012.

MARGOSIAN, M. L. et al. Connectivity of the american agricultural landscape: assessing the national risk of crop pest and disease spread. **BioScience**, Oxford, v. 59, n. 2, p. 141–151, 2009.

MARINO, P. C.; LANDIS, D. A.; HAWKINS, B. A. Conserving parasitoid assemblages of North American pest Lepidoptera: Does biological control by native parasitoids depend on landscape complexity? **Biological Control**, Orlando, v. 37, n. 2, p. 173–185, 2006.

MARTINS, J. F. S. et al. **Situação do Manejo integrado de Insetos-praga na Cultura do Arroz no Brasil.** Pelotas: Embrapa Clima Temperado, 2009. 40 p. (Embrapa Clima Temperado. Documentos, 290).

MASNER, L. The classification and interrelationships of Thoronini (Hymenoptera: Proctotrupoidea, Scelionidae). **The Canadian Entomologist**, Ottawa, v. 104, n. 6, p. 833–849, 1972.

MASNER, L. Revisionary notes and keys to world genera of Scelionidae (Hymenoptera: Proctotrupoidea). **Memoirs of the Entomological Society of Canada**, Ottawa, v. 108, n. 97, p. 1–87, 1976.

MASNER, L.; HUGGERT, L. Revision of the world species of Aradophagini (Hymenoptera: Scelionidae). **The Canadian Entomologist**, Ottawa, v. 111, n. 10, p. 1089–1100, 1979.

MERCKX, T.; PEREIRA, H. M. Reshaping agri-environmental subsidies: from marginal farming to large-scale rewilding. **Basic and Applied Ecology,** Jena, v. 16, n. 2, p. 95–103, 2014.

MONTI, M. M.; NAPPO, A. G.; GIORGINI, M. Molecular characterization of closely related species in the parasitic genus *Encarsia* (Hymenoptera: Aphelinidae) based on the mitochondrial cytochrome oxidase subunit I gene. **Bulletin of Entomological Research**, London, v. 95, n. 5, p. 401-408, 2005.

NEMEC, K. T. et al. Responses of predatory invertebrates to seeding density and plantspecies richness in experimental tallgrass prairie restorations. **Agriculture, Ecosystems and Environment**, Amsterdam, v. 183, p. 11-20, 2014.

NORRIS, R. F.; CASWELL-CHEN, E. P.; KOGAN, M. **Concepts in Integrated Pest Management.** New Jersey: Prentice Hall, 2003. 586 p.

OGAH, E. O. et al. Effect of Abiotic Factors on the Incidence of African Rice Gall Midge, *Orseolia oryzivora* and its Parasitism by *Platygaster diplosisae* and *Aprostocetus procerae*. **Journal of Biology, Agriculture and Healthcare**, Hong Kong, v. 2, n. 8, p. 60-65, 2012.

OMOTO, C.; GUEDES, R. N. C. **Resistência de Pragas a Pesticidas**: Princípios e Práticas. Petrolina: IRAC-BR, 2000. 26 p.

ONODY, H. C. **Estudo da fauna de Hymenoptera parasióides associados a hortas orgânicas e da utilização de extratos vegetais no controle de *Plutella xylostella* (Lepidoptera, Plutellidae).** 2009. 127 f. Tese (Doutorado) - Programa de Pós-Graduação em ecologia e recursos naturais, Universidade Federal de São Carlos, São Carlos, 2009.

PACHECO, D. J. P.; CORRÊA-FERREIRA, B. S. Parasitismo de *Telenomus podisi* Ashmead (Hymenoptera: Scelionidae) em populações de percevejos pragas da soja. **Anais da Sociedade Entomológica do Brasil**, Londrina, v. 29, n. 2, p. 295-302, 2000.

PEREIRA, J. A.; MORAIS, O. P.; CASTRO, E. M. Melhoramento genético do arroz de sequeiro no Nordeste do Brasil. In: QUEIRÓZ, M. A.; GOEDERT, C. O.; RAMOS, S. R. R. (Ed.). **Recursos genéticos e melhoramento de plantas para o nordeste brasileiro**. Petrolina-PE: EMBRAPA Semi árido/ Brasília-DF: EMBRAPA Recursos genéticos e biotecnologia, 1999. Disponível em: < http://www.cpatsa.embrapa.br/catalogo/livrorg/arrozsequeiro.pdf >. Acesso em: 30 jan. 2015.

POLASZEK, A.; RAJMOHANA, K. Taxonomy of the Egg Parasitoids of Rice Black Bug, *Scotinophara* spp. In: JOSHI, R.C.; A.T. BARRION, A.T.; L.S. SEBASTIAN, L.S. (Ed.). **Rice black bugs**: taxonomy, ecology, and management of invasive species. Science Cityof Muñoz, Nueva Ecija: Philippine Rice Research Institute, 2007. p. 351 -360.

PURNOMO, H.; WRIGHT, D. J. Multiple Release of Two Different Hymenoptera Parasitoid of Leafminer Fly, Synergy or Competition. **Agriculture and Agricultural Science Procedia**, Amsterdam, v. 9, p. 64–71, 2016.

PYWELL, R. F. et al. Ecological restoration on farmland can drive beneficial functional responses in plant and invertebrate communities. **Agriculture, Ecosystems and Environment**, Amsterdam, v. 140, n. 1-2, p. 62–67, 2011.

RAHIMI, S. et al. Evaluation of COI and ITS2 sequences ability to distinguish *Lysiphlebus fabarum* and *Lysiphlebus confusus* (Hymenoptera: Aphidiidae). **Journal of Entomological Society of Iran**, Tihrān, v. 31, n. 2, p. 53-66, 2012.

RAJMOHANA, K.; NISHA, M. S. *Telenomus oryzae* (Hymenoptera: Platygastridae), a new egg parasitoid of the rice black bug, Scotinophara (Heteroptera: Pentatomidae) from India. **HALTERES**, Patiala, v. 4, p. 79-86, 2013.

RIFFEL, C. T**. Levantamento e aspectos biológicos de espécies parasitoides de posturas do percevejo-do-colmo-do arroz no estado de Santa Catarina**. 2007. 73 f. Dissertação (Mestrado) - Centro de Ciências Agroveterinárias, UDESC - Universidade do Estado de Santa Catarina, Lages, 2007.

RODRIGUES, G. et al. **Avaliação de Impacto Ambiental da Inovação Tecnológica Agropecuária:** AMBITEC-AGRO. Jaguariúna: Embrapa Meio Ambiente, 2003. 95 p. (Documentos, 34).

RONQUE, M. U. V. et al. Three ways to distinguish species: using behavioural, ecological, and molecular data to tell apart two closely related ants, *Camponotus renggeri* and *Camponotus rufipes* (Hymenoptera: Formicidae). **Zoological Journal of the Linnean Society**, London, v. 176, n. 1, p. 170–181, 2015.

ROOT, R. Organization of a plant-arthropod association in simple and diverse habitats: the fauna of collards (*Brassica oleracea*). **Ecological monographs**, Durham, v. 43, n. 1, p. 95–124, 1973.

SACCAGGI, D. L.; KRUGER, K.; PIETERSEN, G. A multiplex PCR assay for the simultaneous identification of three mealybug species (Hemiptera: Pesudococcidae). **Bulletin of Entomological Research**, London, v. 98, n. 1, p. 27-33, 2008.

SALAZAR CAVEIRO, E. **Inseticidas e acaricidas**: toxicologia: receituário agronômico. 4.ed. Pelotas: UFPel, 1998. 645 p.

SANTOS, R. S. S. dos. Levantamento populacional de percevejos e da incidência de parasitóides de ovos em cultivos orgânicos de soja. **Pesquisa Agropecuária Gaúcha**, Porto Alegre, v. 14, n. 1, p. 41-46. 2008.

SCHLICK-STEINER, B. C. et al. Integrative Taxonomy: A Multisource Approach to Exploring Biodiversity. **The Annual Review of Entomology,** Palo Alto, v. 55, p. 421–38, 2010.

SETTLE, W. H. et al. Managing tropical rice pests through conservation of generalist natural enemies and alternative prey. **Ecology**, Brooklyn, v. 77, n. 7, p. 1975-1988, 1996.

SIMÕES-PIRES, P. R.; JAHNKE.; S. M.; REDAELLI, L. R. Influence of the vegetation management of the leeves in irrigated rice organic in diversity of Hymenoptera parasitoids. **Brazilian Journal of Biology**, São Carlos, v. 76, n. 3, p. 774-781, 2016.

STAHLS, G.; SAVOLAINEN, E. MtDNA COI barcodes reveal cryptic diversity in the *Baetis vernus* group (Ephemeroptera: Baetidae). **Molecular Phylogenetics and Evolution**, San Diego, v. 46, n. 1, p. 82-87, 2008.

SOSBAI., 2014. **Arroz irrigado**: recomendações técnicas da pesquisa para o Sul do Brasil. In: REUNIÃO TÉCNICA DA CULTURA DO ARROZ IRRIGADO, 30., 06 a 08 de agosto de 2014, Bento Goncalves, RS. [**Anais**...] Bento Gonçalves: [s.n.], 2014. 192 p.

SUNNUCKS, P. Efficient genetic markers for population biology. **Trends in Ecology & Evolution**, Amsterdam, v. 15, n. 5, p. 199-203, 2000.

TAEKUL, C. et al. Molecular phylogeny of telenomine egg parasitoids (Hymenoptera: Platygastridae s.l.: Telenominae): evolution of host shifts and implications for classification. **Systematic Entomology,** Oxford, v. 39, n. 1, p. 24–35, 2014.

THIES, C. et al. The relationship between agricultural intensification and biological control: experimental tests across Europe. **Ecological Applications**, Washington, v. 21, n. 6, p. 2187–2196, 2011.

TSCHARNTKE, T. et al. Landscape perspectives on agricultural intensification and biodiversity – ecosystem service management. **Ecology Letters**, Oxford, v. 8, n. 8, p. 857–874, 2005.

TSCHARNTKE, T. et al. Landscape moderation of biodiversity patterns and processes-eight hypotheses. **Biological Reviews**, Cambridge, v. 87, n. 3, p. 661–685, 2012.

UESUGI, R. et al. Molecular evidence for multiple phylogenetic groups within two species of invasive spiny whiteflies and their parasitoid wasp. **Bulletin of Entomological Research**, London, v. 106, n. 3, p. 328–340, 2016.

VAN DRIESCHE, R. G.; BELLOWS JR., T. S. **Biological Control.** London: Champman & Hall, 1996. 593 p.

VENKATESAN, T. et al. Differentiation of some indigenous and exotic trichogrammatids (Hymenoptera: Trichogrammatidae) from India based on Internal transcribed spacer-2 and cytochrome oxidase-I markers and their phylogenetic relationship. **Biological control,** Orlando, v. 101, p. 130–137, 2016.

VLUG, H. J. **Catalogue of the Platygastridae (Platygastroidea) of the world (Insecta: Hymenoptera).** Hymenopterorum Catalogus, v. 19. Amsterdam: SPB Academic Pub, 1995. 168 p.

WÄGELE, H. et al. The taxonomist - an endangered race. A practical proposal for its survival. **Frontiers in Zoology**, London, v. 8, n. 25, 2011.

WAQUIL, J. M.; VIANA, P. A.; CRUZ, I. **Cultivo do Milho**. Manejo integrado de pragas (MIP). Embrapa Milho e Sorgo. Dez, 2006. (Sistemas de Produção, ISSN 1679-012. Versão eletrônica - 2ª ed.).

WAY, M. J.; JAVIER, G. JR. Approaches to a relevant understanding of biodiversity for tropical irrigated rice pest management. In: IMPACT SYMPOSIUM ON EXPLOITING BIODIVERSITY FOR SUSTAINABLE PEST MANAGEMENT, 2000, Kunming, China. **Proceedings**… The Philippines: International Rice Research Institute, 2001. p. 3-14.

XIE, W. et al. Pyrosequencing the *Bemisia tabaci* Transcriptome Reveals a Highly Diverse Bacterial Community and a Robust System for Insecticide Resistance. **PLOS One**, San Francisco, v. 7, n. 4, p. 427-433, 2012.

YARA, K. Relationship between the introduced and indigenous parasitoids *Torymus sinensis* and *T. beneficus* (Hymenoptera: Torymidae) as inferred from mt-DNA (COI) sequences. **Applied Entomology and Zoology**, Tokyo, v. 39, n. 3, p. 427- 433, 2004.

YOUNG, I.; COLEMAN, A. W. The advantages of the ITS2 region of the nuclear rDNA cistron for analysis of phylogenetic relationships of insects: a *Drosophila* example. **Molecular Phylogenetics and Evolution**, San Diego, v. 30, n. 1, p. 236-242, 2004.

ZEPEDA-PAULO, F. et al. Signatures of genetic bottleneck and differentiation after the introduction of an exotic parasitoid for classical biological control. **Biological Invasions**, Dordrecht, v. 18, n. 2, p. 565-581, 2016.

ZHAO, Z. H. et al. Habitat heterogeneity stabilizes the spatial and temporal interactions between cereal aphids and parasitic wasps. **Basic and Applied Ecology**, Jena, v. 16, n. 6, p. 510–518, 2015.

ZILLI, J. B.; BARCELLOS, G. M. Padrão de variação estacional dos preços do arroz no estado do Rio Grande do Sul. **Informações Econômicas**, São Paulo, v. 36, p. 7-17, 2006.

3 ARTIGO 1

Riparian forest fragments in rice fields under different management: differences by hymenopteran parasitoids diversity *

* Artigo formatado conforme as normas da Journal Agricultural and Forest Entomology.

Riparian forest fragments in rice fields under different management: differences by hymenopteran parasitoids diversity

Da Silva, G. de.[1,2]; Jahnke, S. M[2] and Johnson, N. F[3]
[1]giss_rs@yahoo.com.br (corresponding author); [2]UFRGS, Phytosanitary Department, Av. Bento Gonçalves, 7712 - CEP 91540-000 - Porto Alegre - RS - Brasil; [3]The Ohio State University, 1315 Kinnear Road, Columbus - Ohio - USA.

Running title: Riparian forest fragments in rice fields

Abstract

1 Hymenopteran parasitoids are important biological control agents in agroecosystems, and their diversity can be increased with habitat heterogeneity.

2 The objective of this study was to evaluate the contribution of the presence of fragments of natural vegetation (riparian forest) near rice-growing areas and the influence of different management of the crop (organic and conventional) on the diversity of families of hymenopteran parasitoids, through distance gradients, and on the vegetative and reproductive stages of the crop.

3 The work took place in two irrigated rice crops, one with organic management (O.M.) and another with conventional management (C.M.), in the municipality of Nova Santa Rita, RS, Brazil, during the 2013/2014 and 2014/2015 seasons. The parasitoids were collected with Malaise trap arranged at different distances in relation to the riparian forest surrounding the rice crop in both places. Specimens were collected twice a month from seeding until the rice harvest. Average abundance between management, distances and rice development were compared.

4 The most abundant families were Platygastridae, Mymaridae, Encyrtidae, Eulophidae and Trichogrammatidae, their abundances changing over the seasons. Parasitoid average abundance was significantly higher on O.M. only in the second season.

5 There was a negative correlation between distance from native vegetation and parasitoid abundance in C.M. areas.

6 The phenological stages of rice affected the composition of the parasitoid assemblage on site.

Keywords Conservative biological control, parasitoids, rice, habitat heterogeneity, native vegetation.

[1]Gisele de Souza da Silva, UFRGS, Departamento de Fitossanidade, Faculdade de Agronomia, Av. Bento Gonçalves, 7712 - CEP 91540-000 - Porto Alegre - RS – Brasil**.**

Introduction

Rice (*Oryza sativa* L.) is the second most cultivated cereal in the world, occupying an area of 158 million hectares and corresponds to 29% of the grains used for human consumption (SOSBAI, 2014). The rice plant can be damaged by various phytophagous groups (EMBRAPA CLIMA TEMPERADO, 2009). To control these pests, chemical insecticides based on neonicotinoid, diamide, pyrethroid and carbamate are mainly used in conventional management (AGROFIT, 2016). On the other hand, the production of organic rice is based on eliminating the use of synthetic chemical inputs such as fertilizers, pesticides and growth regulators, and promoting alternative technologies such as mechanization, tillage and fertilization in the management of pests, including weeds, diseases and insects (EMBRAPA CLIMA TEMPERADO, 2009). In addition, the maintenance of permanent preservation areas and the mitigation of anthropogenic pressure on natural and modified ecosystems are environmental aspects that organic rice production systems seek to obtain certification (EMBRAPA CLIMA TEMPERADO, 2009).

Parasitoids are one of the most important groups of biological control agents in the control of pest populations in agricultural systems, both by the natural occurrence of the species in the environment and by their use in classic biological control programs (Hanson & Gauld, 2006). Parasitoid diversity associated with different cultivation systems is determined by environmental, biological, and management factors (Chay-Hernandez *et al*., 2006). In large monocultures, the diversity can be suppressed by pesticides, simplification of vegetation, and other environmental disturbances (Altieri, 2003). In less disturbed agricultural ecosystems, the diversity of these agents appears to be related to the diversity of crops, weeds, ground cover and native vegetation next to cultivated systems (Liere *et al*., 2015).

In this context, this study evaluated the contribution of the presence of fragments of Riparian forest near irrigated rice areas and the influence of different management of the crop (organic and conventional) diversity of families of Hymenopteran parasitoids, through distance gradients in rice production systems, and on the vegetative and reproductive stages of plants.

Material and Methods

Study area

The study was carried out in the municipality of Nova Santa Rita, RS, in the metropolitan region of Porto Alegre in the phytogeographic region of the Jacuí watershed, during the 2013/2014 and 2014/2015 seasons. In this region many native trees species occur such as ‘maricá’ (*Mimosa bimucronata* (DC) Kuntze), ‘corticeira’ (*Erythrina falcata* Benth.), fig tree (*Ficus luschnatiana* (Miq.) Miq.), ‘angico’ (*Parapiptadenia rigida* (Benth.) Brenan), Surinam cherry (*Eugenia uniflora* L.), ‘branquilho’ (*Sebastiania commersoniana* (Baill.) L.B. Sm. & Downs), ‘açoita-cavalo’ (*Luehea divaricata* Mart. & Zucc.) and many others (COPTEC, 2010). The vegetation near to irrigated rice area is a riparian forest.

Organic rice crop. The irrigated rice area with organic management (O.M.) is part of the Capela Settlement (Landless Rural Workers Movement Settlement) in Nova Santa Rita. It has a total area of 2169.37 hectares (INCRA, 2007), of which 580 ha belong to COOPAN (Agricultural Production Cooperative Nova Santa Rita). Of these, 220 continuous hectares are allocated for organic rice, which is certified by the Ecological Market Institute (Instituto de Mercado Ecológico - IMO) (Lanner, 2011). In the settlement an area of 273.52 hectares (13.68% of the total) is designated as a permanent preserve (native forest). In the organic rice field, the levees are maintained with wild vegetation.

In the first season (December, 2013 to April, 2014), five points were defined for the installation of traps centered around this coordinate 29° 47’ 16.62” S and 51° 21’ 00.91” W. In the area where the traps were installed, it was used the pre-germinated planting system with cultivar EPAGRI 108 which has late cycle, lodging resistance and indirect iron toxicity. It is moderately resistant to panicle blast and stands out for its excellent grain quality and high reproductive potential (SOSBAI, 2014).

In view of the difficult access to the area in the first year, another five points were defined in the second year (November, 2014 to March, 2015) for the installation of traps centered around this coordinate 29° 46’ 48.90” S, 51° 21’ 48.38” W. The management of the area was the same as in the first year.

In the first year, the traps were separated 100 m from each other, in a distance gradient starting from inside the forest to the middle of the crop, in a straight line (Figure 1). In the second year, the distance was extended to 200 m. Each trap site was named by the location of the Malaise trap, being O5 (Spot 5 - inside the forest), O4 (Spot 4), O3 (Spot 3), O2 (Spot 2), O1 (Spot 1 - greatest distance from forest) (Figure 1).

Conventional rice crop. The irrigated rice area with conventional management (C.M.) is located in the ‘Gaúcha’ Farm, a private property of 300 hectares approximately 2.5 km distant from the organic management area and bordered to the southwest by the Caí River. Tillage is the planting system, and the cultivar used was IRGA428, which has a medium cycle, high productivity potential, tolerance to herbicides, tolerance to toxicity from excess iron, is moderately susceptible to leaf blast and susceptible to blast on panicle (SOSBAI, 2014).

The conventional management adopted by the producer follows the IRGA recommendations, with the use of chemical inputs and application of agricultural pesticides according to the annual manuals for rice management (SOSBAI, 2012). For insect collecting, the experimental design was the same of the organic management area (Figure 1), with the points set between 29° 46’ 16.65” S and 51° 21’ 43.31” W, the same in both seasons. In the conventional rice field, the levees are maintained without wild vegetation by chemicals spraying.

As in the O.M. area, in the first year (December, 2013 to April, 2014), the traps were from each other by 100 m, in a straight line, and in the second (November, 2014 to March, 2015), the distance was extended to 200 m. Each spot also was named by the location of Malaise trap, being C5 (Spot 5), C4 (Spot 4), C3 (Spot 3), C2 (Spot 2), C1 (Spot 1).

In the first season regulators insecticides were used (buprofezin and benzylurea) and in the second season were used non-selective (neurotoxic) insecticides (neonicotinoids and pyrethroids) (farmer personal communication Mr. Denis).

Hymenoptera sampling and identification

For capturing the parasitoids, five Malaise traps (Townes, 1972) were placed in the levees of each area (Figure 1). The collection method was improved, by putting PVC pipes cut in half to simulate a “gutter” in each trap, so that insects which have not reached the collecting head could drop in the “gutter” (containing water and detergent) located on the ground, comprising the entire length of the trap (Gullan & Cranston, 2008).

Samples were collected every two weeks during two rice seasons, 2013/2014 and 2014/2015, from seeding to harvest. The traps remained mounted in the points for 24 hours and thereafter the vials with the collected insects were taken. These were transferred to 70% alcohol, labeled with the collection site, and transported to the Laboratory for Biological Control of Insects (CBLAB) of UFRGS. In the laboratory, the samples were screened using a stereomicroscope Nikon SMZ445, selecting the hymenopteran parasitoids. The identification of families followed the classification adopted by Goulet & Huber (1993) and Sharkey (2007). The specimens were deposited in the Education Collection at Laboratory for Biological Control of Insects (CBLAB) of UFRGS in Agronomy University.

Statistical analyses

Considering the extent of the two areas and their characteristics, it was impossible to make replicas of the samples, so that evaluations were considered exploratory.

The average capture of parasitoids was compared between areas and between crop development periods, considering the four traps installed inside the crop as pseudoreplicas, through Shapiro-Wilk normality test and analysis of variance (Kruskal-Wallis test).

The rice developmental stages were identified according to Counce *et al*. (2000). Here we named indicated O.V or C.V (organic or conventional vegetative stage of rice) and O.R or C.R (organic or conventional reproductive stage of rice), respectively.

For evaluating the abundance of parasitoids over the gradient of distance from traps in relation to the native vegetation, Pearson correlation test was used through the BioEstat 5.3 program (Ayres *et al*., 2011).

Correspondence Analysis (CA) and Bray-Curtis Cluster Analysis plots were built through the PAST program (Hammer *et al*., 2001). Plots are constructed with the main components of lines and columns allowing visualization of the relationship between groups, where the proximity of the points relating to the line (parasitoid families) and column (spots and rice stages) indicates association and the distance indicates repulsion (Greenacre & Hastie, 1987). The Cluster Analysis groups the data in a dendogram, in which the level of similarity (or dissimilarity) is indicated on the vertical scale. On the horizontal axis, the sample elements are reported in a convenient order for the clustering (Mingoti, 2005).

Results

Faunistic data

First Season (2013-2014). In the first season, 1,104 individuals were collected in the rice area with organic management (O.M.), distributed in 21 families; and 860 individuals in the rice area with conventional management (C.M.), distributed in 18 families.

The total average of captured individuals/trap/day was 30.3 ± 5.42 in the O.M. area and 22.3 ± 7.32 in the C.M. area in the first season, with no significant difference (H = 2.08, df = 1, p = 0.1).

Regarding the development stage of rice within each area, in the O.M., the total capture average was significantly lower in the vegetative stage (24.45 ± 6.96) than in the reproductive (40.1 ± 4.74) (H = 5.33; df = 1; p = 0.02). In the C.M., however, there was no significant difference between the vegetative (16.8 ± 10.58) and reproductive stages (29.31 ± 4.06) (H = 3; df = 1; p = 0.08).

Considering the same development stage between areas, in the reproductive stage, a significantly higher average of captures (40.08 ± 4.74) in the O.M. was observed than in the C.M. over this period (29.31 ± 4.06) (H = 5.33; df = 1; p = 0.02). In the vegetative period, there was no significant difference between the O.M. (24.45 ± 6.95) and the C.M. (16.8 ± 10.58) (H = 1.33; df = 1; p = 0.24).

The most abundant families in the O.M. were Platygastridae and Mymaridae. In the C.M., the most abundant were Encyrtidae and Platygastridae (Table 1).

Second Season (2014-2015). In the second year's season, 1,064 parasitoids were collected in the O.M. area, divided into 19 families, and 389 individuals were collected in the C.M. area, distributed in 16 families.

The total average of trapped individuals in the O.M. area was 25.38 ± 6.85 trap/day, significantly higher than in the C.M. area (8.41 ± 3.40) (H = 5.33; df = 1; p = 0.02).

In a comparison of developmental stages within each area, the vegetative stage (17.33 ± 3.12) averaged significantly lower captures than the reproductive (29.41 ± 9.36) in the O.M. (H = 4.08; df = 1; p = 0.04), however, there was no difference between stages in the C.M. (vegetative: 10.06 ± 2.46 and reproductive: 6.7 ± 4.59) (H = 2.08; df = 1; p = 0.14).

Comparison of trap catches in the same development stage of rice between areas showed that in the vegetative stage the O.M. averaged significantly higher captures (17.33 ± 3.12) than the C.M. (10.06 ± 2.46) (H = 5.33; df = 1; p = 0.02), as well as in the reproductive stage, with significantly higher captures in the O.M. (29.41 ± 22.54) than in the C.M. (6.7 ± 2.28) (H = 7.04; df = 1; p = 0.008).

The most abundant families in the O.M. were Eulophidae, Mymaridae and Platygastridae. In the C.M., they were Platygastridae, Mymaridae and Trichogrammatidae (Table 1).

Riparian forest effects on parasitoid abundance in rice fields

In the first season, there was a negative correlation between the number of insects captured and the distance from the forest area for the C.M. (Figure 2A), and 92% of this variation may be explained by the distance in relation to the forest next to the planting area. In the O.M., however, this correlation could not be detected.

In the second season, there was no correlation between the distance gradients in any of the areas (Figure 2B), even with increased distance between traps.

Association between sampling spots, management, phenological stages and parasitoid families

Through correspondence analysis, the points were represented on two axes, indicating that the association between lines (parasitoids families) and columns (spots and rice stages) is two-dimensional, 60% of the relationship being explained in these two axes in season 1 and 69% of the relationship being explained in season 2.

In the first season, samples are mixed on both sides of the x and y axes, showing similar composition between areas (Figure 3). Nonetheless, some families had higher relationships with certain sampling points and phenological periods of the plant. Mymaridae and Trichogrammatidae, showing confluence with the sampling areas of O.M. and both the phenological stages and with the sampling areas of C.M. and its vegetative phenological stage. On the other hand, Encyrtidae showed greater relationship with sampling areas of the C.M. in the reproductive stage. The points Organic 1 (O1) and Organic 2 (O2) were the most dissimilar from the others.

In the second season (Figure 4), the samples of the organic and conventional managements showed dissimilarities between them, since they appear to be distributed on distinct sides, with different families relating to each area. Nevertheless, the most abundant families exhibit similarities to each other along the y axis. Platygastridae, Mymaridade and Encyrtidae appear to be in the same position on the y axis, showing to have the same importance for the composition to which they belong, being Platygastridae, on the right side, related to

C.M.; Eulophidae, on the left side, related to O.M.; and Mymaridae, in center, related to both areas.

Differences between the composition and abundance of families are perceived between the two sampling years for the areas through cluster analysis. The high cophenetic correlation in the two years (0.94 and 0.85, respectively) confirms the adjustment of data to the Bray-Curtis model (Figures 5 and 6).

In the first season, there was similarity between the different sampled points, regardless of the adopted management. Considering a cut-off point in 60%, only the organic management points (O1 and O2) were dissimilar from the others (Figure 5).

In season 2, two clusters are distinct, clearly pointing out similarities between the managements used (Figure 6). All points within the crop of the organic management area showed about 75% similarity. The points relating to the conventional management area showed similarity ranging from 60% to 70%. The lowest percentage of similarity (55%) was that of the organic 5 (O5), presenting itself as independent of the others.

Discussion

A comparison of the results between the two seasons (2013/2014 and 2014/2015) showed that in the O.M. area the abundance of individuals was similar despite the distance between sampling points. However, in the C.M., there was much less abundance in the second season. This may be due to the use of non-selective (neurotoxic) insecticides (neonicotinoids and pyrethroids) applied to the crop in 2014/2015, different from the first season, when growth regulators insecticides were used (buprofezin and benzylurea) (farmer personal communication Mr. Denis). This difference occurs because the products that act on chitin synthesis are either ecdysteroid receptor agonists or are generally more selective to natural enemies and other beneficial insects such as bees, because they act only on immature stages, having a smaller impact on adults (Bastos *et al*., 2006).

Differences in the abundance of parasitoids between crop development stages in the O.M. suggests that in this system the phenological stage of the crop influences the presence of natural enemies. These are possibly related to the hosts, since different pests are related to the distinct development stages of rice. Hence, the higher abundance of Mymaridae, Platygastridae and Eulophidae was expected, given that these families are associated with rice pests in many countries, as Delphacidae in Asia (Gurr *et al*., 2011), Pentatomidae (Maciel *et al*., 2007; Idalgo *et al*., 2013) and Lepidoptera in Brazil (EMBRAPA ARROZ E FEIJÃO, 2008).

In Brazil, Platygastridae, mainly the genera *Telenomus* and *Trissolcus*, are important biological control agents of Pentatomidae in rice crops (Maciel *et al*., 2007; Riffel *et al*., 2010). Their high abundance within the rice fields is associated with resource availability in the crop, therefore, available hosts. Pentatomidae are common both in the vegetative and reproductive stages of rice (SOSBAI, 2014), accounting for the great number of Platygastridae in both development stages of the crop.

Other highlighted families were Eulophidae (O.M.) and Encyrtidae (C.M.). For rice, Gurr *et al*. (2011) listed *Aprostocetus formosanus* (Timberlake, 1921) (Eulophidae) as parasitoids of Delphacidae in the Philippines, Vietnam, Malaysia and Thailand. Other authors have also reported individuals of Eulophidae in rice crops (Nacro *et al*., 1997; Williams *et al*., 1999; Bayegan *et al*., 2015), and Gumovsky *et al*. (2006) described a new species of Eulophidae, genus *Closterocerus*, parasitoid of *Dicladispa armigera* (Olivier, 1808) (Coleoptera: Chrysomelidae), a major rice pest in Southeast Asia and Australasia. In rice cultivation in Rio

Grande do Sul, Eulophidae also was the most abundant parasitoid family and the phytophagous registered were Curculionidae, Pentatomidae, Delphacidae and Cicadellidae (Fritz *et al*., 2011).

The second most abundant family in C.M., Encyrtidae has records of hosts of rice pests in various regions of the world. For example, Kraker *et al*. (1999) noted the parasitism of *Cnaphalocrocis medinalis* (Guenée, 1854) and *Marasmia* spp. (Lepidoptera: Pyralidae), rice pests increasing in abundance since 1960 in many Asian countries, by *Copidosomopsis nacoleiae* (Eady, 1960) (Encyrtidae) (Khan *et al*., 1988; Dale, 1994). *Ooencyrtus nezarae* Ishii, 1928 and *Xenoencyrtus niger* Riek, 1962, both species introduced in the Neotropics, are parasitoids of Pentatomidae eggs (Hanson & Gauld, 2006). In Brazil, *Ooencyrtus submetallicus* (Howard, 1886) was recorded as a parasitoid of *T. limbativentris* eggs in rice crops in Maranhão (Maciel *et al*., 2007).

Mymaridae, a family among the most abundant in both seasons, especially in the vegetative stage in the first season, and reproductive stage in the second one, is known to attack, mostly, Auchenorrhyncha (Hemiptera). Nonetheless, this parasitoid family also attacks Coleoptera, Orthoptera and other Hemiptera (Hanson & Gauld, 2006). These small parasitoids of eggs are recorded attacking leafhoppers, which are rice pests, of Delphacidae present in Asia and Oceania (India, China, Japan, Malaysia, Singapore, Vietnam, Sri Lanka, the Philippines, Thailand, Korea, Taiwan, Indonesia) (Gurr *et al*., 2011). In Brazil, species like *Tagosodes orizicolus* (Muir, 1926) (Hemiptera: Delphacidae), *Graphocephala* sp. and *Estianus* sp. (Hemiptera: Cicadellidae) are recorded in rice (Didonet *et al*., 2001). The presence of Mymaridae species can be related with leafhopper on the crop.

In the C.M., the phenological stage did not influence the parasitoid composition. Other factors such as the habitat heterogeneity or the crop management may have induced the characteristics of the assembly, which has also been recorded in other studies (Tanaka *et al*., 2000; Gurr *et al*., 2011; Zaho *et al.*, 2015).

The clear correlation between the distance from the native forest to the crop in relation to the abundance of parasitoids observed in the C.M. in the first season suggests the importance of this area in the presence of these natural enemies in the crop. The role of these forest fragments in maintaining the richness and abundance of parasitoids has been described by Corbett and Plant (1993), Romeis *et al*. (2005) and Da Silva *et al*. (2016). In the second season, this correlation was not observed due to the large decrease in the abundance of parasitoids, already discussed with relation to the management.

In the organic management area, however, the correlation between the gradient of distance was not demonstrated in any of the seasons. This can possibly be explained by the fact that it is an organic management area, not receiving chemical inputs, which negatively affects the presence of parasitoids, even in central areas of the monoculture. Moreover, as in the O.M. there is wild levees vegetation, including the presence of flowering species that increase the richness of parasitoids (Simões-Pires *et al*., 2016). Therefore, the abundance may not be so dependent on the presence or proximity of the preserved area. Levees can serve as corridors extending the distances traveled by parasitoids (Gurr *et al*., 2011).

In Asia, it is found that even with the harmful effects of insecticides, the level of parasitism in Delphacidae increases when the habitat is manipulated ecologically, emphasizing that adjacent areas can support and allow the persistence of parasitoids even if the rice crops are not present (Gurr *et al*., 2011). The levees also allow a greater richness of phytophages, both of pest species attacking the culture in the vegetative period and of those with no agricultural importance and that can serve as alternative hosts for the parasitoids also found there. This was demonstrated in a study with a *Zizania caduciflora* (Turcz.) (Canadian rice) planting, surrounding a rice crop in China (Yu, 2001). This study shows that this surrounding vegetation supports *Saccharosydne procerus* Matsumura, 1924, a Delphacidae that does not develop in rice (Yu, 2001). However, this leafhopper is parasitized by *Anagrus optabilis* (Perkins, 1905) which is also an important parasitoid of *Nilaparvata lugens* (Stål, 1854) a rice pest (Zheng *et al*., 1999).

The levees have been neglected as a major reserve of plants and resources for natural enemies. Nectar can maximize the longevity and fecundity of parasitoids, and pollen may allow other natural enemies during the period of prey shortage (Zheng *et al*., 2003b). Pest insects and natural enemies were more abundant and rich in the Philippines in rice fields surrounded by vegetated levees than in rice fields without this feature (Marcos *et al*., 2001; Gurr *et al*., 2011). Furthermore, females of *Copidosoma koehleri* Blanchard, 1940 (Encyrtidae) with access to honey were more enduring and parasitized significantly more eggs of *Phthorimaea operculella* (Zeller, 1873) (Lepidoptera: Gelechiidae) than the wasps with access only to water (Baggen & Gurr, 1998). This may be an important advantage, as parasitoids in large monocultures need to forage over large distances, leading to high costs in terms of time and energy (Powell, 1986), affecting their distribution within the crop and consequently the distribution and population of pests (Baggen & Burr, 1998).

We emphasize that this study aimed to evaluate the differences in the complexity of habitats not only with regard to the abundance, but also taking into account other aspects such as richness and distribution of species and individuals. This was also reported by Edwards & Wratten (1981), for whom more complex communities provided a broader spectrum of ecological niches and sustained larger and more diverse populations of predators and parasitoids than the simpler ones. Thus, through correspondence analysis, one can see the relationship between sampling points, rice development stages and management systems, with regard to the diversity and abundance of families of parasitoid Hymenoptera. In addition, cluster analysis combines the samples according to the similarities between them.

In the first season, generally samples are mixed on both sides of the axes, showing a relationship between them. This may be because, although with different managements, both areas are inserted in the same ecosystem with similar adjacent vegetation (COPTEC, 2010) and these environments with native vegetation can increase arthropod diversity, in general, and parasitoid diversity, more specifically, in the cultivated areas (Ferreira *et al*., 2014; Da Silva *et al*., 2016). Notwithstanding, in the second season samples of the organic and conventional managements showed dissimilarities as they appear to be distributed on different sides in the correspondence analysis chart. This may be related to a non-restrictive treatment of chemical inputs in the C.M., leading to a compositional difference between the organic management and the conventional management areas. The similarity of the points in the areas, disassociating the managements, was expected, considering that the extensive use of insecticides affects not only the pests but also beneficial insects (Tanaka *et al*., 2000; Gangurde, 2007), which leads to differences in their composition.

In the first sampling year, the sampling point organic 2 (O2) had a similarity lower than 32% with other samples, being the point with greatest dissimilarity. This may be due to differences between the number of individuals being the point with the lowest abundance of platygastrids and trichogrammatids, besides has the greatest number of ceraphronids, which is the family with greater similarity to the O2. The sampling point O1 was also different from the others, but because of the composition of families, having more singletons (those species in which only one individual has been collected) and doubletons (only two individuals collected) than the others (6). The presence of rare species in an assembly provides higher diversity indices (Magurran, 2011) and may be responsible for the dissimilarities identified.

In season 2, the lowest percentage of similarity (55%) was from the sampling point O5, gathering together the cluster of samples of the conventional management. The point O5 had a low number of mymarids and eulophids in relation to the other points and greater abundance of families Ichneumonidae, Bethylidae, Ceraphronidae and Eupelmidae. This similarity can also be seen through the correspondence analysis, which shows similarity between the point and these families. The association of a family to a certain point should be linked to the use of resources by the group, both of hosts (Plecasa *et al*., 2014) and alternative resources like nectar, pollen or refuge (Gurr *et al*., 2011). Thus, an assessment of the phytophagous fauna present in the area could give an indication of what contributes to the composition of species of parasitoids. This aspect, however, was not evaluated in this study.

Other points showed similar compositions, and families Platygastridae, Mymaridae, Braconidae, Figitidae, Encyrtidae, Trichogrammatidae and Pteromalidae were the ones which contributed most to this in the first season. In the second, the families that contributed most were Platygastridae, Mymaridae, Eulophidae, Encyrtidae, Braconidae and Figitidae.

The differences showed in this research regard to distance gradients of the native riparian forest area in relation to rice crop highlight the importance of this refuge for parasitoids diversity, mainly in the conventional management area, where there is no levees vegetation. In the organic management, it influences is not seen, probably due to levees vegetation presence, that can provide refuge, shelter and ecological corridors for natural enemies. The chemical insecticides in rice crops can change parasitoids diversity through changes of selective inseticides to natural enemies (growth regulators) to non-selective (neurotoxic). The phenological stage of rice influences the parasitoids diversity on site and it must be related to different hosts, oftentimes phytophagous insects, in each crop development.

Acknowledgments

The authors would like to thank COOPAN (Agricultural Production Cooperative Nova Santa Rita), Mr. Denis rice farmer and CNPq for financial support.

References

AGROFIT (2016) *Ministério da Agricultura, Pecuária e Abastecimento – Coordenação Geral de Agrotóxicos e Afins/DFIA/DAS* [WWW document]. URL http://agrofit.agricultura.gov.br/agrofit_cons/principal_agrofit_cons [accessed on 07 August 2016].

Altieri, M. A., Silva, E. N. & Nicholls, C. I. (2003) *O papel da biodiversidade no manejo de pragas.* Ribeirão Preto: Holos.

Ayres, M., Ayres, M. J., Ayres, D.L. & Santos, A.A.S. dos. (2011) *BioEstat 5.3: Aplicações Estatísticas nas Áreas das Ciências Biológicas e Médicas*. 5ª ed. Belém-PA: Publicações Avulsas do Mamirauá.

Baggen, L.R. & Gurr, G.M. (1998) The Influence of Food on *Copidosoma koehleri* (Hymenoptera: Encyrtidae), and the Use of Flowering Plants as a Habitat Management Tool to Enhance Biological Control of Potato Moth, *Phthorimaea operculella* (Lepidoptera: Gelechiidae). *Biological Control*, **11**, 9–17.

Bastos, C.S., Almeida, R.P. & Suinaga, F. (2006) Selectivity of pesticides used on cotton (*Gossypium hirsutum*) to *Trichogramma pretiosum* reared on two laboratory-reared hosts. *Pest Management Science*, Sussex, **62**, 91-98.

Bayegan, Z.A., Hossein, H. & Mohammad, R. Z. (2015) Occurrence of eulophid wasps (Hymenoptera: Chalcidoidea, Eulophidae) in rice fields of eastern Guilan, Iran. *Journal Crop Protection*, **4**(2), 199-205.

Chay-hernandez, D. A., Delfín-gonzález, H. & Parra-tabla, V. (2006) Ichneumonoidea (Hymenoptera) Community Diversity in an Agricultural Environment in the State of Yucatan, Mexico. *Environmental Entomology*, College Park, **35**(5), 1286-1297.

COPTEC (2010) COOPERATIVA DE PRESTAÇÃO DE SERVIÇOS TÉCNICOS LTDA. *PRA - Plano de recuperação do assentamento capela.* Município de Nova Santa Rita, RS. Ministério do Desenvolvimento Agrário, INSTITUTO NACIONAL DE COLONIZAÇÃO E REFORMA AGRÁRIA – INCRA, Superintendência Regional do Rio Grande do Sul – SR-11, 150 p.

Corbett, A. & Plant, R.E. (1993) Role of Movement in the Response of Natural Enemies to Agroecosystem Diversification: A Theoretical Evaluation. *Environmental Entomology*, **22**(3), 519-531.

Counce, P., Keisling, T.C. & Mitchell, A.J. (2000) A uniform, objective, and adaptative system for expressing rice development. *Crop Science*, **40**(2), 436-443. http://dx.doi.org/10.2135/cropsci2000.402436x.

Dale, D. (1994) Insect pests of the rice plant – their biology and ecology. In: E.A. HEINRICHS, ed. *Biology and management of rice insects*. pp. 363–485, Wiley Eastern Ltda.

Da Silva, G. de S., Jahnke, S.M. & Ferreira, M.L.G. (2016) Hymenoptera parasitoids in protected area of Atlantic Forest biomes and organic rice field: 2 compared assemblages. *Revista Colombiana de Entomologia,* **42**(2), 110-117.

Didonet, J., Didonet, A.P.P., Erasmo, E.L. & Santos, G.R. (2001) Incidência e densidade populacional de pragas e inimigos naturais em arroz de terras altas, em Gurupi-TO. *Bioscience Journal,* **17**, 67-76.

Edwards, P. J. & Wratten, S. D. (1981) *Ecologia das interações entre insetos e plantas*. vol. 27, São Paulo: EDUSP.

EMBRAPA ARROZ E FEIJÃO (2008) *Informações Técnicas para a Cultura do Arroz Irrigado no Estado do Tocantins. Manejo dos principais insetos fitófagos.* Documentos / Embrapa Arroz e Feijão, ISSN 1678-9644, 218, 136p [WWW document]. URL https://www.agencia.cnptia.embrapa.br/Repositorio/doc_218_000g0qz6ick02wx5ok026zxpg0lrxr0k.pdf [accessed on 05 September 2016].

EMBRAPA CLIMA TEMPERADO (2009) *Cultivo de arroz irrigado orgânico no Rio Grande do Sul.* (Sistemas de produção / Embrapa Clima Temperado, ISSN 1676-7683; 17), 161p. Editores técnicos, Maria LauraTurino Mattos, José Francisco da Silva Martins [WWW document]. URL http://ainfo.cnptia.embrapa.br/digital/bitstream/item/46576/1/sistema-17.pdf [accessed on 01 September 2016].

Fagundes, N.A. & Gastal, C.V. de S., 2008. Diagnóstico ambiental e delimitação de Áreas de Preservação Permanente em um assentamento rural. *Acta Scientiarum Biological Sciences*, Maringá, **30**(1), 29-38.

Ferreira, M. L. G., Jahnke, S.M., Morais, R.M. & Da silva, G.S. de. (2014) Diversidad de insectos depredadores en área orizícola orgánica y de conservación, en Viamão, RS. Brasil. *Revista Colombiana de Entomologia*, 40, 120-128.

Fritz, L. L., Heinrichs, E. A., Machado, V., Andreis, T.F., Pandolfo, M., Salles, S.M. de., Oliveira, J.V. de. & Fiuza, L.M. (2011) Diversity and abundance of arthropods in subtropical rice growing areas in the Brazilian south. *Biodiversity and Conservation*, **20**, 2211–2224.

Gangurde, S. (2007) Aboveground arthropod pest and predator diversity in irrigated rice (*Oryza sativa* L.) production systems of the Philippines. *Journal of Tropical Agriculture*, **45**, (1-2), 1-8.

Goulet, H. & Huber, J. T. (1993) *Hymenoptera of the World: an identification guide to families.* Ottawa: Agriculture Canada Publication.

Greenacre, M. & Hastie, T. (1987) The geometric interpretation of correspondence analysis. *Journal of the American Statistical Association*, **82**, 437-447.

Gullan, P. J. & Cranston, P. S. (2008) *Os Insetos:* um resumo de entomologia. 3. Ed. São Paulo: Roca Ltda.

Gumovsky, A., Polaszek, A., Murphy, S.T., Rabbi, M.F. & Zhu, C. D. (2006) *Closterocerus oryzamyntor* (Hymenoptera: Eulophidae: Entedoninae), a larval parasitoid of the rice hispa *Dicladispa armigera* in Bangladesh (Coleoptera: Chrysomelidae: Hispinae). *Zootaxa*, **1241**, 51–59.

Gurr, G.M., Liu, L., Read, D.M.Y., Catindig, J.L.A., Cheng, J.A., Lan, L.P. & Heong, K.L. (2011) Parasitoids of Asian rice planthopper (Hemiptera: Delphacidae) pests and prospects for enhancing biological control by ecological engineering. *Annals of Applied Biology*, **158**, 149-176. http://dx.doi.org/10.1111/j.1744-7348.2010. 00455.x

Hammer, O., Harper, D.A.T. & Ryan, P.D. (2001) PAST: paleontological statistics software package for education and data analysis. *Palaeontologia Electronica*, **4**(1), 1-9.

Hanson, P. E. & Gauld, I. D. (2006) *Hymenoptera de la Región Neotropical.* v. 77. Gainesville: The American Entomological Institute.

Idalgo, T.D.N., Sant'ana, J., Redaelli, L.R. & Pires, P.D.S. (2013) Parasitismo de ovos de *Tibraca limbativentris* Stål (Hemiptera: Pentatomidae) em lavoura de arroz irrigado, Eldorado do Sul, RS Arq. Inst. Biol. São Paulo, **80**(4), 453-456.

INCRA – INSTITUTO NACIONAL DE COLONIZAÇAÕ E REFORMA AGRÁRIA (2007) *Relatório Ambiental do Projeto de Assentamento Capela.* Porto Alegre: Incra.

Khan, Z.R., Barrion, A.T., Litsinger, J.A., Castilla, N.P. & Joshi, R.C. (1988) Mini review: a bibliography of rice leaffolders (Lepidoptera: Pyralidae). *Insect Science and its Applications*, **9**, 129–174.

Kraker, J., Van Huis, A., Heong, K.L., Van Lenteren, J.C. & Rabbinge, R. (1999) Population dynamics of rice leaffolders (Lepidoptera: Pyralidae) and their natural enemies in irrigated rice in the Philippines. *Bulletin of Entomological Research*, **89**, 411– 421.

Lanner, A. J. (2011) *A Cooperativa de produção agropecuária Nova Santa Rita Ltda (COOPAN) do Assentamento Capela, Nova Santa Rita (RS): questões da atividade suinícola*. Porto Alegre: Faculdade de Ciências Econômicas da UFRGS, 104 p. Trabalho de Conclusão do Curso de Graduação Tecnológica em Planejamento e Gestão para o Desenvolvimento Rural – PLAGEDER.

Liere, H., Kim, T.N., Werling, B.P., Meehan, T.D., Landis, D.A. & Gratton, C. (2015) Trophic cascades in agricultural landscapes: indirect effects of landscape composition on crop yield. *Ecological Applications*, **25** (3), 652–66.

Maciel, A. A. S., Lemos, R.N.S. de., Souza, J.R. de., Costa, V.A., Barrigossi, J.A.F. & Chagas, E.F. das. (2007) Parasitismo de Ovos de *Tibraca limbativentris* Stal (Hemiptera: Pentatomidae) na Cultura do Arroz no Maranhão. *Neotropical Entomology*, **36** (4), 616-618.

Magurran, A. E. (2011) *Medindo a diversidade biológica*. Editora UFPR.

Marcos, T.F., Flor, L.B., Velilla, A.R., Schoenly, K.G., Manalo, J. O., Ofilas, O.M., Teng, P.S., Ulep, J.R., Tinguil, M.B., Estoy, A.B., Cocson, L.G. & Obien, S.R. (2001) Relationships between pests and natural enemies in rainfed rice and associated crop and wild habitats in Ilocos Norte, Philippines. In: T.W. MEW, E. BORROMEO AND B. HARDY eds *Proceedings of the Impact Symposium on Exploiting Biodiversity for Sustainable Pest Management*, Kunming China, 21–23 August 2000. pp. 23–24. The Philippines: International Rice Research Institute.

Mingoti, S. A. (2005) Análise de dados através de métodos de estatística multivariada – uma abordagem aplicada. Belo Horizonte: Editora UFMG.

Nacro, S., Dakouo, D. & Heinrichs, E. A. (1997) Population dynamics, host plant damage and parasitism associated with the African rice gall midge in southern Burkina Faso. *Insect Science and its Application*, **16**, 251-257.

Powell, W. (1986) Enhancing parasitoid activity in crops. In: J. WAAGE and D. GREATHEAD, eds. *Insect Parasitoids*, pp. 319–340, London: Academic Press.

Plecasa, M., Gagi, V., Jankovic, M., Petrovic-Obradovic, O., Kavallieratos, N.G., Tomanovic, Z., Thies, C., Tscharntkee, T. & Cetkovic, A. (2014) Landscape composition and configuration influence cereal aphid–parasitoid–hyperparasitoid interactions and biological control differentially across years. *Agriculture, Ecosystems and Environment***,** **183**, 1–10.

Riffel, C.T., Prando, H.F. & Boff, M.I.C. (2010) Primeiro Relato de Ocorrência de *Telenomus podisi* (Ashmead) e *Trissolcus urichi* (Crawford) (Hymenoptera: Scelionidae) como Parasitoides de Ovos do Percevejo-do-Colmo-do-Arroz, *Tibraca limbativentris* (Stål) (Hemiptera: Pentatomidae), em Santa Catarina. *Neotropical Entomology*, **39** (3), 447-448.

Romeis, J., Babendreier, D., Wackers, F.L. & Shanower, T.G. (2005) Habitat and plant specifity of *Trichogramma* egg parasitoids – underlying mechanisms and implications. *Basic and Applied Ecology*, **6**, 215-236.

Sharkey, M.J. (2007) Phylogeny and Classification of Hymenoptera. *Zootaxa*, **1668**, 521–548.

Simões-Pires, P.R., Jahnke., S. M. & Redaelli, L. R. (2016) Influence of the vegetation management of the leeves in irrigated rice organic in diversity of Hymenoptera parasitoids. *Brazilian Journal Biology*. http://dx.doi.org/10.1590/1519-6984.06215

SOSBAI (2012) *Arroz irrigado: recomendações técnicas da pesquisa para o Sul do Brasil*. XXIX Reunião Técnica da Cultura do Arroz Irrigado, 01 a 03 de agosto de 2012, Gravatal, SC. - Itajaí.

SOSBAI (2014) *Arroz irrigado: recomendações técnicas da pesquisa para o Sul do Brasil.* XXX Reunião Técnica da Cultura do Arroz Irrigado, 06 a 08 de agosto de 2014, Bento Goncalves, RS.

Tanaka, K., Endo, S. & Kazano, H. (2000) Toxicity of insecticides to predators of rice planthoppers: Spiders, the mirid bug and the dryinid wasp. *Applied Entomology and Zoology*, **35**(1), 177-187.

Townes, H. (1972) A light-weight Malaise trap. *Entomological News*, Philadelphia, **83**(9), 239-247.

Williams, C. T., Okhidievbie, O., Harris, K. M. & Ukwungwu, M. N. (1999) The host range, annual cycle and parasitoids of the African rice gall midage *Orseoli oryzivora* (Diptera: Cecidomyiidae) in central and southeast Nigeria. *Bulletin of Entomological Research*, **89**, 589-597.

Zhao, Z.H., Hui, C., Li, Z.H. & Li, B. L. (2015) Habitat heterogeneity stabilizes the spatial and temporal interactions between cereal aphids and parasitic wasps. *Basic and Applied Ecology*, **16**, 510–518.

Zheng, X., Yu, X., Lu, Z. & Chen, J. (1999) Dispersal patterns of natural enemies of rice planthoppers between zizania and rice fields. *Acta Agriculturae Zhejiangensis*, **11**, 339–343.

Zheng, X., Yu, X., Lu, Z., Chen, J. & Xu, H. (2003b) Effects of different nutritional resources on the longevity and parasitic ability of egg parasitoid *Anagrus nilaparvatae. Chinese Journal of Applied Ecology*, **14,** 1751–1755.

Table 1. Hymenoptera parasitoids families sampled in the first (2013/2014) and second crop season (2014/2015) over vegetative stage (Veg) and reprodutive stage (Rep) of rice crop in organic management area (O.M.) and conventional management area (C.M.), Nova Santa Rita, RS.

	1° Crop Season						**2° Crop Season**					
	O.M.			**C.M.**			**O.M.**			**C.M.**		
Family	**Veg**	**Rep**	**Fr (%)**	**Veg**	**Rep**	**Fr (%)**	**Veg**	**Rep**	**Fr (%)**	**Veg**	**Rep**	**Fr (%)**
Platygastridae	131	137	24.2	81	94	20.3	59	120	16.8	60	55	29.5
Mymaridae	106	79	16.7	102	43	16.8	47	186	21.9	37	43	20.5
Eulophidae	49	81	11.8	12	15	3.1	58	212	25.4	17	10	6.9
Encyrtidae	54	67	10.9	27	182	24.2	12	50	5.8	15	18	8.5
Trichogrammatidae	79	54	12	56	78	15.5	14	38	4.9	21	29	12.8
Ichneumonidae	45	27	6.5	12	5	2	25	65	8.5	6	6	3.1
Ceraphronidae	16	11	2.4	18	50	7.9	8	13	2	7	6	3.3
Braconidae	21	28	4.4	16	20	4.2	16	36	4.9	20	7	6.9
Figitidae	19	11	2.7	13	0	1.5	9	20	2.7	8	3	2.8
Diapriidae	9	5	1.3	8	1	1	3	6	0.8	3	1	1
Bethylidae	16	3	1.7	2	1	0.3	7	5	1.1	4	2	1.5
Chalcididae	8	4	1.1	5	2	0.8	1	13	1.3	3	1	1
Eupelmidae	9	1	0.9	2	2	0.5	2	10	1.1	1	1	0.5
Pteromalidae	3	0	0.3	5	2	0.8	4	9	1.2	0	1	0.3
Aphelinidae	5	5	0.9	1	1	0.2	0	3	0.3	1	0	0.3
Chrysididae	4	1	0.5	0	0	0	1	2	0.3	0	0	0
Evaniidae	3	2	0.5	0	0	0	1	2	0.3	0	0	0
Signiphoridae	0	1	0.1	0	0	0	0	4	0.4	0	0	0
Dryinidae	2	0	0.2	1	0	0.1	0	3	0.3	0	0	0
Torymidae	3	0	0.3	0	0	0	0	0	0	0	0	0
Megaspilidae	0	0	0	1	1	0.2	0	0	0	0	0	0
Eurytomidae	3	2	0.5	1	0	0.1	0	0	0	0	0	0
Proctrotupidae	0	0	0	0	0	0	0	0	0	0	3	0.8
TOTAL	**585**	**519**	**100**	**363**	**497**	**100**	**267**	**797**	**100**	**203**	**186**	**100**

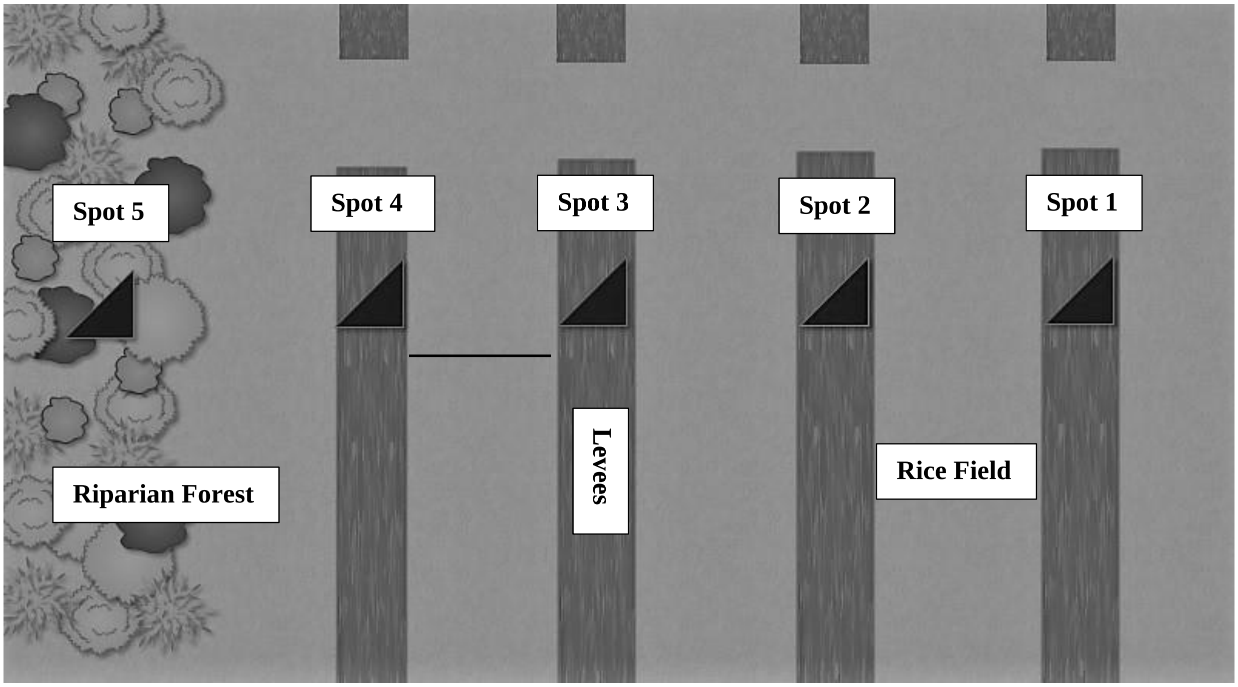


Figure 1. Layout showing Malaise traps (◢) position on rice field and riparian forest in Organic Management Area (O.M.) and Conventional Management Area (C.M.), in Nova Santa Rita, RS. (—) Distance between traps (100m first season; 200m second season).

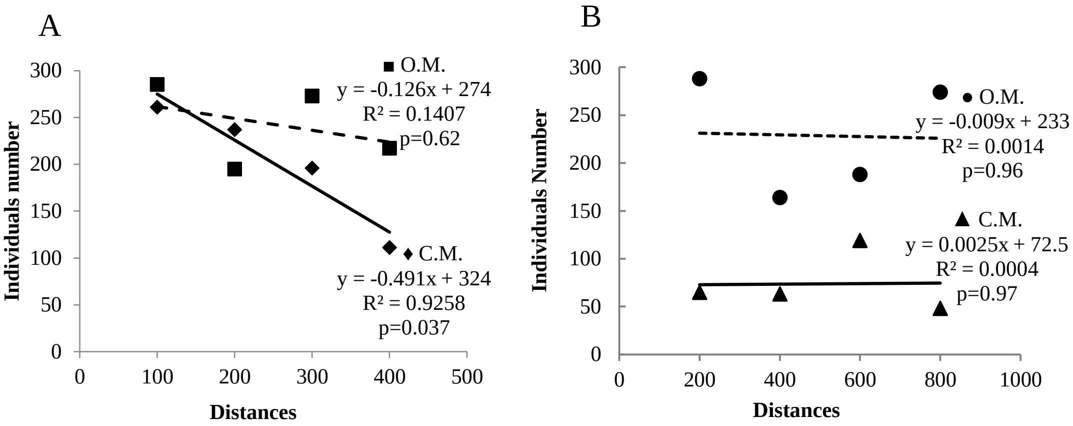


Figure 2. Correlation between samples spots with 0, 100m, 200m, 300m e 400m distances in first crop season (A) from riparian forest (O.M. $p > 0.05$ e C.M. $p < 0.05$. Pearson Test). Correlation between samples spots with 0, 200m, 400m, 600m e 800m distances in second crop season (B) from native vegetation (O.M. $p > 0.05$ e C.M. $p > 0.05$. Pearson Test).

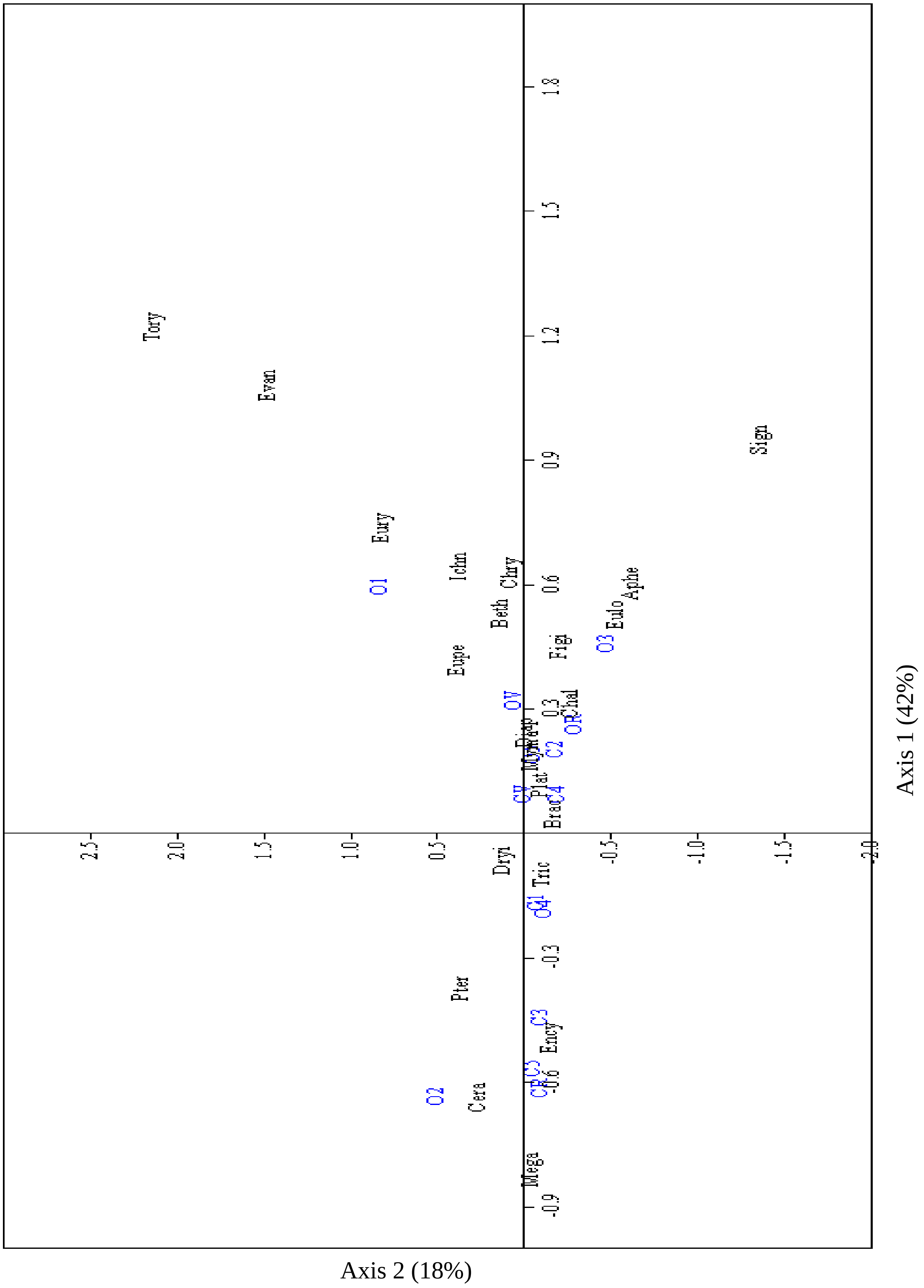


Figure 3. Correspondence Analyses. Relation between sample spot in each rice crop development stages (V= vegetative; R= reproductive) in each point of the areas with organic management (O) and conventional (C) and parasitoids families in the first season (2013/2014).

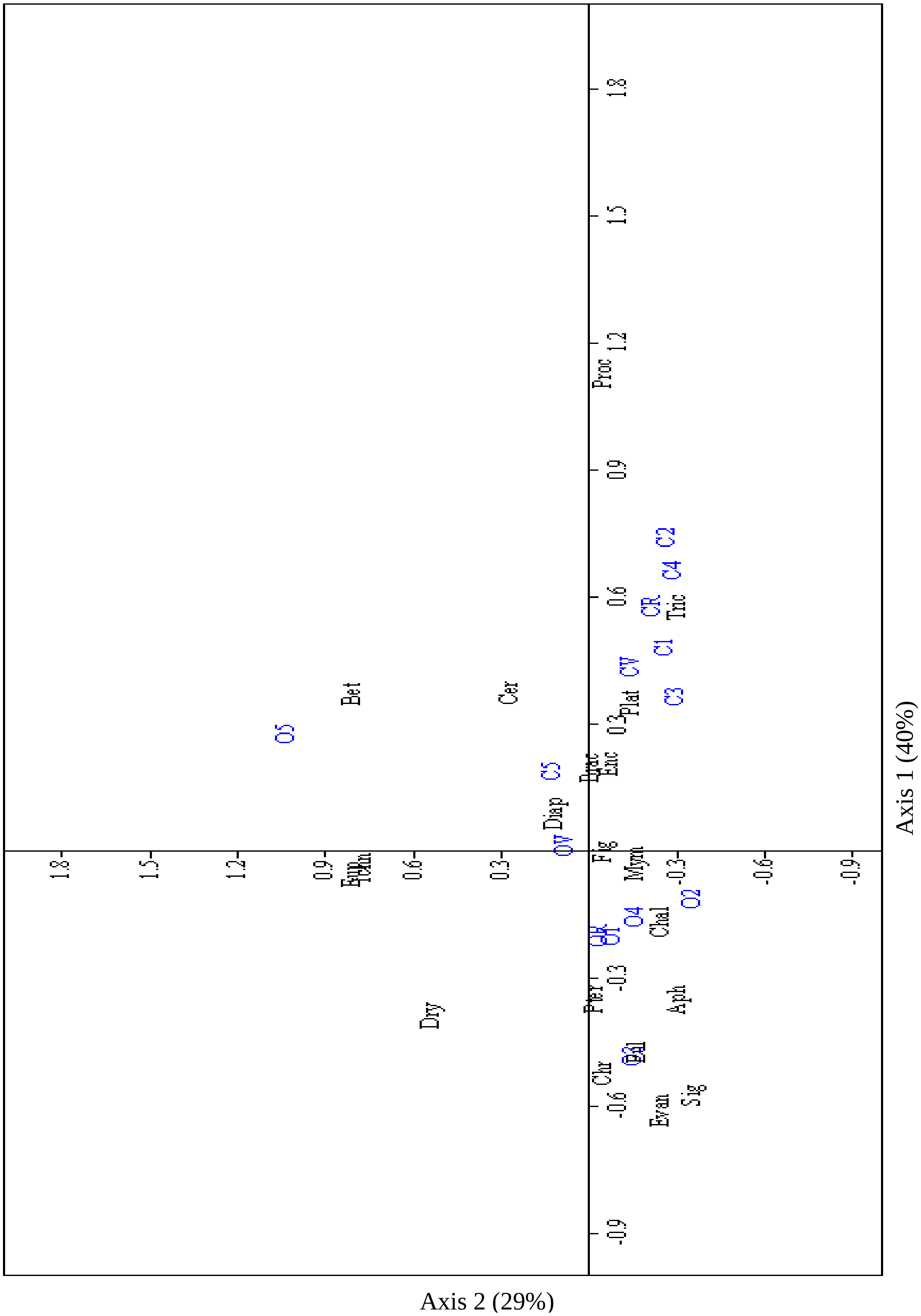


Figure 4. Correspondence Analyses. Relation between sample spot in each rice crop development stages (V= vegetative; R= reproductive) in each point of the areas with organic management (O) and conventional (C) and parasitoids families in the second season (2014/2015).

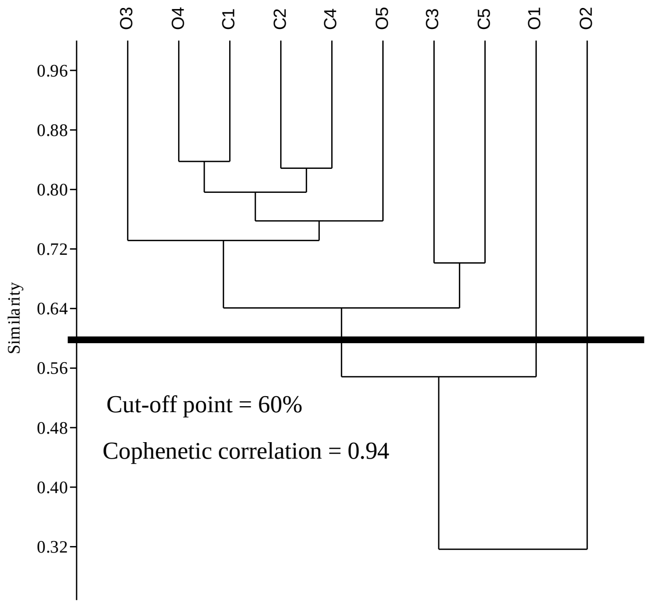


Figure 5. Cluster Analysis of similarity (Bray-Curtis Index). Relation between abundance distribution in each family and sample spot in both areas (O.M. and C.M.) in first season (2013/2014).

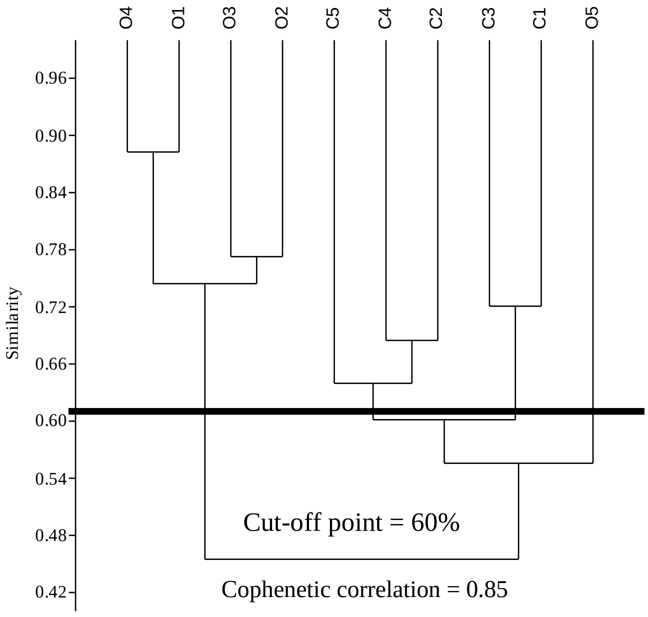


Figure 6. Cluster Analysis of similarity (Bray-Curtis Index). Relation between abundance distribution in each family and sample spot in both areas (O.M. and C.M.) in second season (2014/2015).

4 ARTIGO 2

Platygastridae diversity in rice crops with organic and conventional management in southern Brazil*

* Artigo formatado conforme as normas da Neotropical Entomology.

Section “Biological Control”

Gisele De Souza Da Silva, giss_rs@yahoo.com.br (corresponding author); UFRGS,
Phytosanitary Department, Av. Bento Gonçalves, 7712 - CEP 91540-000 - Porto Alegre - RS -
Brasil

Platygastridae diversity in rice crops with organic and conventional management in southern Brazil

G. DE S. DA SILVA[1], S. M. JAHNKE[1], N. F. JOHNSON[2]

[1]UFRGS, Phytosanitary Department, Av. Bento Gonçalves, 7712 - CEP 91540-000 - Porto Alegre - RS – Brasil, [2] The Ohio State University, 1315 Kinnear Road, 43212, Columbus, Ohio, USA.

Running title: Platygastroids wasps in rice crops

ABSTRACT - Platygastridae parasitoids have been referred as important biological control agents in several agricultural systems, mainly to rice crop. Thus, we studied the richness, abundance and populational fluctuation of these Hymenoptera parasitoids through distance gradients of vegetation near cultivated areas under different management of the rice crop (organic and conventional) and under two development stages of plant. The work took place in two irrigated rice crops, one with organic management (O.M.) and another with conventional management (C.M.), in the municipality of Nova Santa Rita, RS, Brazil, during the 2013/2014 and 2014/2015 seasons. The parasitoids were collected with Malaise trap arranged at different distances in relation to the native vegetation surrounding the rice crop in both places. Specimens were collected twice a month from seeding until the rice harvest. The most abundant genera were *Idris*, *Telenomus* and *Baeus*. *Telenomus podisi* Ashmead, *Telenomus* sp.3, *Telenomus* sp.2 and *Telenomus* sp.1, were the most abundant morphospecies, respectively, and their abundances changing over the seasons. The rice phenological stage influenced the diversity over the two seasons and, in the second, possibly the pesticides use had a negative pressure upon parasitoids assemblage in conventional management. The high abundance of this family indicates that the natural biological control can be occurring in the rice crop, mainly in the organic management.

Keywords: Conservative biological control, egg parasitoids, irrigated rice, native vegetation

Introduction

Natural enemies like parasitoids play a key role on agriculture management decreasing pests population density and, consequently, the damage to them (Heinrichs & Barrion 2004). Among them, Platygastridae (Hymenoptera: Scelioninae, Teleasinae and Telenominae) have been referred as important biological control agents in several agricultural systems, such as

Telenomus and *Trissolcus* in soybean crop and horticultural species (Santos 2008, Favetti *et al* 2013).

Parasitoids eggs have high specificity in relation to the hosts (Hanson & Gauld 2006). This is a desirable feature in natural enemies, especially for an applied biological control (Van Driesche & Bellows 1996). Some species have been used for this purpose, such as *Telenomus podisi* Ashmead and *Trissolcus basalis* (Wollaston) (Corrêa-Ferreira & Moscardi 1996, Corrêa-Ferreira 2002, Ehler 2002). In Brazil, Corrêa-Ferreira & Moscardi (1996) showed that a inoculative release can control stink bugs populations. It has been used in southern Brazil in soybean (Corrêa-Ferreira 2002).

In rice crop (*Oryza sativa* L.), which is important because it can be grown in small, medium and large areas (SOSBAI, 2014), platygastoids belonging to Telenominae are associated mainly to Hemiptera (Ehler 2002, Bambaradeniya & Edirisinghe 2008, Idalgo *et al* 2013, Rajmohana & Nisha 2013). In Asian, the black rice bug *Scotinophara* sp. (Hemiptera: Pentatomidae), from India, is parasitized by many platygastroids species such as *Telenomus triptus* Nixon, *Telenomus cyrus* Nixon, *Telenomus chloropus* (Thomson), *Telenomus gifuensis* Ashmead (Polaszek & Rajmohana 2007) and *Telenomus oryzae* Rajmohana & Nisha (Rajmohana & Nisha 2013). This parasitoid family always appears with high number of individuals in researches with rice crop diversity, as for example in India, where 40 parasitoids species were found and being 29 of Platygastridae (Gnanakumar *et al* 2012).

Some researches in Brazil show the importance of Platygastridae in rice fields through natural or conservative biological control, as a controller of pests abundance (Fritz *et al* 2008, Fritz *et al* 2011, Idalgo *et al* 2013, Da Silva *et al* 2016). *Trissolcus basalis* and *T. podisi* are the parasitoids which show highest efficiency in parasitism on *Nezara viridula* (Linnaeus) and *Euschistus heros* (Fabricius) eggs (Ferreira 2003).

Thus, the aims of this research were to evaluate the richness, abundance and populational fluctuation of Platygastridae (Scelioninae, Teleasinae and Telenominae) through distance gradients of preserved vegetation near cultivated areas under different management of the irrigated rice crop (organic and conventional) and under two development stages of rice.

Material and Methods

Study area

The study was carried out in the municipality of Nova Santa Rita, RS, in the metropolitan region of Porto Alegre in the phytogeographic region of the Jacuí watershed, during the 2013/2014 and 2014/2015 seasons. In this region, many native trees species occur such as ‘maricá’ (*Mimosa bimucronata* (DC) Kuntze), ‘corticeira’ (*Erythrina falcata* Benth.), fig tree (*Ficus luschnatiana* (Miq.) Miq.), ‘angico’ (*Parapiptadenia rigida* (Benth.) Brenan), Surinam cherry (*Eugenia uniflora* L.), ‘branquilho’ (*Sebastiania commersoniana* (Baill.) L.B. Sm. & Downs), and ‘açoita-cavalo’ (*Luehea divaricata* Mart. & Zucc.) and many others (COPTEC, 2010). The vegetation near to irrigated rice area is a riparian forest.

Organic rice crop

The irrigated rice area with organic management (O.M.) is part of the Capela Settlement (Landless Rural Workers Movement Settlement) in Nova Santa Rita. It has a total area of 2169.37 hectares (INCRA, 2007), of which 580 ha belong to COOPAN (Agricultural Production Cooperative Nova Santa Rita). Of these, 220 continuous hectares are allocated for organic rice, which is certified by the Ecological Market Institute (‘Instituto de Mercado Ecológico’ - IMO) (Lanner, 2011). In the settlement an area of 273.52 hectares (13.68% of the total) is designated as a permanent preserve (native forest). In the organic rice field, the levees are maintained with wild vegetation.

The Capela Settlement is located southwest of the Caí River. To the north, in a range of 417 m, it borders the Mineiro stream, which is 7m wide on average. It is also watered by smaller streams, but the main water resource is the Padre weir, which occupies 67 hectares of the property and has a dam of 300 m length. Previous wetland areas have been exploited for rice-growing activity (Fagundes and Gastal, 2008). There are 100 families settled in the region, with an average area of 21.69 hectares per lot (INCRA, 2007).

Data samplings were made in different rice lots at each season.

In the first season (December, 2013 to April, 2014), five points were defined for the installation of traps centered around this coordinate 29° 47’ 16.62” S and 51° 21’ 00.91” W. In the area where the traps were installed, it was used the pre-germinated planting system with cultivar EPAGRI 108. It has late cycle, lodging resistance, indirect iron toxicity, moderately resistant to panicle blast, stands out for its excellent grain quality and high reproductive potential (SOSBAI, 2014).

In view of the difficult access to the area in the first year, another five points were defined in the second year (November, 2014 to March, 2015) for the installation of traps centered around this coordinate 29° 46’ 48.90” S, 51° 21’ 48.38” W. The management of the area was the same as in the first year.

In the first year, the traps were separated 100 m from each other, in a distance gradient starting from inside the forest to the middle of the crop, in a straight line (Fig 1). In the second year, the distance was extended to 200 m. Each trap site was named by the location of the Malaise trap, being O5 (Spot 5 - inside the forest), O4 (Spot 4), O3 (Spot 3), O2 (Spot 2), O1 (Spot 1 - greatest distance from forest) (Fig 1).

Conventional rice crop

The irrigated rice area with conventional management (C.M.) is located in the 'Gaúcha' Farm, a private property of 300 hectares, bordered to the southwest by the Caí River. Tillage is the planting system, and the cultivar used was IRGA428. It has a medium cycle, high productivity potential, tolerance to Only and Kifix herbicides, tolerance to toxicity from excess iron, is moderately susceptible to leaf blast and susceptible to blast on panicle (SOSBAI, 2014).

The conventional management adopted by the producer follows the IRGA recommendations, with the use of chemical inputs and application of agricultural pesticides according to the annual manuals for rice management (SOSBAI, 2012). For insect collecting, the experimental design was the same of the organic management area (Fig 1), with the points set between 29° 46' 16.65" S and 51° 21' 43.31" W. This area is approximately 2.5 km distant from the organic management area. The area for trap installation was the same in both seasons. In the conventional rice field, the levees are maintained without wild vegetation by chemicals spraying.

As in the O.M. area, in the first year (2013/2014), the traps were from each other by 100 m, in a straight line, and in the second (2014/2015), the distance was extended to 200 m. Each spot also was named by the location of Malaise trap, being C5 (Spot 5), C4 (Spot 4), C3 (Spot 3), C2 (Spot 2), C1 (Spot 1).

In the first season analyzed regulators insecticides were used (buprofezin and benzylurea) and in the second season were used non-selective (neurotoxic) insecticides (neonicotinoids and pyrethroids) (farmer personal communication Mr. Denis).

Platygastridae sampling and identification

For capturing the parasitoids five Malaise traps (Townes 1972) were placed in the levees of each of the areas (Fig 1). The collection method was improved, by putting PVC pipes cut in half to simulate a “gutter” in each trap, so that insects which have not reached the vials could drop in the “gutter” (containing water and detergent) located on the ground, comprising the entire length of the trap (Gullan & Cranston, 2008).

Samples were collected every two weeks during two rice seasons, 2013/2014 and 2014/2015, from seeding to harvest. The traps remained mounted in the points for 24 hours and thereafter the vials with the collected insects were taken. These were transferred to 70% alcohol, labeled with the collection site and transported to the Laboratory for Biological Control of Insects (CBLAB) of UFRGS. In the laboratory, the samples were screened using a stereomicroscope Nikon SMZ445, selecting the Platygastridae (Scelioninae, Teleasinae and Telenominae) hymenopteran parasitoids. The specimens were mounted on entomological pins with double mounting and placed in a reference collection. After, identified in specific level through Keys (Johnson 1984, Johnson 1987, Johnson & Musetti 2011, Masner 1976, Masner 1980, Masner 1983, Muesebeck 1977) and compared with the specimens on C.A. Triplehorn Insect Collection, Ohio State University, Columbus, OH.

.

Statistical analyses

Considering the extent of the two areas and their characteristics, it was impossible to make replicas of the samples, so that evaluations were considered exploratory.

The rice development stages were identified according to Counce *et al* (2000) into vegetative and reproductive stages. Here we named indicated O.V or C.V (organic or conventional vegetative stage of rice) and O.R or C.R (organic or conventional reproductive stage), respectively.

Fluctuations in the abundance of individuals of the most abundant species over the samples and rice management in both season were evaluated.

Rarefaction curves were constructed to compare richness between the both places of rice crop management (O.M. and C.M.) through the PAST Program (Hammer *et al* 2001). Estimated richness was calculated for each study site via the Chao 1 and Bootstrap estimates, using EstimateS software, version 9.1.0 (Colwell 2013).

Correspondence Analysis (CA) and Bray-Curtis Cluster Analysis plots were built through the PAST program (Hammer et al., 2001). Plots are constructed with the main components of lines and columns allowing visualization of the relationship between groups, where the proximity of the points relating to the line (Scelioninae, Teleasinae and Telenominae genera) and column (spots and rice stages) indicates association and the distance indicates repulsion (Greenacre and Hastie, 1987). The Cluster Analysis groups the data in a dendogram, in which the level of similarity (or dissimilarity) is indicated on the vertical scale. On the horizontal axis, the sample elements are reported in a convenient order for the clustering (Mingoti, 2005).

Results

Faunistic data

Among the collected genera in both seasons, it highlights for *Idris* spp. (11 morphospecies), *Telenomus* spp. (8 morphospecies) and *Baeus* spp. (5 morphospecies) for the higher richness. Several genera have the first record for Rio Grande do Sul, Brazil (Table 1).

First season

In the first season, 268 individuals were collected in the rice area with organic management (O.M), distributed in 31 morphospecies and 172 individuals were collected in the rice area with conventional management (C.M.), distributed in 24 morphospecies.

There was variation between species in each area and development stages of rice crop (Table 1). *Telenomus podisi* was the most abundant in both areas with 31.30% in O.M and 38.4% in C.M, and *Telenomus* sp.3 the second most abundant with 21.03% (O.M.) and 15.1% (C.M.).

The abundance of these species varied over the season (Fig 2). In both areas, *T. podisi* and *Telenomus* sp.3 were more abundant in the reproductive stage than in the vegetative.

Second season

In the second season, 151 individuals were collected in the rice area with organic management (O.M.), distributed in 34 morphospecies and 93 individuals were collected in the rice area with conventional management (C.M.), distributed in 21 morphospecies.

Telenomus podisi was the most abundant in both areas with 23.8% in O.M. and 49.5% in C.M. The second most abundant in O.M. area was *Telenomus* sp.2 (9.3%) and in C.M., *Telenomus* sp.1 (18.3%) (Table 1).

In both areas, *T. podisi* was more abundant in the reproductive stage than vegetative (Fig 3). *Telenomus* sp.1 had higher abundance in the vegetative stage of C.M. and *Telenomus* sp.2 was most abundant in the reproductive stage of O.M.

Association between platygastroids genera, sampling spots, management, and phenological stages

Through correspondence analysis, the points were represented on two axes, indicating that the association between lines (Scelioninae, Teleasinae and Telenominae genera) and columns (spots and rice stages) is two-dimensional, 50% of the relationship being explained in these two axes in season 1 and 44% of the relationship explained in season 2.

In the first season, samples are mixed on both sides of the x and y axes, showing similar composition between areas (Fig 4). Some genera, such as *Telenomus*, *Trissolcus*, *Macroteleia* and *Triteleia* showed relationships with certain sampling points and phenological periods of the plant CR and OR. On the other hand, *Xenomerus* and *Baryconus* genera appear to be distributed on distinct sides far away from the axes and had no conexion with sampling points. The points organic 5 (O5) and conventional 5 (C5) were the most dissimilar from the others.

In the second season (Fig 5), the genera showed dissimilarities between them, being more dispersed on chart than season before. *Telenomus* spp. and *Macroteleia* spp. had the same similarity with reproductive stages of O.M. and C.M. In the other hand, *Anteris* and *Probaryconus* genera had not relationship with any sampling points. The points O5, C3 and C5 were the most dissimilar from the others.

Regarding all sampling (assembling both seasons), differences between species composition and abundance are recognized among phenological stages in both season through cluster analysis. The high cophenetic correlation (0.83) confirms the adjustment of data to the Bray-Curtis model (Fig 6).

There was similarity among phenological stages, independent of rice management. Thereby, in the first season, the diversity similarity was influenced by crop phenological stages (65% in vegetative and 64% in reproductive) and was not by management. In the second season, however, it was not visible.

Species richness

The species accumulation curves (S) at each area indicates that richness was not fully sampled, as illustrated by the ascending curves (Fig 7). The richness sampled to O.M. was 45 morphospecies and, to conventional, 32 morphospecies. The variables to estimate areas richness

(Magurran 2011), in O.M. there were 9 singletons, 12 doubletons, 13 unicates and 12 duplicates and in C.M. there were 12 singletons, 5 doubletons, 14 unicates and 6 duplicates.

The rarefaction curve shows differences between the two areas for Scelionidae diversity (Fig 8), because in the cut-off point (around 250 individuals) the observed diversity in the smaller community (C.M.) did not reach the 95% confidence interval of the larger community (O.M.).

Discussion

Among the genera with the highest species richness, *Idris* and *Baeus* belong to the Baeini tribe and are known for parasite spiders eggs (Stevens & Austin 2007, Valerio *et al* 2013). Spiders are frequent in rice crops, so several species from this group were expect (Bambaradeniya & Edirisinghe 2008, Fritz *et al* 2011). The noteworthy abundance of *Telenomus* species indicates them importance on local trophic chain, acting in biological control of pests or others herbivorous on the crop and adjacent areas. The host specificity is an important feature and makes them effective on biological control (Hanson & Gauld 2006). We found it in higher or lower degree within some *Telenomus* group (Johnson 1984), for example, *Telenomus arzamae* Riley, *Telenomus californicus* Ashmead and *Telenomus dalmanni* (Ratzeburg) only attack Lepidoptera; *Telenomus crassiclava* Nixon parasitize Fulgoridae; *Telenomus floridanus* (Ashmead), Lygaeidae; *Telenomus laricis* Walker, Miridae; *Telenomus nigrocoxalis* Ashmead, Rhopalidae; *T. podisi*, Pentatomoidea and *Telenomus tabanivorus* (Ashmead), Diptera (Tabanidae, Asilidae, Stratiomyiidae) (Hanson & Gauld 2006). Therefore, when to determine the *Telenomus* species will be possible infer the host association.

Also, several species of *Telenomus* spp. were collected in rice crop in Philippines in a research about trophic interactions (Schoenly *et al* 1996). Others species are associated to rice pests, such as *Telenomus nr. triptus* Nixon and *Telenomus rowani* (Gahan, 1925) collected in rice crops in SriLanka at crop and rice levees (Bambaradeniya & Edirisinghe 2008). In India, *T. rowani* was the parasitoid emerged from yellow stem borer *Scirpophaga incertulas* (Walker) (Chakraborty *et al* 2016).

Telenomus podisi, the most abundant specie in both areas and seasons, is known for parasitize Pentatomidae eggs in many cops. In rice fields in Brazil, pentatomids are pests that damage the plant stems and grain, such as rice stem bug *Tibraca limbativentris* Stål and the small rice stink bug *Oebalus poecilus* (Dallas) (Ferreira & Barigossi 2001, Idalgo & Sant'Ana 2010, Machado & Garcia 2010). A parasitism rate of 23.4% was found in *T. limbativentris* in Maranhão with *T. podisi* being more frequent (Maciel *et al* 2007). In rice crops in Santa Catarina, a parasitism rate of 70% was found with the same species in rice stem bug (Riffel 2007). In Rio Grande do Sul, *T. podisi* had a parasitism rate of 75% over *T. limbativentris* (Idalgo *et al* 2013). Regarding to small rice stink bug, *Oebalus* spp. eggs are parasitized by *Telenomus mormidae* Lima (Ferreira & Barrigossi 2004, Panizzi 2008).

Trissolcus, also present in this survey, together with *Telenomus* spp., are considered the platygastroids genera more important for Pentatomidae biological control (Hanson & Gauld 2006).

Other genera from this family also have hosts insects associated to rice fields (Schoenly *et al* 1996, Gangurde 2007, Fritz *et al* 2011). For example, *Calliscelio* spp. (Masner *et al* 2009), *Cremastobaeus* spp. (Loiacono & Mulvany 1987, Masner & Hanson 2006), *Duta* spp. (Masner 1991, Masner & Hanson 2006), *Paridris* spp. (Talamas *et al* 2012) that parasite Gryllidae eggs. *Calotelea* species was registered in Orthoptera and Odonata eggs in rice fields (Kononova & Fursov 2007) and *Triteleia* parasitize Orthoptera (Popovici *et al* 2011).

Regarding to phenological stages of crop, *T. podisi* (O.M. and C.M.), *Telenomus* sp.2 (O.M.) and *Telenomus* sp.3 (O.M. and C.M.) were most abundant in reproductive stages, while *Telenomus* sp.1 (C.M.) and *Trissolcus* spp. (O.M. and C.M.) were most abundant in vegetative stage. The specific difference can be associated to pentatomids pests that cause damage in the stem and grain, such as rice stem bug and the small rice stink bug (Ferreira & Barigossi 2001, Idalgo & Sant'Ana 2010, Machado & Garcia 2010). These pests are more abundant in reproductive stage (SOSBAI 2014). In southern Brazil, a higher richness of Platygastridae in vegetative stage in rice crop was found (Simões-Pires *et al* 2016). On the other hand, according with our research, Bambaradeniya & Edirisinghe (2008) in SriLanka, found more diversity in the reproductive stage. Arthropod diversity variation (phytophagous and natural enemies) had relationship with rice phenological stage (75% correlation coefficient) and parasitoid density had high positive correlation with pest density, therefore, phytophagous as well as parasitoids, have association to crop phenological stage (Bambaradeniya & Edirisinghe 2008).

The points O5 and C5 were the most dissimilar in both season, through correspondence analysis. These points were inside native vegetation (preservation area) and can be the reason of the difference with the others on the crop.

Some genera had relationship with one of these points, such as *Phanuromyia* and *Scelio* (O5) in the first season and *Trimorus* (O5), in the second season. *Phanuromyia* is a genus known for parasitize Fulgoridae and Issidae eggs (Johnson & Musetti 2003), *Scelio* for parasitizing Acrididae (Yoder *et al* 2009, Yoder *et al* 2014) and *Trimorus*, Carabidae (Masner & Hanson 2006). *Anteris* and *Probaryconus* were the most dissimilar genera, showing a relationship with conventional points C3 and C5 in the second season. Both genera have records in egg parasitism of Orthoptera, mainly in Grylloidea (Gryllidae) (Masner & Hanson 2006). There are records of sub-aquatic Grylloidea, Phalangopsidae, in Neotropical region (Sperber *et al* 2003), justifying their presence in some sampling points.

In the first season, *Baryconus* and *Xenomerus* were further away from all sampling points, probably because their lower abundance and association with some point in organic management. *Baryconus* spp. are known for parasitize Tettigoniidae (Muesebeck 1977, Ritchie & Masner 1983, Masner & Hanson 2006), while *Xenomerus* have unknown hosts.

Besides *Telenomus* and *Idris* genera cited above, *Macroteleia* and *Gryon* showed similarity with several sampling points of both management and seasons. *Macroteleia* spp. are known to parasitize Tettigoniidae (Masner & Hanson 2006, Chen *et al* 2013) and *Gryon* spp. are known to parasitize Heteroptera eggs (Masner & Hanson 2006).

The similarity influenced by crop phenological stage can appears on cluster analysis, that reached up to 65% in the first season. Both areas shared the same vegetation profile, i.e. the preserved areas near to the crop have similar faunistic composition (COPTEC 2010), so probably the parasitoids assemblage in theses refuges areas are alike. Thus, platygastroids assemblage composition in the rice fields was more influenced by rice phenological stage, which attracted different hosts and, consequently, different parasitoids were attracted to the local.

In the second season, there was no similarity found and the management may have had a greater influence on composition. In the first season, in conventional management growth regulating insecticides were used (Buprofezin and Benzoylurea), which are more selective to natural enemies; in the second, however, the farmer used neurotoxic products (Neonicotinoids and Pyrethroids) (personal communication, Mr. Denis), not selective to natural enemies.

Therefore, in the first season, the management did not have a large effect in Platygastridae assemblage composition, being more influenced by adjacent vegetation and crop development phases. While in the second season, a more harmful human intervention can have affected the assemblages in conventional management.

The species accumulation curves (S) at each area indicates that richness was not fully sampled, since are on the rise on the line graph. Invertebrate diversity is still poorly documented and assemblages are not closed systems, thus, the cumulative species list must rise indefinitely when new colonizers arrive. For Magurran (2011), the best thing we can reach is an estimate of species richness and they are based on the numbers of rare species (singletons and doubletons), their representativeness throughout the sample period (constant species or accessories - unicates and duplicates) and their proportion regarding to richness and abundance of total sampling in each assemblage. Both areas have a high number of rare species (47% and 53% in organic management and conventional, respectively), therefore it was expected a high richness pointed out by estimators.

Chao 1 estimated that 94.22% of richness in O.M. and 69.03% in C.M. was sampled. Chao 1 is a simple estimator of absolute number of species in an assemblage (Chao 1984), being based on rare species number (Magurran 2011). Therefore, it is the best for estimating the minimum number of species in an assemblage (Gotelli & Colwell 2011) and a good estimator to evaluate our data.

In O.M. the doubletons numbers were larger than singletons, hence the high index percentage, while in C.M., the opposite was observed, resulting in a lower index.

The Boostrap estimator requires incidence data (Smith & Van Belle 1984) and differs from the others by use data from all species collected to estimate the total richness, using the unicates and duplicates numbers (Colwell 2013) and not only rare species; therefore, it is generally the lowest value estimator. According to it, 87.90% of richness from O.M. and 84.49% of richness from C.M. was sampled.

In our analysis, we choose to evaluate the richness with more than one estimator because rarity levels are exaggerated in researches with insects assemblages and when a single sampling technique is employed, being a factor that causes the estimators to fail (Longuino *et al* 2002).

Thus, through the richness estimators, the areas had different diversity patterns. By applying simultaneously, the curves of accumulation of species and Chao 1, it is possible a significate view of species diversity and estimate of total richness (Magurran 2011).

Rarefaction curves of both areas corroborate estimators data and show differences in species diversity among them, because the observed diversity in C.M. in cut-off point is not within 95% confidence interval of rarefaction curve of O.M., which is the larger community.

The greatest diversity of parasitoids in O.M. in both season must be due to the difference on crop management without agrochemicals, reducing the impacts upon the insects. Decrease on phytophagous, predators and parasitoids diversity after agrochemicals application is well known. Besides of, a faster increase in pests than in natural enemies population after the pesticide effect, called pests resurgence, have been emphasized by many researchers (Pingali & Gerpacio 1997, Tanaka *et al* 2000, Gangurde 2007; Bambaradeniya & Edirisinghe 2008).

For finals considerations, the rice phenological stage influenced the diversity over the two seasons with morphospecies and abundances different in both stages. It must be related to different hosts, oftentimes phytophagous insects, in each crop development. Investigations related to it can bring important information about the dynamics and relationships of these populations in the rice system. However, in the second season, possibly the pesticides use had a negative pressure upon parasitoids assemblage in conventional management. The chemical insecticides in rice crops can change parasitoids richness and abundance through changes of selective inseticides to natural enemies (growth regulators) to non-selective inseticides (neurotoxic).

The records of this work highlight the importance of the Platygastridae for the biological control of pests in rice fields. The high abundance of this family indicates that the natural biological control can be occurring in the rice crop, mainly in the organic management. Several genera have the first record for Rio Grande do Sul, Brazil.

Acknowledgments

The authors would like to thank COOPAN (Cooperative of Farming Production Nova Santa Rita Ltda), Mr. Denis rice farmer, C.A. Triplehorn Insect Collection, Ohio State University, Columbus, OH, for technical assistance, and CAPES and CNPq for financial support.

References

Bambaradeniya CNB, Edirisinghe JP (2008) Composition, structure and dynamics of arthropod communities in a rice agro-ecosystem. Ceylon J Sci Biol Sci Colombo, Sri Lanka 37 (1): 23-48.

Chakraborty K, Moitra MN, Sanyal AK, Rath PC (2016) Important natural enemies of paddy insect pests in the upper gangetic plains of west Bengal, India. International Journal of plant, animal and environmental sciences, 6 (1): 35-40.

Chao A (1984) Nonparametric estimation of the number of classes in a population. Scand Stat Theory Appl, 11265–270.

Chen H, Johnson NF, Masner L, Xu Z (2013) The genus Macroteleia Westwood (Hymenoptera, Platygastridae s. l., Scelioninae) from China. ZooKeys 300: 1–98.

Corrêa-Ferreira BS, Moscardi F (1996) Biological control of soybean stink bugs by inoculative releases of *Trissolcus basalis*. Entomol Exp Appl 79:1- 7.

Corrêa-Ferreira BS (2002) *Trissolcus basalis* para o controle de percevejos da soja. In: Parra JRP, Botelho PSM, Corrêa-Ferreira BS, Bento JMS (Ed.). Controle biológico no Brasil: parasitoides e predadores. São Paulo: Manole, p 449- 476.

Corrêa-Ferreira BS (2003) Soja Orgânica: Alternativas para o Manejo dos Insetos-Pragas. Londrina: Embrapa-CNPSo, 83p.

COPTEC (2010) Cooperativa de prestação de serviços técnicos ltda. PRA - Plano de Recuperação do Assentamento capela. Município de Nova Santa Rita, RS.

Counce PA et al. (2000) A Uniform, Objective, and Adaptive System for Expressing Rice Development. Crop Sci. 40: 436-443.

Colwell RK (2013) EstimateS 9: statistical estimation of species richness and shared species from samples. Hartford: University of Connecticut. Disponível em: <http:// viceroy.eeb.ucon.edu/estimates>. Acessed 30 October 2016.

Da Silva G de S, Jahnke SM, Ferreira MLG (2016) Hymenoptera parasitoids in protected area of Atlantic Forest biomes and organic rice field: 2 compared assemblages. Revista Colombiana de Entomologia, vol. 42, n°2, pp. 110-117.

Ehler LE (2002) An evaluation of some natural enemies of *Nezara viridula* in northern California. Biocontrol 47: 309-325.

Favetti BM, Krinski D, Butnariu AR, Loiácono, MS (2013) Egg parasitoids of *Edessa meditabunda* (Fabricius) (Pentatomidae) in lettuce crop. Rev Bras Entomol 57(2): 236–237.

Ferreira E, Barrigossi JAF, Vieira NRA (2001) Percevejos das panículas do arroz: fauna Heteroptera associada ao arroz. Embrapa Arroz e Feijão. Circular Técnica, 43.

Ferreira E, Barrigossi JAF (2004) Reconhecimento e controle dos principais percevejos Oebalus spp. que atacam as panículas de arroz. Santo Antônio de Goiás: Embrapa Arroz e Feijão. (Embrapa Arroz e Feijão. Comunicado técnico, 76), 6p.

Fritz LL, Heinrichs EA, Pandolfo M, Salles SMde, Oliveira JVde, Fiuza LM (2008) Agroecossistemas orizícolas irrigados: insetos-praga, inimigos naturais e manejo integrado. Oecologia brasiliensis, Rio de Janeiro 12(4): 720-732.

Fritz LL, Heinrichs EA, Machado V, Andreis TF, Pandolfo M, Salles SMde, Oliveira JVde, Fiuza LM (2011) Diversity and abundance of arthropods in subtropical rice growing areas in the Brazilian south. Biodivers. Conserv., London, 20: 2211–2224.

Gangurde S (2007) Aboveground arthropod pest and predator diversity in irrigated rice (Oryza sativa L.) production systems of the Philippines. J. Trop. Agric., 45 (1-2): 1-8.

Gnanakumar M, Rajmohana K, Bijoy C, Balan, D, Nish, R (2012) Diversity of Hymenopteran Egg Parasitoids in Organic and Conventional Paddy Ecosystems. Trop. Agric. Res. 23 (4): 300–308.

Gotelli NJ, Entsminger GL (2001) Ecosim null model software ecology. Version 6.0 Acquired Intelligence Inc. & Keysey-Bear. Disponível em: <http://www.uvm.edu/~ngotelli/EcoSim/EcoSim.html>. Acessed 24 October 2012.

Gotelli NJ, Colwell RK (2011) Estimating species richness. Biological diversity: frontiers in measurement and assessment, 12: 39-54.

Greenacre M, Hastie T (1987) The geometric interpretation of correspondence analysis. J Am Stat Assoc 82: 437-447.

Hammer O, Harper DAT, Ryan PD (2001) PASt: Paleontological statistics software package for education and data analyses. Palaeontol Electronica, Oslo, 4 (1) 9 p.

Hanson PE, Gauld ID (2006) Hymenoptera de la Región Neotropical. v. 77. Gainesville: The American Entomological Institute.

Heinrichs EA, Barrion AT (2004) Rice-Feeding Insects and Selected Natural Enemies in West Africa: biology, ecology, identification. Manila: International Rice Research Institute, 242p.

Idalgo TDN & Sant'ana J (2010) Aspectos morfológicos, biologia, danos e controle do percevejo-do-colmo-do-arroz, *Tibraca limbativentris* Stål, 1860. Disponível em: <http://www.infobibos.com/Artigos/2010_2/tibraca/index.htm>. Acessed 08 April 2015.

Idalgo TDN, Sant'Ana J, Redaelli LR, Pires PDS (2013) Parasitismo de ovos de *Tibraca limbativentris* Stål (Hemiptera: Pentatomidae) em lavoura de arroz irrigado, Eldorado do Sul, RS Arq. Inst. Biol. São Paulo, 80 (4): 453-456.

INCRA – Instituto Nacional de Colonizaçaõ e Reforma Agrária. Relatório Ambiental do Projeto de Assentamento Capela. Porto Alegre, Setembro, 2007. 95 p.

Johnson NF (1984) Systematics of nearctic *Telenomus*: classification and revisions of the *podisi* and *phymatae* species groups [*Hymenoptera: Scelionidae*]. *Bulletin Ohio Biological Survey*, Columbus, 6:1–113.

Johnson NF (1987) Systematics of New World *Trissolcus*, a genus of pentatomid egg-parasitoids (Hymenoptera: Scelionidae): Neotropical species of the *flavipes* group. J. Nat. Hist., (21): 285-304.

Johnson NF, Musetti L (2011) Redescription and revision of the Neotropical genus *Pseudoheptascelio* Szabó (Hymenoptera, Platygastridae, Scelionidae), parasitoids of eggs of short-horned grasshoppers (Orthoptera, Acrididae). ZooKeys 136: 93-112.

Kononova SV, Fursov VN (2007) A Review of the Genera *Calotelea*, *Calliscelio*, and *Oxyscelio* (Scelioninae, Scelionidae, Proctotrupoidea) from the Palaearctic Fauna. Entomological Review,87(1): 92–105.

Lanner AJ (2011) A Cooperativa de produção agropecuária Nova Santa Rita Ltda (COOPAN) do Assentamento Capela, Nova Santa Rita (RS): questões da atividade suinícola. Porto Alegre. Trabalho de Conclusão do Curso de Graduação Tecnológica em Planejamento e Gestão para o Desenvolvimento Rural – PLAGEDER, da Faculdade de Ciências Econômicas da UFRGS. 104f.

Longuino JT, Coddington J, Colwell RK (2002) The ant fauna in tropical rain forest: estimating species richness three different ways. Ecology, Washington, 83: 689-702.

Loiacono MS, Mulvany SH (1987) Sistematica y analisis fenetico de seis nuevas espécies del gênero *Cremastobaeus* Ashmead 1893 (Hymenoptera – Proctotrupoidea). Revista de la Asociacion de Ciencias Naturales del Litoral 18: 13-28.

Machado RCM, Garcia FRM (2010) Levantamento de pragas e inimigos naturais ocorrentes em lavoura de arroz no município de Cachoeirinha, Rio Grande do Sul. Revista de Ciências Ambientais 4(2): 57-68.

Maciel AAS, Lemos RNSde, Souza JRde, Costa VA, Barrigossi JAF, Chagas EFdas (2007) Parasitismo de Ovos de *Tibraca limbativentris* Stal (Hemiptera: Pentatomidae) na Cultura do Arroz no Maranhão. Neotrop. Entomol., Londrina 36(4): 616-618.

Magurran AE (2011) Medindo a diversidade biológica. Editora UFPR. 261p.

Masner L (1976) Revisionary notes and keys to world genera of Scelionidae (Hymenoptera: Proctotrupoidea). Memoirs of the Entomological Society of Canada, 97:1–87.

Masner L (1980) Key to genera of scelionidae of the Holartic Region, with descriptions of new genera and species (Hymenoptera: Proctotrupoidea). Memoirs of the Entomological Society of Canada, 113p.

Masner L (1983) A revision of *Gryon* Haliday in North America (Hymenoptera: Proctotrupoidea: Scelionidae). Byosystematics Research Institute, Agriculture Canada, Ottawa. Can. Entomol.

Masner L (1991) The neartic species of *Duta* Nixon (Hymenoptera: Scelionidae), egg parasitoids of ground crickets (Orthoptera: Gryllidae). Can. Entomol., 123: 777-793.

Masner L, Hanson PE (2006) Família Scelionidae. In: HANSON, PE; GAULD, ID (eds). Hymenoptera de la Región Neotropical. Gainesville: The American Entomological Institute. p. 254-265.

Masner L, Johnson NF, Musetti L (2009) *Calliscelio elegans* (Perkins), a tramp species, and a review of the status of the genus *Caenoteleia* Kieffer (Hymenoptera: Platygastridae). Zootaxa, 2237: 59–66.

Mingoti S A (2005) Análise de dados através de métodos de estatística multivariada – uma abordagem aplicada. Belo Horizonte: Editora UFMG.

Muesebeck CFW (1977) The Parasitic Wasp of the Genus *Macroteleia* Westwood of the New World (Hymenoptera, Proctotrupoidea, Scelionidae). Technical Bulletin 1565, US. Dept of Agriculture.

Panizzi A (2008) Small Rice Stink Bug, *Oebalus poecilus* (Dallas) (Hemiptera: Heteroptera: Pentatomidae). Encyclopedia of Entomology, Publisher: Springer Netherlands, pp. 3420-3421.

Pingali PL, Gerpacio RV (1997) Living with reduced insecticide use for tropical rice in Asia. Food Policy, 22 (2): 107-118.

Polaszek A, Rajmohana K (2007) Taxonomy of the Egg Parasitoids of Rice Black Bug, *Scotinophara* spp. In: R.C. Joshi, A.T. Barrion and L.S. Sebastian (eds.).

Rice black bugs: taxonomy, ecology, and management of invasive species. Science City of Muñoz, Nueva Ecija: Philippine Rice Research Institute 351 -360pp.

Popovici, OA, Bin F, Masner L, Popovici M, Notton D (2011) *Triteleia peyerimhoffi* comb. n., a remarkably variable circum-Mediterranean scelionid (Hymenoptera, Platygastroidea). ZooKeys 140: 71–99.

Rajmohana K, Nisha MS (2013) *Telenomus oryzae* (Hymenoptera: Platygastridae), a new egg parasitoid of the rice black bug, *Scotinophara* (Heteroptera: Pentatomidae) from India. Halteres, 4: 79-86.

Ritchie J, Masner L (1983) Revision of the Nearctic species of *Baryconus* (Hymenoptera: Scelionidae, Scelioninae). Canadian Journal, 2001. 61: 704-720.

Riffel CT (2007) Levantamento e aspectos biológicos de espécies parasitoides de posturas do percevejo-do-colmo-do arroz no estado de Santa Catarina. 2007. 73 f. Dissertação (Mestrado) - Centro de Ciências Agroveterinárias, UDESC - Universidade do Estado de Santa Catarina, Lages.

Santos RSS dos (2008) Levantamento populacional de percevejos e da incidência de parasitoides de ovos em cultivos orgânicos de soja. Pesquisa Agropecuária Gaúcha, Porto alegre, 14(1): 41- 46.

Schoenly K, Cohen JE, Heong KL, Litsinger JA, Aquino GB, Barrion AT, Arida G (1996) Food web dynamics of irrigated rice fields at five elevations in Luzon, Philippines. Bulletin of Entomological Research, 86:451-466.

Simões-Pires PR, Jahnke SM, Redaelli LR (2016) Influence of the vegetation management of the leeves in irrigated rice organic in diversity of Hymenoptera parasitoids. Braz J Biol. Available: < http://dx.doi.org/10.1590/1519-6984.06215>

SOSBAI. Arroz irrigado: recomendações técnicas da pesquisa para o Sul do Brasil (2012) XXIX Reunião Técnica da Cultura do Arroz Irrigado, 01 a 03 de agosto de 2012, Gravatal, SC. - Itajaí.179 p.

Smith EP, VAN Belle G (1984) Nonparametric estimation of species richness. Biometrics, Washington, 40: 119-129.

Sperber CF, Rocha A, Lopes-Andrade C, Mesa A (2003) *Izecksohniella puri* sp. n., a new Brazilian cricket species (Orthoptera: Grylloidea: Phalangopsidae) from Atlantic Forest remnants. Zootaxa 224: 1-12.

Stevens NB, Austin AD (2007) Systematics, distribution and biology of the Australian 'micro-flea' wasps, *Baeus* spp. (Hymenoptera: Scelionidae): parasitoids of spider eggs. Zootaxa 1499: 1-45.

Talamas EJ, Masner L, Johnson NF (2012) *Paridris* Kieffer of the New World (Hymenoptera, Platygastroidea, Platygastridae). ZooKeys 233: 31–90.

Tanaka K, Endo S, Kazano H (2000) Toxicity of insecticides to predators of rice planthoppers: Spiders, the mirid bug and the dryinid wasp. Appl. Entomol. Zool. (Jpn.) 35 (1): 177-187.

Townes H (1972) A light-weight Malaise trap. Entomol. News, Philadelphia, 83(9): 239-247

Valerio AA, Austin AD, Masner L, Johnson NF (2013) Systematics of Old World *Odontacolus* Kieffer s.l. (Hymenoptera, Platygastridae s.l.): parasitoids of spider eggs. ZooKeys 314: 1–151.

VAN Driesche RG, Bellows JRTS (1996) Biological Control. London: Champman & Hall, 593p.

Valerio AA, Masner L Austin AD (2010) Systematics of *Cyphacolus* Priesner (Hymenoptera: Platygastridae s.l.), an Old World genus of spider egg parasitoid. Zootaxa 2645:1–48.

Yoder MJ, Valerio AA, Polaszek A, Masner L, Norman FJ (2009) Revision of *Scelio pulchripennis* - group species (Hymenoptera, Platygastroidea, Platygastridae) ZooKeys 20: 53 – 118.

Yoder MJ, Valerio AA, Polaszek A, Noort SVan, Masner L, Norman FJ (2014) Monograph of the Afrotropical species of *Scelio* Latreille (Hymenoptera, Platygastridae), egg parasitoids of acridid grasshoppers (Orthoptera, Acrididae). ZooKeys 380: 1–188.

Table 1 Morphospecies of Platygastridae (Scelioninae, Teleasinae and Telenominae) sampled in the first (2013/2014) and second crop season (2014/2015) over vegetative and reproductive stage of rice crop in organic management area (O.M.) and conventional management area (C.M.), Nova Santa Rita, RS.

	1° Season						**2° Season**					
	O.M			**C.M**			**O.M**			**C.M**		
Platygastridae	**Veg**	**Rep**	**Fr (%)**	**Veg**	**Rep**	**Fr (%)**	**Veg**	**Rep**	**Fr (%)**	**Veg**	**Rep**	**Fr (%)**
Anteris sp.1*	0	0	0.0	0	0	0.0	0	0	0.0	2	0	2.2
Baeus sp.1*	0	0	0.0	0	0	0.0	2	1	2.0	1	0	1.1
Baeus sp.2*	3	0	1.1	0	0	0.0	1	0	0.7	0	0	0.0
Baeus sp.3*	0	0	0.0	1	0	0.6	0	1	0.7	0	0	0.0
Baeus sp.4*	0	0	0.0	0	0	0.0	1	2	2.0	0	0	0.0
Baeus sp.5*	0	2	0.8	3	5	4.7	0	0	0.0	1	0	1.1
Baryconus sp.1*	7	1	3.0	0	0	0.0	0	2	1.3	0	1	1.1
Calliscelio sp.1*	5	1	2.2	3	3	3.5	1	0	0.7	0	0	0.0
Calotelea sp.1*	0	0	0.0	2	1	1.7	0	1	0.7	0	0	0.0
Cremastobaeus sp.1*	0	1	0.4	2	0	1.2	0	3	2.0	1	0	1.1
Cremastobaeus sp.2*	0	1	0.4	0	0	0.0	0	6	4.0	0	0	0.0
Duta sp.1*	4	6	3.7	7	0	4.1	0	2	1.3	0	1	1.1
Duta sp.2*	0	1	0.4	0	0	0.0	1	4	2.9	1	0	1.1

Table 1 continue

Eumicrosoma sp.1*	0	0	0.0	0	0	0.0	0	2	1.3	0	0	0.0
Gryon sp.1	1	0	0.4	0	0	0.0	1	6	4.6	2	0	2.2
Gryon sp.2	0	0	0.0	0	0	0.0	2	0	1.3	0	0	0.0
Idris sp.1*	0	0	0.0	0	0	0.0	0	1	0.7	0	0	0.0
Idris sp.2*	0	0	0.0	0	0	0.0	1	1	1.3	0	0	0.0
Idris sp.3*	0	0	0.0	0	0	0.0	0	2	1.3	0	0	0.0
Idris sp.4*	1	0	0.4	0	0	0.0	0	1	0.7	0	0	0.0
Idris sp.5*	0	0	0.0	0	2	1.2	0	0	0.0	0	2	2.2
Idris sp.6*	0	1	0.4	0	0	0.0	0	1	0.7	0	1	1.1
Idris sp.7*	0	0	0.0	0	1	0.6	2	0	1.3	0	0	0.0
Idris sp.8*	1	0	0.4	0	0	0.0	0	1	0.7	0	0	0.0
Idris sp.10*	0	0	0.0	1	1	1.2	0	0	0.0	0	0	0.0
Idris sp.11*	1	0	0.4	1	0	0.6	0	0	0.0	0	0	0.0
Idris sp.12*	0	1	0.4	0	0	0.0	0	0	0.0	0	0	0.0
Macroteleia sp.1*	3	8	4.1	2	4	3.4	0	2	1.3	1	0	1.1
Opisthacantha sp.1*	3	3	2.2	2	1	1.7	4	1	3.3	1	0	1.1
Paridris sp.1*	3	0	1.1	0	0	0.0	1	0	0.7	0	0	0.0
Phanuromyia sp.1*	7	2	3.4	0	1	0.6	0	7	4.6	0	2	2.2
Probaryconus sp.1*	0	0	0.0	0	0	0.0	0	0	0.0	2	0	2.2
Probaryconus sp.2*	0	0	0.0	0	0	0.0	0	0	0.0	0	1	1.1
Scelio sp.1*	1	2	1.1	0	0	0.0	0	0	0.0	0	0	0.0
Trimorus sp.1*	0	1	0.4	0	0	0.0	2	1	2.0	0	0	0.0
Trimorus sp.2*	11	1	4.5	6	1	4.1	1	1	1.3	2	0	2.2
Trissolcus sp.1	0	0	0.0	1	0	0.6	2	0	1.3	0	0	0.0
Trissolcus sp.2	1	0	0.4	2	0	1.2	0	0	0.0	0	0	0.0
Trissolcus sp.3	0	0	0.0	1	0	0.6	0	0	0.0	0	0	0.0
Triteleia sp.1*	0	3	1.1	0	0	0.0	0	0	0.0	0	0	0.0
Telenomus sp.1	8	5	4.9	7	4	6.4	5	7	8.0	14	3	18.3
Telenomus sp.2	9	3	4.5	3	1	2.3	1	13	9.3	1	0	1.1
Telenomus sp.3	12	45	21.3	11	15	15.1	7	5	8.0	5	1	6.5
Telenomus sp.4	0	0	0.0	0	0	0.0	0	4	2.7	0	0	0.0
Telenomus sp.5	5	6	4.1	9	0	5.2	0	2	1.3	0	1	1.1
Telenomus sp.6	31	53	31.3	22	44	38.4	11	25	23.8	15	31	49.5
Telenomus sp.7	1	0	0.4	1	0	0.6	0	0	0.0	0	0	0.0
Telenomus sp.8	2	0	0.8	1	0	0.6	0	0	0.0	0	0	0.0
Xenomerus sp.1*	1	0	0.4	0	0	0.0	0	0	0.0	0	0	0.0
Total	**121**	**147**	**100.0**	**88**	**84**	**99.9**	**46**	**105**	**99.9**	**49**	**44**	**99.9**

*Genera with first record for Rio Grande do Sul, Brazil.

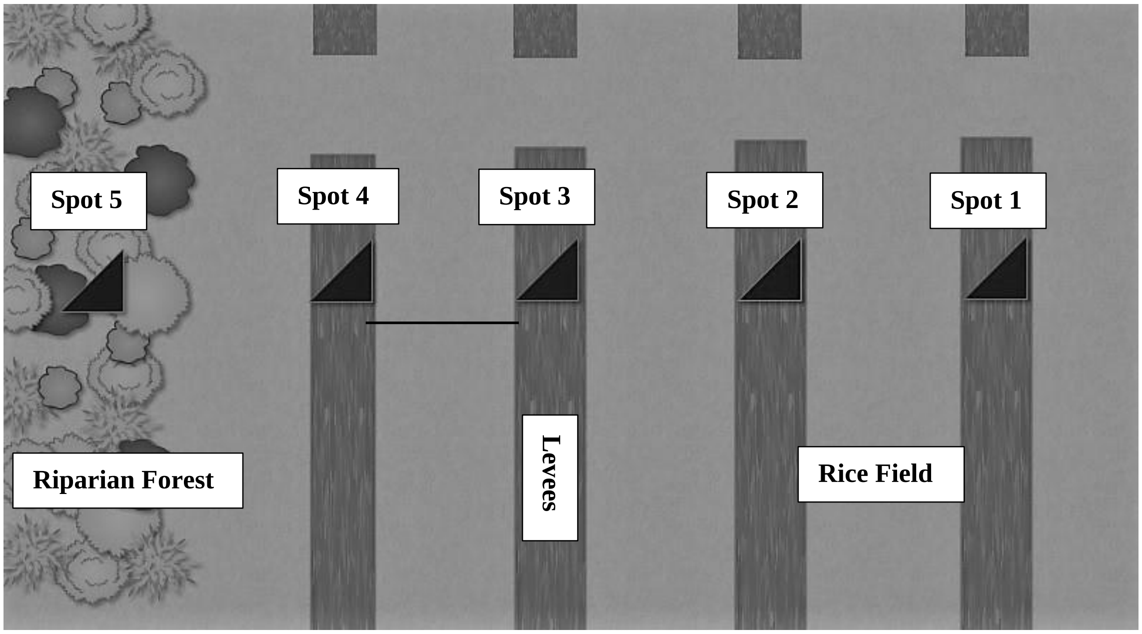


Fig 1 Layout showing Malaise traps (◢) position on rice field and riparian forest in both areas, Organic Management Area (O.M.) and Conventional Management Area (C.M.), in Nova Santa Rita, RS. (▬) Distance between traps (100m first season; 200m second season).

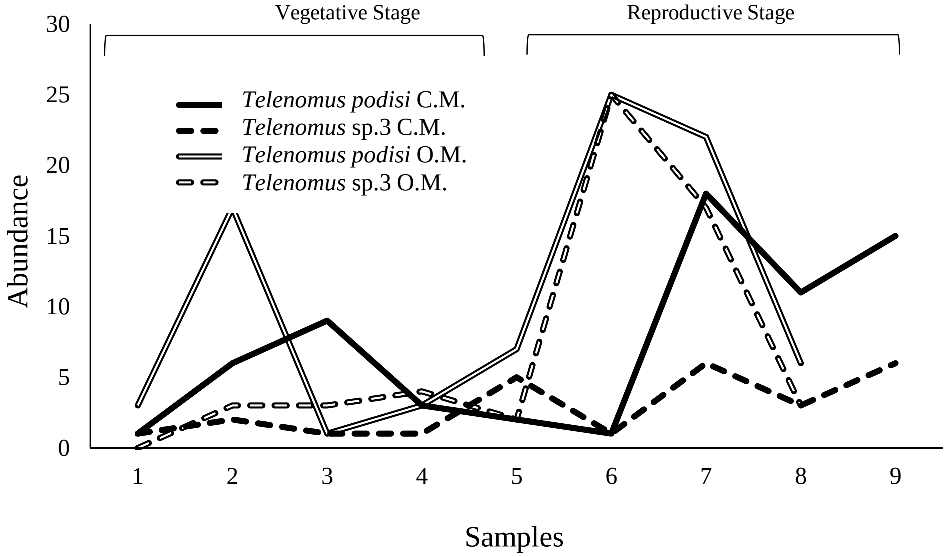


Fig 2 Fluctuations in the abundance of individuals of the most abundant species (*Telenomus podisi* and *Telenomus* sp.3) in rice fields with organic management (O.M.) and conventional management (C.M.). Nova Santa Rita, RS, Brazil (December, 2013 to April, 2014).

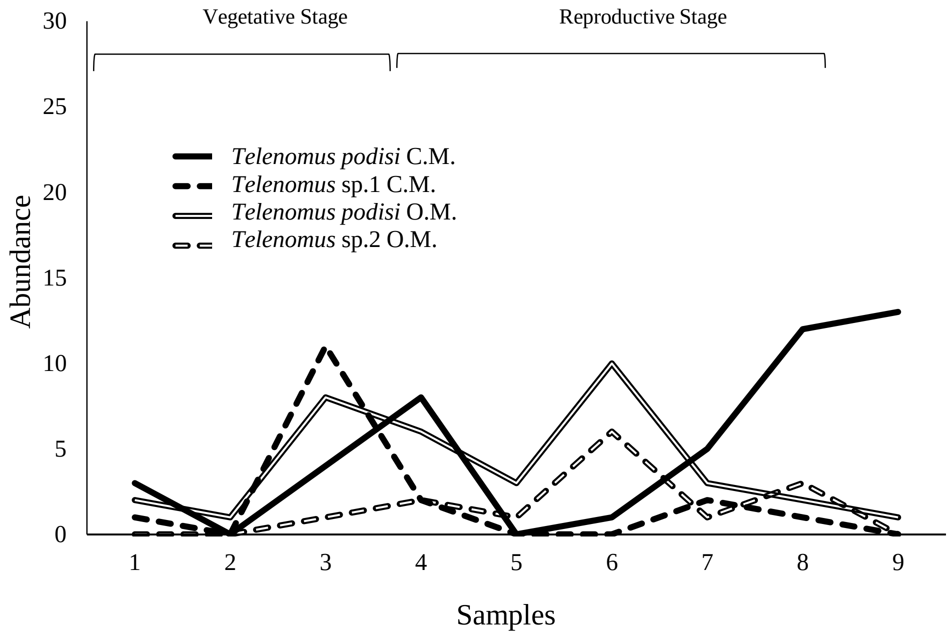


Fig 3 Fluctuations in the abundance of individuals of the most abundant species (*Telenomus podisi*, *Telenomus* sp.1 and *Telenomus* sp.2) in rice fields with organic management (O.M.) and conventional management (C.M.). Nova Santa Rita, RS, Brazil (November, 2014 to March, 2015).

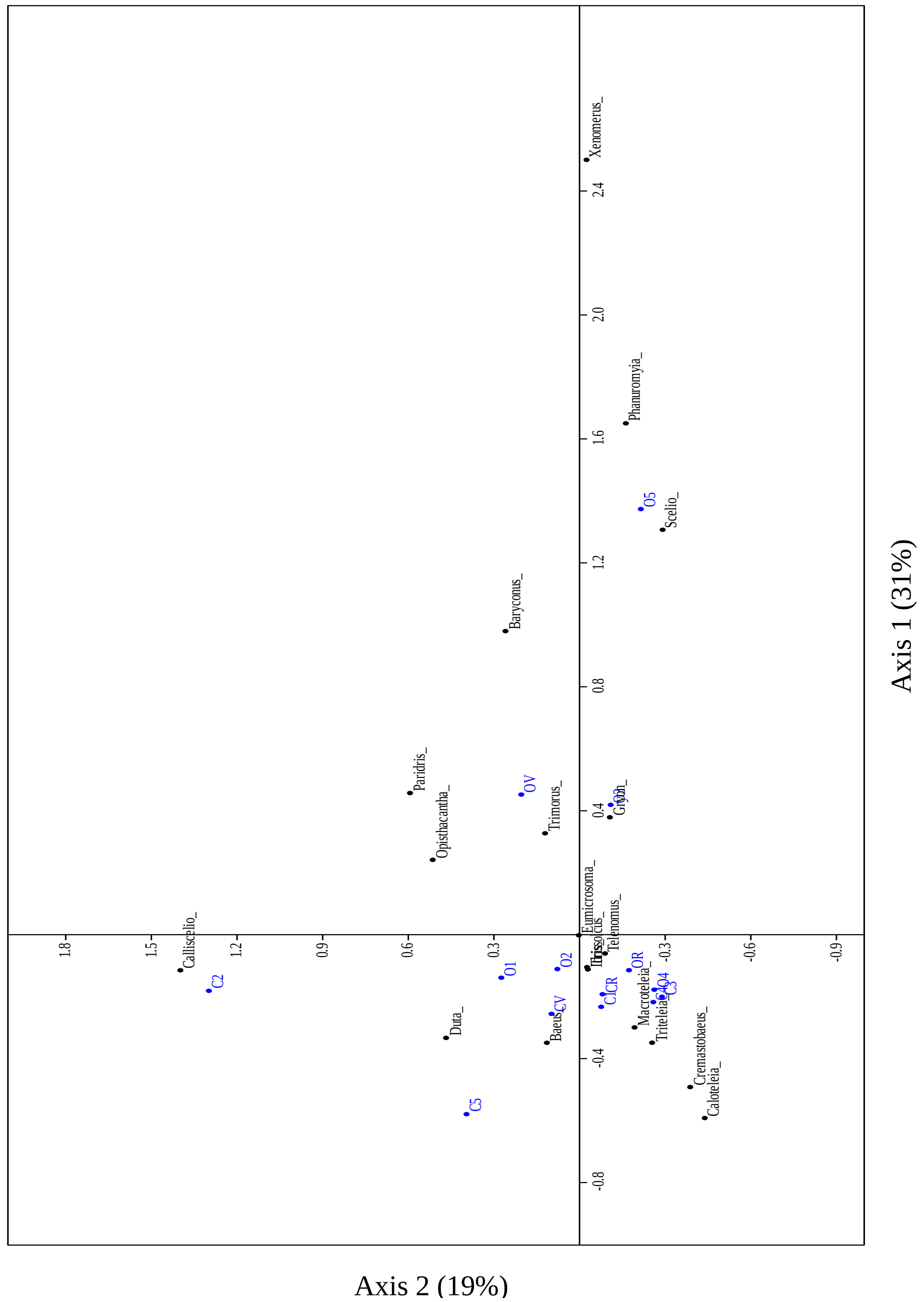


Fig 4 Correspondence Analyses. Relation between sample spot in each management, rice crop development stages (V= vegetative; R= reproductive) in each point of the areas with organic management (O) and conventional (C) and platygastroids species in the first season (2013/2014), Nova Santa Rita, RS, Brazil.

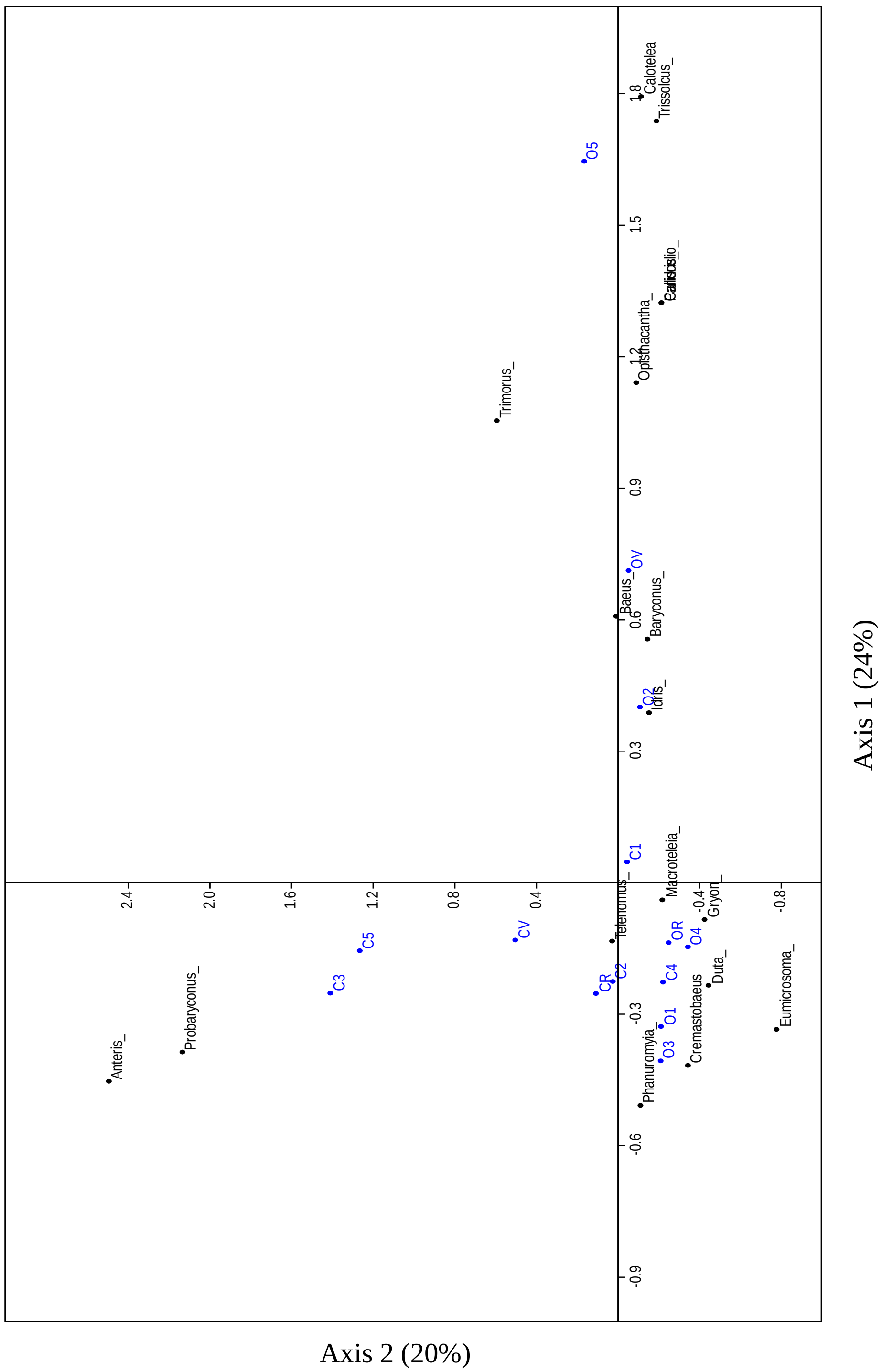


Fig 5 Correspondence Analyses. Relation between sample spot in each management, rice crop development stages (V= vegetative; R= reproductive) in each point of the areas with organic management (O) and conventional (C) and platygastroids species in the second season (2014/2015), Nova Santa Rita, RS, Brazil.

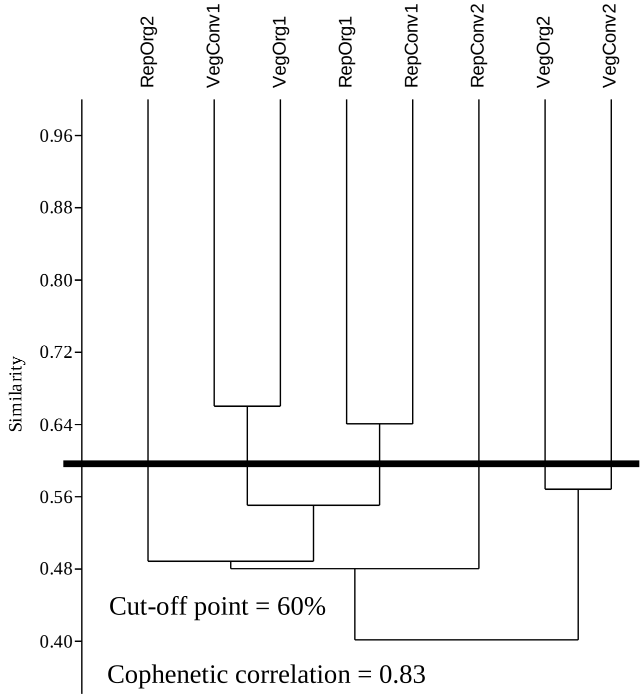


Fig 6 Cluster Analysis of similarity (Bray-Curtis Index). Relation between platygastroids abundance distribution and rice phenological stages vegetative (Veg) and reproductive (Rep) in both areas (organic = Org and conventional = Conv) in first season (2013/2014 = 1) and second season (2014/2015 = 2), Nova Santa Rita, RS, Brazil. Cophenetic correlation = 0.83; Cut-off point = 60%

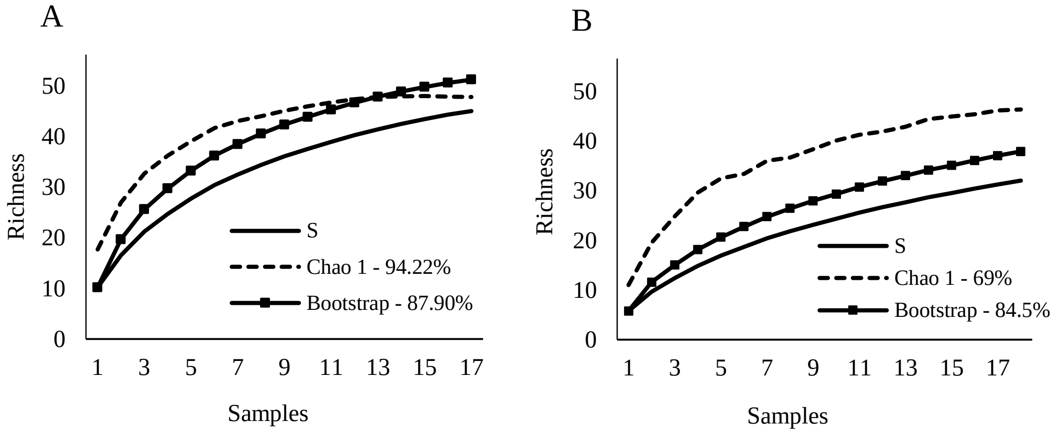


Fig 7 Estimated richness curves (% of estimated richness) of platygastroids species to Chao 1 and Bootstrap estimators (randomized 500 times) and accumulation curve (S), at the organic rice management (O.M.) (A) and conventional rice management (C.M.) (B) from both seasons, 2013/2014 and 2014/2015. Nova Santa Rita, RS, Brazil.

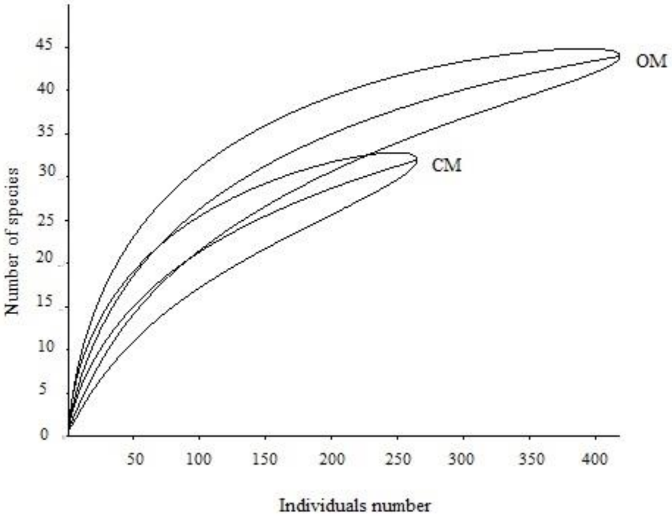


Fig 8 Rarefaction curves of Platygastridae parasitoids collected at the organic rice management (O.M.) and conventional rice management (C.M.) from both seasons, 2013/2014 and 2014/2015. Nova Santa Rita, RS, Brazil.

5 ARTIGO 3

Molecular diversity and phylogeography of *Telenomus podisi* (Hymenoptera: Platygastridae)*

* Artigo formatado conforme as normas da Zootaxa

Molecular diversity and phylogeography of *Telenomus podisi* (Hymenoptera: Platygastridae)

GISELE DE SOUZA DA SILVA[1,2], NORMAN F JOHNSON[3], HUA-YAN CHEN[4], SIMONE MUNDSTOCK JAHNKE[2,5]

[1] *E-mail: giss_rs@yahoo.com.br (corresponding author);*
[2] *UFRGS, Phytosanitary Department, Av. Bento Gonçalves, 7712 - CEP 91540-000 - Porto Alegre – RS, Brasil;*
[3] *The Ohio State University, Columbus, Ohio, USA, E-mail: johnson.2@osu.edu.*
[4] *The Ohio State University, Columbus, Ohio, USA, E-mail: huayanc@gmail.com*
[5] *E-mail: mundstock.jahnke@ufrgs.br*

Abstract

Telenomus podisi Ashmead (Hymenoptera: Platygastridae) is an important species in biological control of agricultural pests in many countries. Despite its importance in agricultural field, some taxonomic questions remain unclear. Thus, more studies are needed to understand the relationships between themselves. The objective of this study was to use population genetic methods in conjunction with two molecular markers: COI and ITS2, to address relationships between *T. podisi* specimens from different biogeographic regions. One hundred and forty-nine specimens identified as *T. podisi* were sampled from 18 localities in seven different countries from 1991 to 2016. Seventy-three COI and ITS2 haplotypes were identified. The haplotypes were the same for both genes. Haplotype 73 (H73) was the most frequent (13%) occurring in 22% of localities. H6 was the second most frequent haplotype (11%) occurring in 28% of localities and H8 represented (8%) also occurring in 28% of localities. Four main clades are revealed in the phylogenetic tree. Haplotype 72 was the most basal to all others haplotypes. In sequence, 3 branches that originate 3 clades (haplotypes H73 to H41) and a monophyletic group formed from H39 to H1 (haplotypes H40 to H1). More than 70% of haplotypes were singletons and 89% unique to a geographic area. The presence of many singletons may indicate a recent origin for them. Haplotype H6 from Arizona, Texas (Bastrop State Park and Cooke County), Ohio and Brazil can be establishing in small populations across geographic area. Haplotype H8 from Texas (Bastrop State Park and Lick Creek Park), Ohio, Cuba and Brazil can be spread out for long time ago with good establishment or/and have more than one population colonizing in the same region. Some haplotypes seem to be evolving through different pathways and independently of geographic location. Other features may be putting pressure on these haplotypes, such as climatic barriers, shift of host and flora associated. It is important inside biological control context, because differences in each population can lead to different methodologies regard to have an effective biological control.

Key words: Genetic diversity, biological control, biogeography, haplotypes

Introduction

Telenomus podisi Ashmead (Hymenoptera: Platygastridae) is an important species in biological control of agricultural pests in many countries (Corrêa-Ferreira 2002; Ehler 2002). It parasitizes Pentatomidae eggs, many of which are agricultural pests (Hanson & Gauld 2006). In Brazil, it is recorded parasitizing *Tibraca limbativentris* Stål (Hemiptera: Pentatomidae), where parasitism rates up to 75% in rice crops (Maciel *et al*. 2007; Riffel 2007; Idalgo *et al*. 2013). In soybean, the parasitism over *Euschistus heros* (Fabricius), *Podisus connexivus* Bergoth and *Dichelops melacanthus* (Dallas) (Hemiptera: Pentatomidae) eggs rates up to 73%, 61% and 50%, respectively (Corrêa-Ferreira & Moscardi 1996). In United States, *T. podisi* showed a higher parasitism over the Pentatomidae *Nezara viridula* (Linnaeus) and *Euschistus servus* (Say) in corn, peanut and cotton farmscapes (Tillman 2011). Also, the important pest brown marmorated stink bug *Halyomorpha halys* (Stål) (Hemiptera: Pentatomidae) has been found parasitized by *T. podisi* (Talamas *et al*. 2015). Despite its importance in agricultural field, some taxonomic questions about this species remain unclear.

Platygastridae belongs to superfamily Platygastroidea with 6011 species described (Hymenoptera online 2016). The subfamily Telenominae includes 905 species, being 652 valid species described in *Telenomus* Haliday genus (Taekul *et al*. 2014*)*. There is some disagreement about the classification of this subfamily (Kozlov 1970*;* Kozlov & Kononova 1983; Masner 1972; 1976; Masner & Huggert 1979) and the relationships at lower taxonomic levels are also problematic. According to Murphy *et al.* (2007), this subfamily is monophyletic, but some genera like *Telenomus*, showed a nonmonophyly. More recently Taekul *et al*. (2014) also fail to settle the *Telenomus* monophyly and found a nonmonophyly in *podisi* group. Johnson (1984) describe *T. podisi* belongs to Neartic species with others species within *podisi* group from Neotropical Region, however, in this region diversity is greater and do not show a fixed diagnostic. So, more studies about this group to try understand taxonomic relationships at a finer level are necessary.

Through the study of genetics population, we can investigate the connection between demographic features and the molecular genetic variants, which influence speciation and taxonomic hierarchy (Sunnucks 2000) and some researches are conducted for this purpose. Miranda *et al.* (2016) identified two population groups of *Partamona rustica* Pedro & Camargo (Hymenoptera: Apidae) in west and east of the São Francisco River in Brazil through four mitochondrial genes and eight microsatellite loci. A paper that examined the impacts of an initial bottleneck and subsequent expansion on genetic structure of introduced wasp *Polistes chinensis antennalis* (Fabricius) (Hymenoptera, Vespidae) in New Zealand from East Asia was conducted by Tsuchida *et al*. (2014). Both researches found differences in genetic structure of studied populations through different geographic distribution.

Studies regarding host location and acceptance have begun to raise questions as to whether *T. podisi* is a single species. A study of *T. podisi* raised from specimens from Brazil and United States found differences between them in responses to host walking traces, cold tolerance, cuticular hydrocarbon composition and cross mating (Borges *et al*. 2003), leading a doubt on the idea that the two populations belong to the same species.

Taxonomy and biological systematics are sciences of discovering, describing, classifying and naming organisms (Tancoigne *et al*. 2011). It is the basic scientific discipline of biology, postulating hypotheses of identity and relationships, on which all other natural sciences dealing with organisms relies (Wägele *et al*. 2011). Taxonomic knowledge is essential whether studying whole organisms, their organs, their specific bio-molecules or biochemical pathways. The study only can be considered robust enough to discuss species-specific traits or attributes, if a species identity is unambiguous (Wägele *et al*. 2011). Identification of a target species of study impacts all subsequent comparisons, predictions, and possible replication of the study (Wägele *et al*. 2011).

Many researchers disagree about the concept of species and the limits of this. De Queiroz (2007) argued that the key to reconciling the alternative species concepts is identifying a common element, which implies a single, more general, concept of species. It refers to equate species with evolving metapopulation lineages separately, or more specifically, with segments of such lineages (De Queiroz 2007). The 'lineage' refers to an ancestor-descendant series (Simpson 1961; Hull 1980) in this case of metapopulations or simply a metapopulation extended through time (Simpson 1951). So, the evolutionary species concept (ESC), is the primary concept while the others are secondary species criteria (De Queiroz 2007).

Among the genes used as molecular markers to identify species and populations genetics, there are the mitochondrial gene COI (cytochrome oxidase subunit I) and the ITS2 (rDNA internal transcribed spacer 2). These genes have been used to identify many insects species such as *Encarsia* spp. (Hymenoptera: Aphelinidae) (Monti *et al*. 2005), blow flies (Diptera: Calliphoridae) (Khullar *et al*. 2016), *Eumerus* sp. (Diptera: Syrphidae) (Chroni *et al*. 2016); *Lysiphlebus* sp. (Braconidae) (Rahimi *et al.* 2012), *Horismenus* sp. (Eulophidae) (Kenyon *et al*. 2015) and Trichogrammatidae (Almeida & Stouthamer 2015; Venkatesan 2016). Thus, these tools can answer questions about the phylogeny and species delimitation of a group. This is also important because Platygastridae are biological control agents and the strains may have host specificity. This information can have a major impact on the success of biological control.

The objective of this study is to use population genetic methods in conjunction with two molecular markers: the mitochondrial protein-coding gene COI, and the nuclear protein-coding gene ITS2, to address relationships between *Telenomus podisi* specimens from different biogeography regions.

Materials and Methods

Taxa sampling

One hundred and forty-nine specimens identified as *T. podisi* and one specimen identified as *Trissolcus brochymenae* (Ashmead) (outgroup) based on morphology were sorted from hymenopteran collected by Malaise traps or reared from eggs of stink bugs from 18 localities in seven different countries from 1991 to 2016 (Table 1 and Appendix 1). The label data for all specimens have been georeferenced and recorded in the Hymenoptera On-Line database (Hymenoptera online 2016). Details of these specimens can be accessed entering the identifier in the form (note the space between the acronym and the number). All insects were stored in 95% ethanol at -20 °C until DNA extraction. After nondestructive DNA extraction the voucher specimens were deposited in the C. A. Triplehorn Insect Collection (OSUC).

DNA extraction, amplification, and sequencing

Genomic DNA from whole specimens was extracted using a nondestructive protocol as described in Taekul *et al*. (2014). Following extraction a 597-bp fragment of the mitochondrial cytochrome oxidase subunit 1 (COI) was amplified using the SCEL-F1/HCO-2198 primer pair (Gariepy *et al*. 2014), and the entire internal transcribed spacer 2 (ITS2) region was amplified using the ITS2-F/ITS2-R primer pair (Ji *et al.* 2003). Polymerase chain reactions (PCRs) were performed using GoTaq® Green Master Mix (Promega) and conducted in a Mastercycler® nexus gradient (Eppendorf). Thermocycling conditions were: an initial denaturing step at 95°C for 4 min, followed by 35 cycles of 95°C for 45 s, 54°C for 45 s, 72°C for 45 s and an additional extension at 72°C for 5 min. The PCR products were detected by electrophoresis on a 1.2% agarose gel stained with ethidium bromide and purified using the QIAquick PCR purification kit protocol when necessary. Amplicons were directly sequenced in both directions with forward and reverse primers by Beckman Coulter Genomics (Danvers, MA). Chromatograms were assembled with Sequencher v4.0 (Gene Codes Corporation, Ann Arbor, MI). Sequences for COI and for ITS2 are listed in Appendix 4 and 5, respectively. Sequences will be submitted to GenBank.

Phylogenetic analysis and haplotype network

The sequences of both the COI gene and the ITS2 region were aligned by MAFFT v7 (Katoh & Standley 2013) and unique haplotype was determined using DnaSP5 (Librado & Rozas 2009). The genetic differences, including haplotype diversity (h) and nucleotide diversity within populations were estimated by an analysis of molecular variance (AMOVA) using Arlequin 3.5 (Excoffier & Lischer 2010) with 10,000 permutations. Regional haplotype diversity was visualized as pie charts on a map using PhyloGeoViz (Tsai 2010).

Bayesian analyses were performed in MrBayes 3.2 (Ronquist *et al.* 2012) for both genes and the concatenated matrix. jModelTest2 (Darriba *et al.* 2012) was used to test for the best-fit model of evolution for each gene. GTR + I + G was selected for both genes and the concatenated alignment by the corrected Akaike Information Criterion (AICc) (Darriba *et al.* 2012). Two independent Markov chains were run for 5 million generations and convergence was maximized by ensuring that the average standard deviation of split frequencies was below 0.01. Trees were sampled every 1000 generations and the first 25% of each run was discarded as burn-in. The species *T. brochymenae* was used as outgroup. FigTree version 1.4.3 (Rambaut 2016) and TreeGraph2 (Stöver & Müller 2010) was used to visualize the results.

Results

Spatial distribution of genetic and haplotype diversity

Among the 149 examined individuals representing 18 populations, 73 COI and ITS2 haplotypes (h) were identified (Table 1). The haplotypes were the same for both genes.

Genetic diversity measures include haplotype diversity, i.e. the probability that two randomly chosen haplotypes are different; and nucleotide diversity, i.e. the average number of nucleotide differences per site between two randomly chosen DNA sequences (Nei & Li 1979). For the total sample measures showed high haplotype diversity (h-mean 0.735; range: 0–1.000) and high nucleotide diversity (π -mean 0.053; range: 0–0.199). High haplotype and genetic diversity showed in Ohio (OH), Arkansas (AR), Kansas (KS), Texas Cooke county (TXcc), Texas Lick Creek (TXlc), Cuba (CUBA) and Brazil (BRA RS) samples (h range: 0.667-1.000; π range: 0.064 – 0.199). High haplotype diversity and low genetic diversity showed in Texas Star county (TXsc), Texas Kennedy Ranch (TXkr), Arizona (AZ), Tennessee (TN) and Dominican Republican Armando Bermudez (DRab) (h range: 0.900-1.000; π range: 0.000 – 0.024). Low haplotype and genetic diversity showed in Mexico (MEX), Dominican Republican Morne Trois Pitons (DRmt), Panama (PAN) and Bolivia (BOL) (h:0; π: 0) (Table 1).

Single haplotypes represented 76.7% (56/73) of all haplotypes. Haplotype 73 (H73) was the most frequent, representing 13% (19/149) of the total sample, and being the only haplotype found in Bolivia, Dominican Republic (Morne Trois Pitons), Panama and Mexico. H6 was the second most frequent haplotype representing 11% (16/149), and was found in five localities (AZ, TXbs, TXcc, OH and BRA RS). H8 represented 8% (12/149) and also, was spread among five localities (TXcc, TXlc, OH, Cuba and BRA RS). The remaining frequent haplotypes found in more than one locality was H49, H68, H35, H9 and H19. In total, were found 65 unique haplotypes (89% of total), i.e. haplotypes unique to a geographic area. Geographical distribution of haplotypes diversity is showed in Figure 1.

Phylogenetic and phylogeographic analyses

Three trees were generated by Bayesian Inference analysis with COI genes (Appendix 2), ITS2 region (Appendix 3) and a concatenate tree of both molecular markers (Figure 2). All trees had a high posterior probability values.

Four main polyphyletic clades are revealed in the phylogenetic tree. Haplotype 72 was the most basal to all others haplotypes. In sequence, three branches that originates three clades (haplotypes H73 to H41) and a monophyletic group formed from H39 to H1 (haplotypes H40 to H1). The haplotypes H73 (BOL, PAN, MEX and DRmt) formed the same subclade with H70, H71 and H69 from BRA RS. The next subclade was formed by haplotypes from Ohio, Texas (TXlc and TXkr), Arkansas and Brazil (H65, H67, H68, H66). The next clade was entirely composed of haplotypes detected in the populations placed in Ohio and Tennessee. The third one, is compounded by haplotypes from Brazil (4), Cuba (1) and Texas (1-TXsc). A monophyletic group formed by three subclades have haplotypes from Arkansas (1), Kansas (1), Arizona (4) and Brazil (1) in the first one; Ohio (12), Texas (TXlc-2 and TXcc-3) and Kansas (3) in the second subclade, and in the third one, haplotypes from Ohio (10), Arkansas (1), Texas (TXlc-5, TXcc-3, TXbs-1), Arizona (1), Cuba (1), Drab (1) and Brazil (3) (Figure 2).

Discussion

The large numbers of singleton haplotypes revealed in this study are quite striking. In fact, more than 70% of haplotypes are singletons and 89% are unique to a geographic area. The presence of many singletons may indicate a recent origin for them (Crandal & Templeton 1993) or local adaptation. Contrasting is that the haplotype most frequent H73 is from Mexico, Dominican Republican (Morne Trois Pitons), Panama and Bolivia. All these countries are in Central America, except by Bolivia in the middle South America, and are closer countries compared to USA and South America. These populations had low haplotype and genetic diversity. Population with small haplotype and genetic diversity can be trough recent population bottleneck or founder event by single or a few DNA lineages (Grand & Bowen 1998). A geographical or climatic barrier could prevent many haplotypes from establish in determined local and then increase effective population sizes and a large amount of within-population genetic variation as recorded also for other insects (Ferreira & Ferguson 2010; Tan *et al.* 2016). These results can suggest two pathways for them. First, the population spread out from Central

America through South America or second, the opposite happened with the stopped spread population in Central America by geographic or climatic barriers.

The second most frequent haplotype was H6 (AZ, TXbs, TXcc, OH and BRA RS). In these populations, some have high haplotype diversity and low genetic diversity (TXbs and AZ), that can mean population bottleneck followed by rapid population growth and accumulation of mutations (Grand & Bowen 1998). The genetic diversity of invasive populations is always considered low due to the reduced size of propagules and bottleneck events (Nei *et al.* 1975). Then, these haplotypes can be establishing in small populations across geographic area.

The third most frequent was H8 (TXcc, TXlc, OH, Cuba and BRA RS). All these population have high haplotype and genetic diversity that can mean large stable population with long evolutionary or secondary contact between differentiated lineages (Grand & Bowen, 1998). Then, they can be spread out for long time ago with good establishment or/and have more than one population colonizing in the same region. Multiple invasions/colonization would be an alternative explanation for the high genetic diversity observed (Guidolin *et al*. 2014).

Phylogeography is a powerful tool to infer evolutionary processes at the intraspecific level and among closely related species (Avise 1998, 2009). The use of both cytoplasmic and nuclear markers is preferred over use of a single gene to reveal the phylogeographic patterns (Presa *et al*. 2002; Mardulyn *et al*. 2011; Turmelle *et al*. 2011; Cornetti *et al*. 2014). From the results, we can see through the phylogenetic analysis two different groups within the populations. Some haplotypes seem to be evolving through different pathways and independently of geographic location. Other features may be putting pressure on these haplotypes.

Although it is not clear how mitochondrial DNA selection evolves (Meiklejohn *et al*. 2007), mutation of mitochondrial DNA has been directly linked with phenotypic selection (Ballard & Melvin 2010), resulting in phenotypes expressing diverse fitness traits (Ballard & Melvin 2010; Rand *et al*. 2004). This can occur in spread pest disease, with some haplotype of insect vector being associated with specific haplotype (Guidolin *et al.* 2014). *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) for example, is recognized as a species complex of 34 species that are morphologically indistinguishable (Boykin & De Barro 2014); however, putative species exhibit differences in host range, phylogeographical clustering and potential to transmit viruses (Legg *et al.* 2014; Wainaina *et al.* 2016). Thus, it can occur with parasitoids indistinguishable morphologically.

The shift of host also can be associated with differences on haplotypes. A research with the parasitoid *Pnigalio mediterraneus* Ferriere & Delucchi (Hymenoptera: Eulophidae) showed lower genetic diversity of these species on *Cameraria ohridella* Deschka & Dimic (Lepidoptera: Gracillariidae) than on *Bactrocera oleae* Rossi (Diptera: Tephritidae). That could be explained by a recent shift to *C. ohridella* or by the fact these host feed on a toxic plant, which could serve as a barrier to the adaptation of many haplotypes to this host (Gebiola *et al.* 2014).

Temperature tolerance (climactic barrier) can be observed in different insects species (Gebiola *et al.* 2014; Tan *et al*. 2016). Borges *et al*. (2003) showed differences in *T. podisi* populations from Brazil (Brasilia) and USA (Maryland) in cold tolerance. Although this aspect was not analyzed by the authors, these populations can have differences in haplotype level, as we can see in this work in some haplotypes from Brazil and USA, justifying the thermotolerance between them.

Telenomus podisi is known by parasite Pentatomidae eggs (Johnson 1984; Hanson & Gauld 2006) and others stink bugs in crops. Many individuals in this research were sampled in crops, such as BRA RS (rice crop), CUBA (beans), TN (organic crops), so it can be associated to pests species. On the other hand, samples such as AZ, AR, TX, OH were sampled in natural areas (forest, prairie), so, may have other hosts (Johnson 1984). More researches associating these haplotypes with hosts can indicate genetic differences regard to their hosts.

The genetic variability of the populations, in general, is higher in the origin regions of the species as compared to those where the species was introduced, as exemplified in the works of Gariepy *et al.* (2014b) and Xu *et al.* (2014) that describe only a single COI haplotype and two COII haplotypes in specimens collected from the USA and Canada, in contrast with native Asian range, where are recorded 21 COI haplotypes and 18 COII haplotypes of *H. halys* (Hemiptera: Pentatomidae). For biological control of an exotic species, a population of parasitoid with a larger range of haplotypes would be better to try, because of the greater genetic diversity which can lead a good establishment of the introduced parasitoid; or could to improve some better feature from determined area, such as thermotolerance. For example, from present results, to use specimens from Central America or Bolivia with one kind of haplotype is not a great option, unless these species had some specific recognized important fitness trait.

Speciation can be conceptualized in terms of a few general evolutionary processes: mutation, natural selection, migration (or the lack thereof), and genetic drift and the characters affected by those processes, however, are highly diverse (De Queiroz 2007). They may be genotypic or phenotypic; qualitative or quantitative; selectively advantageous, disadvantageous, or neutral. About the species concept problem, the important point is that changes in these characters lead to the acquisition of a number of different properties by diverging lineages (De Queiroz 2007). In this study, we can see variation within populations that can lead to future speciation. It is important inside biological control context, because can change relation of these populations regarding some host insects (acceptance or not, host shift) (Gebiola *et al.* 2014), as well as local flora and association (Popkin *et al*. 2016), physiological features (Borges *et al*. 2003), insecticides resistance (Vontas *et al*. 2002; Guidolin *et al.* 2014) and transgenic response (Gantz *et al.* 2015; Xia *et al*. 2016).

Differences in each population can lead to different methodologies regarding to biological control. Then, methodological adaptations should be created according to geographical area of work being account intrinsic characteristics of each population to have an effective biological control.

Acknowledgments

The authors would like to thank C.A. Triplehorn Insect Collection, Ohio State University, Columbus, OH, for technical assistance, and CAPES and CNPq for financial support.

TABLE 1. Sampling sites with their coordinates and abbreviation, number of individuals (N), haplotype (h) and nucleotide (π) diversity of each populations grouped according to geographical origin of *Telenomus podisi*.

Locality	Abbreviation	Coordinates	N	Number of Haplotypes	h (SD)	π (SD)	Haplotype distribution
USA/ Ohio	OH	39.59936°N 83.02809°W	41	31	0.972 ± 0.016	0.123 ± 0.061	H1(2), H2(1), H3(1), H5(1), H6(1), H8(1), H9(1), H12(1), H14(1), H15(1), H17(1), H18(4), H19(6), H20(1), H21(1), H22(1), H23(1), H24(1), H26(1), H30(1), H40(2), H49(1), H51(1), H52(1), H53(1), H54(1), H55(1), H57(1), H61(1), H68(1)
USA/Arkansas	AR	34.303162°N 93.031013°W	3	3	1.000 ± 0.272	0.199 ± 0.150	H4(1), H35(1), H67(1)
USA/Kansas	KS	39.062476N 96.36329W	4	4	1.000 ± 0.177	0.092 ± 0.0621	H19(1), H27(1), H28(1), H39(1)
USA/Texas, Cooke Co.	TXcc	33.400199N 97.210596W	8	6	0.928 ± 0.084	0.065 ± 0.0368	H6(2), H7(1), H8(2), H19(1), H25(1), 32(1)
USA/Texas, Lick Creek Park	TXlc	30.340198N 96.123917W	12	9	0.935 ± 0.051	0.138 ± 0.072	H8(2), H9(1), H10(1), H13(1), H16(2), H29(1), H33(1), H45(2), H68(1)
USA/Texas, Starr Co.	TXsc	26.371746N 98.445322W	1	1	1.000 ± 0.000	0.000 ± 0.000	H47(1)
USA/Texas, Kenedy Ranch	TXkr	27.133262N 97.474576W	1	1	1.000 ± 0.000	0.000 ± 0.000	H66(1)
USA/Texas, Bastrop State Park	TXbs	30.063665N 97.171284W	1	1	1.000 ± 0.000	0.000 ± 0.000	H6(1)
USA/Arizona, Appleton Whittell	AZ	31.361156N 110.302686W	5	4	0.900 ± 0.161	0.006 ± 0.005	H35(2), H36(1), H37(1), H38(1)
USA/Arizona, Coronado National Forest	AZ	31.441505N 110.453574W	1	1	1.000 ± 0.000	0.000 ± 0.000	H6(1)
USA/Tennessee, Knox Co.	TN	35.591487N 83.583112W	11	9	0.964 ± 0.051	0.025 ± 0.014	H48(1), H49(1), H50(1), H56(1), H58(1), H59(2), H60(1), H62(2), H63(1)

…Continued on the next page

TABLE 1. (Continued)

Locality	Abbreviation	Coordinates	N	Number of Haplotypes	h (SD)	π (SD)	Haplotype distribution
Mexico/Oaxaca	MEX	16.042812N 96.28099W	4	1	0.000 ± 0.000	0.000 ± 0.000	H73(4)
Cuba/Manicaragua	CUBA	22.084796N 79.584086W	3	2	0.667 ± 0.314	0.127 ± 0.096	H8(2), H44(1)
Dominican Republic/ Armando Bermúdez National Park	DRab	19.103281N 71.030015W	1	1	1.000 ± 0.000	0.000 ± 0.000	H11(1)
Dominican Republic/Morne Trois Pitons NP	DRmt	15.20953N 61.20556W	3	1	0.000 ± 0.000	0.000 ± 0.000	H73(3)
Panama/Veraguas	PAN	8.3031N 81.0710W	3	1	0.000 ± 0.000	0.000 ± 0.000	H73(3)
Bolivia/Santa cruz	BOL	17.50124S 64.23454W	9	1	0.000 ± 0.000	0.000 ± 0.000	H73(9)
Brazil/Rio Grande do Sul	BRA RS	29.471662S 51.210091W	38	14	0.859 ± 0.035	0.180 ± 0.089	H6(11), H8(5), H9(1), H34(1), H41(8), H42(1), H43(1), H46(1), H64(1), H65(1), H69(4), H70(1), H71(1), H72(1)
Average					0.735 ± 0.645	0.053 ± 0.033	

References

Almeida, R.P. & Stouthamer, R. (2015) ITS-2 sequences-based identification of *Trichogramma* species in South America. *Brazilian Journal of Biology*, 75 (4).

Avise, J. (1998) The history and purview of phylogeography: a personal reflection. *Molecular Ecology*, 7, 371–379.

Avise, J. (2009) Phylogeography: retrospect and prospect. *Journal of Biogeography*, 36, 3–15.

Ballard, J.W.O. & Melvin, R.G. (2010) Linking the mitochondrial genotype to the organismal phenotype. *Molecular Ecology* 19, 1523–1539.

Borges, M., Colazza, S., Ramirez-Lucas, P., Chauhan, K.R., Moraes, M.C.B. & Aldrich, J.R. (2003). Kairomonal effect of walking traces from *Euschistus heros* (Heteroptera: Pentatomidae) on two strains of *Telenomus podisi* (Hymenoptera: Scelionidae). *Physiological entomology*, 28(4), 349-55.

Boykin, L.M. & De Barro, P. J. (2014) A practical guide to identifying members of the *Bemisia tabaci* species complex: and other morphologically identical species. *Frontiers in Ecology and Evolution*, 2(August), 1–5. doi:10.3389/fevo.2014.00045

Chroni, A., Djan, A.M., Vidaković, D.O., Petanidou, T. & Vujić, A. (2016) Molecular species delimitation in the genus *Eumerus* (Diptera: Syrphidae) *Bulletin of Entomological Research*, p. 1-13, doi:10.1017/S0007485316000729

Cornetti, L., Menegon, M., Glovine, G., Heulin, B. & Vernesi C. (2014) Mitochondrial and nuclear DNA survey of *Zootoca vivipara* across the eastern Italian Alps: Evolutionary relationships, historical demography and conservation implications. —*PLoS ONE* 9, 1–10.

Corrêa-Ferreira, B.S. & Moscardi, F. (1996) Biological control of soybean stink bugs by inoculative releases of *Trissolcus basalis*. *Entomologia Experimentalis et Applicata*, 79, 1- 7.

Corrêa-Ferreira, B.S. (2002) *Trissolcus basalis* para o controle de percevejos da soja. In: Parra, J.R.P.; Botelho, P.S.M.; Corrêa-Ferreira, B.S.; Bento, J.M.S. (Eds.). *Controle biológico no Brasil*: parasitoides e predadores. São Paulo: Manole, p. 449- 476.

Crandall, K.A. & Templeton, A.R. (1993) Empirical tests of some predictions from coalescent theory with applications to intraspecific phylogeny reconstruction. — *Genetics*, 134, 959–969.

Darriba, D., Taboada, G.L., Doallo, R. & Posada D. (2012) jModelTest 2: more models, new heuristics and parallel computing. *Nature methods*, 9(8), 772.

De Queiroz, K. (2007) Species Concepts and Species Delimitation. *Systematic Biology*, 56 (6), 879–886.

Ehler, L.E. (2002) An evaluation of some natural enemies of *Nezara viridula* in northern California. *Biocontrol*, 47, 309-325.

Excoffier, L. & Lischer, H.E. L. (2010) Arlequin suite ver 3.5: A new series of programs to perform population genetics analyses under Linux and Windows. *Molecular Ecology Resources*, 10, 564-567.

Ferreira, M. & Ferguson, J. (2010) Do Mediterranean crickets *Gryllus bimaculatus* De Geer (Orthoptera: Gryllidae) come from the Mediterranean? Largescale phylogeography and regional gene flow. *Bulletin of Entomological Research*, 100, 49–58.

Gantz, V.M., Jasinskiene, N., Tatarenkova, O., Fazekas, A., Macias, V.M., Bier, E. & James, A.A. (2015) Highly efficient Cas9-mediated gene drive for population modification of the malaria vector mosquito *Anopheles stephensi*. *Proceedings of the National Academy of Sciences,* 112 (49), www.pnas.org/cgi/doi/10.1073/pnas.1521077112

Gariepy, T.D., Haye, T. & Zhang, J. (2014) A molecular diagnostic tool for the preliminary assessment of host–parasitoid associations in biological control programmes for a new invasive pest. *Molecular Ecology*, 23, 3912–3924.

Gariepy, T.D., Haye, T., Fraser, H. & Zhang, J. (2014b) Occurrence, genetic diversity, and potential pathways of entry of *Halyomorpha halys* in newly invaded areas of Canada and Switzerland. *Journal of Pest Science*, 87, 17–28.

Gebiola, M., Lopez-Vaamonde, C., Nappo, A.G. & Bernardo, U. (2014) Did the parasitoid Pnigalio mediterraneus (Hymenoptera: Eulophidae) track the invasion of the horse chestnut leafminer? *Biological Invasions*, 16, 843–857 DOI 10.1007/s10530-013-0542-8

Guidolin, A.S., Fresia, P. & Consoli, F.L. (2014) The Genetic Structure of an Invasive Pest, the Asian Citrus Psyllid *Diaphorina citri* (Hemiptera: Liviidae) *PLOS ONE,* DOI:10.1371/journal.pone.0115749

Grand, W.S. & Bowen, B.W. (1998) Shallow population histories in deep evolutionary lineages of marine fishes: insights from sardines and anchovies and lessons for conservations. *Journal of Heredity*, 89, 415-426.

Hanson, P. E. & Gauld, I. D. (2006) *Hymenoptera de la Región Neotropical***.** v.77. Gainsville: The American Entomological Institute.

Hull, D. L. (1980) Individuality and selection. *Annual Review of Ecology and Systematics,* 11, 311–332.

Hymenoptera Online (HOL). [Online] Available from http://hol.osu.edu. (accessed 19 November 2016)

Idalgo, T.D.N., Sant'Ana J., Redaelli, L.R. & Pires, P.D.S. (2013) Parasitismo de ovos de *Tibraca limbativentris* Stål (Hemiptera: Pentatomidae) em lavoura de arroz irrigado, Eldorado do Sul, RS. *Arquivos do Instituto Biológico,* 80 (4), 453-456.

Ji, Y.-J., Zhang, D.-X., He, L.-J. (2003) Evolutionary conservation and versatility of a new set of primers for amplifying the ribosomal internal transcribed spacer regions in insects and other invertebrates. *Molecular Ecology*, 3, 581-585.

Johnson, N.F. (1984) Systematics of nearctic *Telenomus*: classification and revisions of the *podisi* and *phymatae* species groups [Hymenoptera: Scelionidae]. *Bulletin Ohio Biological Survey,* 6,1–113.

Katoh, K. & Standley, D.M. (2013) MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Molecular Biology and Evolution*, 30,772–780.

Kenyon, S.G., Buerki, S., Hansson, C., Alvarez, N. & Benrey, B. (2015) Uncovering Cryptic Parasitoid Diversity in *Horismenus* (Chalcidoidea, Eulophidae). *PLoS ONE,* 10 (9), doi:10.1371/journal. pone.0136063

Khullar, N., Singh, D. & Jha, C.K. (2016) Short COI marker: A valuable tool for identification and phylogenetic analysis of 6 forensically important blow fly species from India. *Journal of Entomology and Zoology Studies,* 4 (3), 27-31.

Kozlov, M.A. (1970) Supergeneric groupings of Proctotrupoidea (Hymenoptera). *Entomologicheskoye Obozreniye*, 49, 203–226.

Kozlov, M.A. & Kononova, S.V. (1983) *Telenominae of the Fauna of the USSR.* Nauka, Leningrad.

Legg, J. P., Sseruwagi, P., Boniface, S., Okao-Okuja, G., Shirima, R., Bigirimana, S., Gashakae, G., Herrmannf, H-W., Jeremiahg, S., Obieroh, H., Ndyetabulai, I., Tata-Hangyj, W., Masembe, C. & Brown, J. K (2014) Spatio-temporal patterns of genetic change amongst populations of cassava *Bemisia tabaci* whitef lies driving virus pandemics in East and Central Africa. *Virus Research*, 186, 61–75. doi:10.1016/j.virusres.2013.11.018

Librado, P. & Rozas, J. (2009) DnaSP v5: a software for comprehensive analysis of DNA polymorphism data. *Bioinformatics* 25, 1451–1452.

Maciel, A. A. S., Lemos, R.N.S. de., Souza, J.R. de., Costa, V.A., Barrigossi, J.A.F. & Chagas, E.F. das. (2007) Parasitismo de Ovos de *Tibraca limbativentris* Stal (Hemiptera: Pentatomidae) na Cultura do Arroz no Maranhão. *Neotropical Entomology*, 36, (4), 616-618.

Mardulyn, P., Othmezouri, N., Mikhailov, Y.E. & Pasteels, J.M. (2011) Conflicting mitochondrial and nuclear Phylogeographic signals and evolution of host-plant shifts in the boreo-montane leaf beetle *Chrysomela lapponica*. — *Molecular phylogenetics and Evolution*, 61, 686–696.

Masner, L. (1972) The classification and interrelationships of Thoronini (Hymenoptera: Proctotrupoidea, Scelionidae). *The Canadian Entomologist*, 104, 833–849.

Masner, L. (1976) Revisionary notes and keys to world genera of Scelionidae (Hymenoptera: Proctotrupoidea). *Memoirs of the Entomological Society of Canada*, 97, 1–87.

Masner, L. & Huggert, L. (1979) Revision of the world species of Aradophagini (Hymenoptera: Scelionidae). *The Canadian Entomologist*, 111, 1089–1100.

Meiklejohn, C.D., Montooth, K.L. & Rand, D.M. (2007) Positive and negative selection on the mitochondrial genome. *Trends in Genetics* 23, 259–263.

Miranda, E.A., Batalha-Filho, H., Congrains, C., Carvalho, A.F., Ferreira, K.M. & Del Lama, M.A. (2016) Phylogeography of *Partamona rustica* (Hymenoptera, Apidae), an Endemic Stingless Bee from the Neotropical Dry Forest Diagonal. *PLOS ONE*. DOI:10.1371/journal.pone.0164441

Monti, M. M., Nappo, A. G. & Giorgini, M. (2005) Molecular characterization of closely related species in the parasitic genus *Encarsia* (Hymenoptera: Aphelinidae) based on the mitochondrial cytochrome oxidase subunit I gene. *Bulletin of Entomological Research*, 95, 401-408.

Murphy, N.P.; Carey, D.; Castro, L.R.; Dowton, M. & Austin, A.D. (2007) Phylogeny of the platygastroid wasps (Hymenoptera) based on sequences from the 18S rRNA, 28S rRNA and cytochrome oxidase *I* genes: implications for the evolution of the ovipositor system and host relationships. *Biological Journal of the Linnean Society*, 91, 653–669.

Nei, M., Muruyama, T. & Chakraborty, R. (1975) The bottleneck effect and genetic variability in populations. *Evolution*, 29, 1–10.

Nei, M. & Li, W.H. (1979) Mathematical models for studying genetic variation in terms of restriction endonucleases. *Proceedings of the National Academy of Sciences of the United States of America*, 76, 5269–5273.

Popkin, M., Piffaretti, J., Clamens, A.L., Qiao, G.X., Chen, J., Vitalis, R., Vanlerberghemasutti, F., Gupta, R.K., Lamaari, M., Langella, O., D'acier, A.C. & Jousselin, E. (2016) Large-scale phylogeographic study of the cosmopolitan aphid pest *Brachycaudus helichrysi* reveals host plant associated lineages that evolved in allopatry. *Biological Journal of the Linnean Society*.

Presa, P., Pardo, B.G., Marinez, P. & Bernatchez L. (2002) Phylogeographic congruence between mtDNA and rDNA ITS markers in brown trout. — *Molecular Biology and Evolution*, 19, 2161–2175.

Rahimi, S., Hosseini,R., Hajizadeh, J. & Sohani, M.M. (2012) Evaluation of COI and ITS2 sequences ability to distinguish *Lysiphlebus fabarum* and *Lysiphlebus confusus* (Hymenoptera: Aphidiidae). *Journal of Entomological Society of Iran*, 31 (2), 53-66.

Rand, D.M., Haney, R.A. & Fry, A.J. (2004) Cytonuclear coevolution: the genomics of cooperation. *Trends in ecology & Evolution*, 19, 645–653.

Rambaut, A. (2016) FigTree v1.4.3: Tree Figure Drawing Tool. tree.bio.ed.ac.uk/software/figtree/.

Riffel, C. T. (2007) *Levantamento e aspectos biológicos de espécies parasitoides de posturas do percevejo-do-colmo-do arroz no estado de Santa Catarina*. 2007. Dissertação (Mestrado) - Centro de Ciências Agroveterinárias, UDESC - Universidade do Estado de Santa Catarina, Lages. 73p.

Ronquist, F., Teslenko, M., van der Mark, P., Ayres, D.L., Darling, A. & Hohna S. (2012). MrBayes 3.2: Efficient Bayesian Phylogenetic Inference and Model Choice Across a Large Model Space. *Systematic Biology*, 61(3), 539–42.

Simpson, G. G. (1951). The species concept. *Evolution*, 5, 285–298.

Simpson, G. G. (1961). Principles of animal taxonomy. Columbia University Press, New York.

Stöver, B.C. & Müller, K. F. (2010) TreeGraph 2: Combining and visualizing evidence from different phylogenetic analyses. BMC *Bioinformatics*, 11, 7. http://treegraph.bioinfweb.info/Download DOI: 10.1186/1471-2105-11-7

Sunnucks, P. (2000) Efficient genetic markers for population biology. *Trends in Ecology & Evolution*, 15 (5).

Taekul, C., Valerio, A. A., Austin, A. D., Klompen, H. & Johnson, N. F. (2014) Molecular phylogeny of telenomine egg parasitoids (Hymenoptera: Platygastridae s.l.: Telenominae): evolution of host shifts and implications for classification. *Systematic Entomology*, 39, 24–35.

Talamas, E.J., Herlihy, M.V., Dieckhoff, C., Hoelmer, K.A., Buffington, M.L., Bon, M.C. &

Weber, D.C. (2015) *Trissolcus japonicus* (Ashmead) (Hymenoptera, Scelionidae) emerges in North America. *Journal of Hymenoptera Research*, 43, 119–128.

Tan, K., Qu, Y., Wang, Z., Liu, Z., Engel, M.S. (2016) Haplotype diversity and genetic similarity among populations of the Eastern honey bee from Himalaya-Southwest China and Nepal (Hymenoptera: Apidae). *Apidologie*, 47, 197–205, DOI: 10.1007/s13592-015-0390-x

Tancoigne, E., Bole, C., Sigogneau, A. & Dubois, A. (2011) Insights from Zootaxa on potential trends in zoological taxonomic activity. *Frontiers in Zoology*, 8, (5).

Tillman, P. G. (2011) Natural Biological Control of Stink Bug (Heteroptera: Pentatomidae) Eggs in Corn, Peanut, and Cotton Farmscapes in Georgia. *Environmental Entomology*, 40 (2), 303-314. http://dx.doi.org/10.1603/EN10154

Tsai, Y-HE (2010) PhyloGeoViz: a web-based program that visualizes genetic data on maps. *Molecular Ecology Resources,* 11, 557–561.

Tsuchida, K.; Kudo, K. & Ishiguro, N. (2014) Genetic structure of an introduced paper wasp, *Polistes chinensis antennalis* (Hymenoptera, Vespidae) in New Zealand. *Molecular Ecology*, 23, 4018–4034. doi: 10.1111/mec.12852

Turmelle, A.S., Kunz, T.H. & Sorenson, M.D. (2011) A tale of two genomes: contrasting patterns of phylogeographic structure in a widely distributed bat. — *Molecular Ecology*, 20, 357–375.

Venkatesan, T., More, R.P., Baskar, R., Jalali, S.K., Lalitha, Y. & Ballal, C.R. (2016) Differentiation of some indigenous and exotic trichogrammatids (Hymenoptera: Trichogrammatidae) from India based on Internal transcribed spacer-2 and cytochrome oxidase-I markers and their phylogenetic relationship. *Biological control*, 101,103-137.

Vontas, J.G., Small, G.J., Nikou., D.C., Ranson, H. & Hemingway, J. (2002) Purification, molecular cloning and heterologous expression of a glutathione S-transferase involved in insecticide resistance from the rice brown planthopper, *Nilaparvata lugens. The Biochemichal Journal,* 362, 329±337 (Printed in Great Britain).

Wägele, H., Kolb, A. K., Kuhlmann, M., Haszprunar, G., Lindberg, D., Koch, A. & Wägele, J.W. (2011) The taxonomist - an endangered race. A practical proposal for its survival. *Frontiers in Zoology*, 8 (25).

Wainaina, J.M., De Barro, P., Kubatko, L., Kehoe, M.A., Harvey, J., Karanja, D., Boykin, L.M. (2016) Genetic Diversity, Population Structure and Species Delimitation of *Trialeurodes vaporariorum* (greenhouse whitefly). *bioRxiv.org: the preprint server for biology,* doi: http://dx.doi.org/10.1101/067769.

Xia, H., Zhang, H., Wang, W., Yang, X., Wang, F., Su, J., Xia, H., Xu, K., Cai, X. & Lu, B.R. (2016) Ambient insect pressure and recipient genotypes determine fecundity of transgenic crop-weed rice hybrid progeny: Implications for environmental biosafety assessment. *Evolutionary Applications*, ISSN 1752-4571. doi:10.1111/eva.12369.

Xu, J., Fonseca D., Hamilton, G., Hoelmer, K. & Nielsen A (2014) Tracing the origin of US brown marmorated stink bugs, *Halyomorpha halys*. *Biological Invasions,* 16, 153–166.

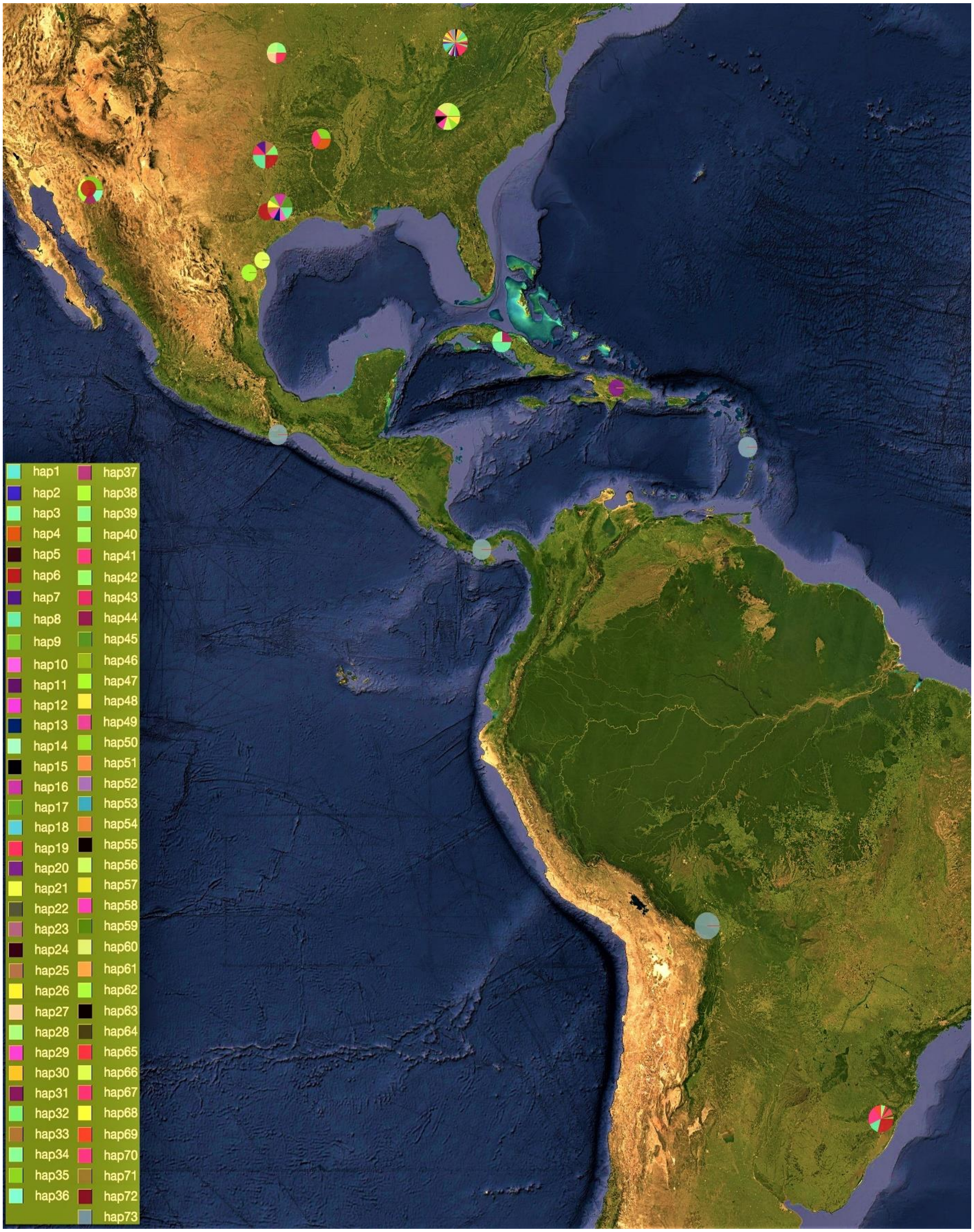


FIGURE 1. Geographic distribution of the 73 haplotypes among the 18 sampled localities. Each pie represents a locality.

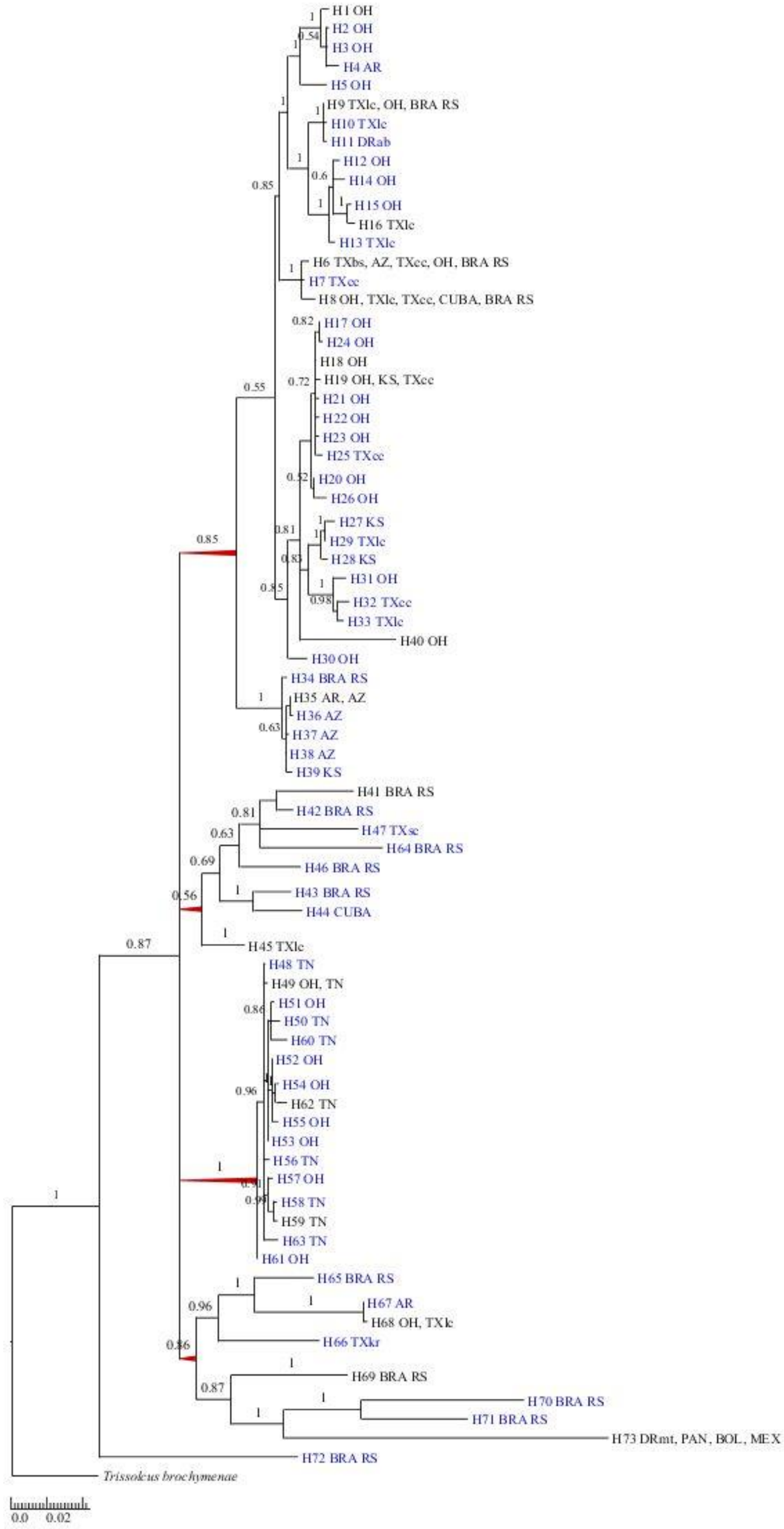


FIGURE 2. Bayesian consensus concatenate tree of the COI gene and ITS2 haplotypes of *Telenomus podisi* with posterior probability values showed over the branches. *Branches of the four main clades are in red color and singletons haplotypes are highlighted in blue color.

6 CONSIDERAÇÕES FINAIS

As diferenças apontadas neste trabalho a respeito do gradiente de distância da vegetação nativa em relação à lavoura do arroz indicam que fragmentos de vegetação nativa são importantes para a diversidade e abundância de himenópteros parasitoides, principalmente em áreas do manejo convencional, onde a vegetação nas taipas não está presente. Nas áreas com manejo orgânico, nas quais as taipas possuem vegetação espontânea, esta influência não é claramente percebida, possivelmente porque estas servem de refúgio, abrigo e corredor ecológico para os inimigos naturais.

Os estágios fenológicos de desenvolvimento do arroz podem influenciar a composição de famílias de parasitoides e, dentro da família Platygastridae (Scelioninae, Teleasinae e Telenominae) especificamente, com diferentes morfoespécies e em densidades discrepantes nos dois períodos da cultura. Esse aspecto deve estar relacionado aos diferentes hospedeiros, muitas vezes insetos fitófagos, presentes em cada fase da cultura. Investigações referentes a isso podem trazer importantes informações a respeito da dinâmica e das relações destas populações no sistema orizícola.

Os inseticidas químicos podem alterar a riqueza e abundância de parasitoides nas áreas de arroz, o que foi constatado em razão da mudança do manejo realizado na área do convencional pelo produtor que, na primeira safra utilizou inseticidas considerados seletivos aos inimigos naturais e, na segunda aplicou produtos não seletivos (neurotóxicos), decrescendo a abundância de parasitoides no local.

Os registros deste trabalho destacam a importância da família Platygastridae para o controle biológico de pragas em áreas de arroz, indicando que um controle biológico natural pode estar ocorrendo no local, principalmente na área do manejo orgânico.

O terceiro capítulo assinala a variação entre as populações de *T. podisi* e esboça aspectos que conduzem a uma futura especiação. Isto é importante dentro do contexto do controle biológico, pois essas variações podem levar a mudanças nas relações dos parasitoides com determinados insetos hospedeiros, planta hospedeira, características fisiológicas e resistência a inseticidas. Assim, adaptações metodológicas deveriam ser desenvolvidas de acordo com a área geográfica de trabalho considerando características intrínsecas de cada população específica para se ter um efetivo controle biológico.

7 APÊNDICES

APÊNDICE 1. List of specimens included in this study.

Taxa	**Lab Code**	**Voucher no.**	**COI**	**ITS2**
Telenomus podisi	G0002	OSUC 555922	Y	Y
Telenomus podisi	K0025	OSUC 372813	Y	Y
Telenomus podisi	K0020	OSUC 372810	Y	Y
Telenomus podisi	K0044	OSUC 557737	Y	Y
Telenomus podisi	K0034	OSUC 372818	Y	Y
Telenomus podisi	K0032	OSUC 557729	Y	Y
Telenomus podisi	K0040	OSUC 557733	Y	Y
Telenomus podisi	K0027	OSUC 557726	Y	Y
Telenomus podisi	K0019	OSUC 557723	Y	Y
Telenomus podisi	K0024	OSUC 372812	Y	Y
Telenomus podisi	K0042	OSUC 557735	Y	Y
Telenomus podisi	G0003	OSUC 555923	Y	Y
Telenomus podisi	K0001	OSUC 372802	Y	Y
Telenomus podisi	K0033	OSUC 372817	Y	Y
Telenomus podisi	K0037	OSUC 372819	Y	Y
Telenomus podisi	K0009	OSUC 557716	Y	Y
Telenomus podisi	K0038	OSUC 557732	Y	Y
Telenomus podisi	K0005	OSUC 557715	Y	Y
Telenomus podisi	K0016	OSUC 557722	Y	Y
Telenomus podisi	K0046	OSUC 557739	Y	Y
Telenomus podisi	K0047	OSUC 372821	Y	Y
Telenomus podisi	K0014	OSUC 557720	Y	Y
Telenomus podisi	K0015	OSUC 557721	Y	Y
Telenomus podisi	K0041	OSUC 557734	Y	Y
Telenomus podisi	K0045	OSUC 557738	Y	Y
Telenomus podisi	K0051	OSUC 557743	Y	Y
Telenomus podisi	K0013	OSUC 372807	Y	Y
Telenomus podisi	K0039	OSUC 372820	Y	Y
Telenomus podisi	K0018	OSUC 372809	Y	Y
Telenomus podisi	K0002	OSUC 557713	Y	Y
Telenomus podisi	K0017	OSUC 372808	Y	Y

continuação APÊNDICE 1. List of specimens included in this study.

Taxa	**Lab Code**	**Voucher no.**	**COI**	**ITS2**
Telenomus podisi	K0008	OSUC 372806	Y	Y
Telenomus podisi	K0011	OSUC 557718	Y	Y
Telenomus podisi	K0048	OSUC 557740	Y	Y
Telenomus podisi	K0049	OSUC 557741	Y	Y
Telenomus podisi	K0050	OSUC 557742	Y	Y
Telenomus podisi	K0004	OSUC 372803	Y	Y
Telenomus podisi	K0023	OSUC 557725	Y	Y
Telenomus podisi	K0003	OSUC 557714	Y	Y
Telenomus podisi	K0035	OSUC 557730	Y	Y
Telenomus podisi	K0095	OSUC 372832	Y	Y
Telenomus podisi	K0053	OSUC 557744	Y	Y
Telenomus podisi	K0054	OSUC 557745	Y	Y
Telenomus podisi	K0052	OSUC 372823	Y	Y
Telenomus podisi	K0068	OSUC 557756	Y	Y
Telenomus podisi	K0066	OSUC 557754	Y	Y
Telenomus podisi	K0067	OSUC 557755	Y	Y
Telenomus podisi	K0065	OSUC 557753	Y	Y
Telenomus podisi	K0071	OSUC 557758	Y	Y
Telenomus podisi	K0077	OSUC 557764	Y	Y
Telenomus podisi	K0078	OSUC 557765	Y	Y
Telenomus podisi	K0070	OSUC 557757	Y	Y
Telenomus podisi	K0073	OSUC 557760	Y	Y
Telenomus podisi	K0069	OSUC 372826	Y	Y
Telenomus podisi	K0075	OSUC 557762	Y	Y
Telenomus podisi	K0072	OSUC 557759	Y	Y
Telenomus podisi	K0061	OSUC 557750	Y	Y
Telenomus podisi	K0085	OSUC 557770	Y	Y
Telenomus podisi	K0063	OSUC 557752	Y	Y
Telenomus podisi	K0059	OSUC 557748	Y	Y
Telenomus podisi	K0060	OSUC 557749	Y	Y
Telenomus podisi	K0082	OSUC 557767	Y	Y
Telenomus podisi	K0087	OSUC 557772	Y	Y
Telenomus podisi	K0084	OSUC 557769	Y	Y
Telenomus podisi	K0081	OSUC 372828	Y	Y
Telenomus podisi	K0086	OSUC 557771	Y	Y
Telenomus podisi	K0094	OSUC 557776	Y	Y
Telenomus podisi	K0092	OSUC 372831	Y	Y
Telenomus podisi	K0090	OSUC 557774	Y	Y
Telenomus podisi	K0091	OSUC 372830	Y	Y
Telenomus podisi	K0096	OSUC 372833	Y	Y
Telenomus podisi	K0104	OSUC 372836	Y	Y
Telenomus podisi	K0108	OSUC 557785	Y	Y

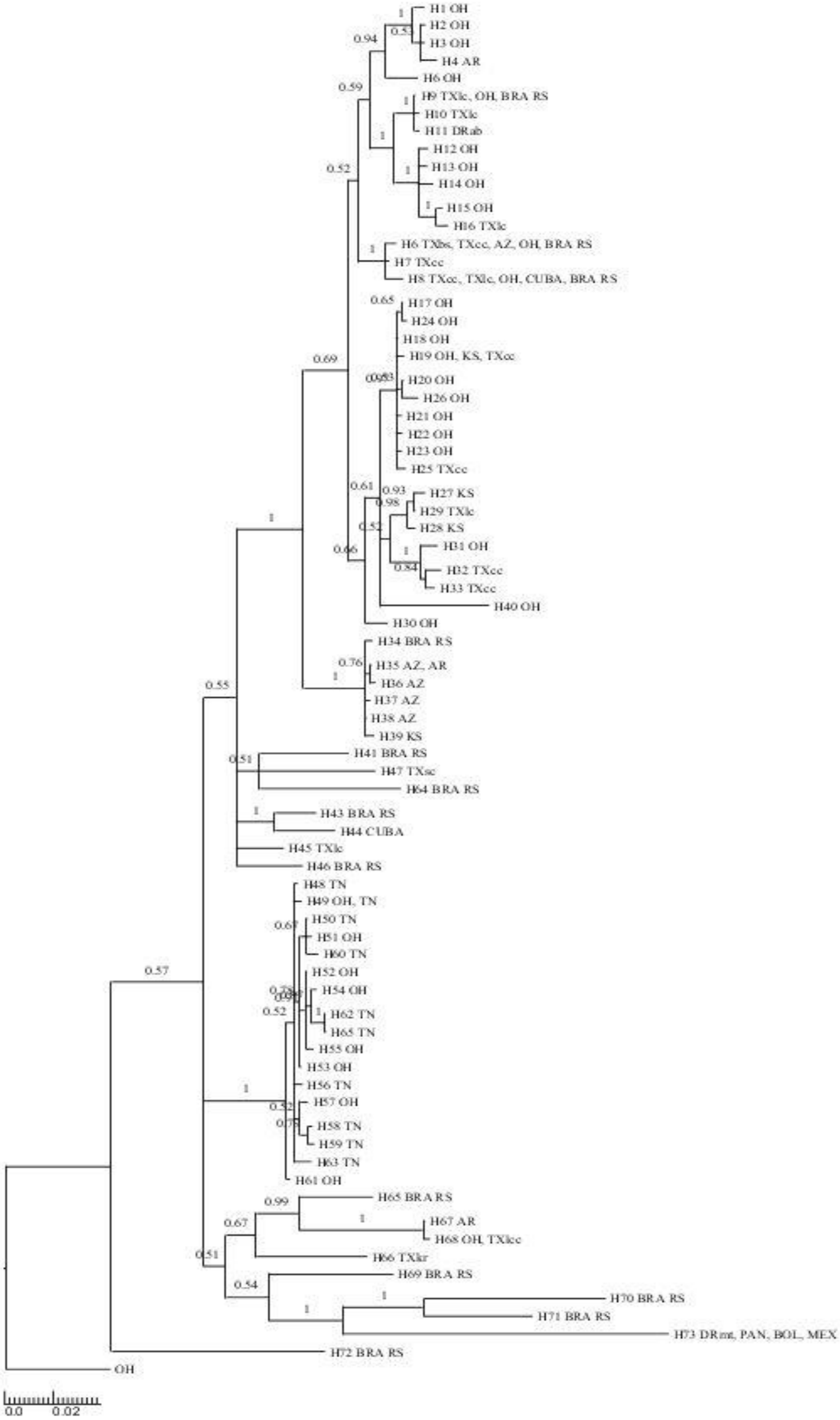
continuação APÊNDICE 1. List of specimens included in this study.

Taxa	**Lab Code**	**Voucher no.**	**COI**	**ITS2**
Telenomus podisi	K0105	OSUC 557782	Y	Y
Telenomus podisi	K0106	OSUC 557783	Y	Y
Telenomus podisi	K0107	OSUC 557784	Y	Y
Telenomus podisi	K0080	OSUC 557766	Y	Y
Telenomus podisi	G0095	OSUC 553316	Y	Y
Telenomus podisi	G0108	OSUC 553324	Y	Y
Telenomus podisi	G0106	OSUC 553322	Y	Y
Telenomus podisi	G0101	BMSB 1155	Y	Y
Telenomus podisi	G0097	BMSB 1146	Y	Y
Telenomus podisi	G0098	OSUC 553318	Y	Y
Telenomus podisi	G0109	OSUC 553325	Y	Y
Telenomus podisi	G0104	BMSB 1157	Y	Y
Telenomus podisi	G0103	OSUC 553320	Y	Y
Telenomus podisi	G0105	OSUC 553321	Y	Y
Telenomus podisi	G0100	OSUC 553319	Y	Y
Telenomus podisi	G0005	OSUC 553194	Y	Y
Telenomus podisi	G0007	OSUC 553196	Y	Y
Telenomus podisi	G0008	OSUC 553197	Y	Y
Telenomus podisi	G0009	OSUC 553198	Y	Y
Telenomus podisi	G0014	OSUC 553203	Y	Y
Telenomus podisi	G0017	OSUC 553206	Y	Y
Telenomus podisi	G0018	OSUC 553207	Y	Y
Telenomus podisi	G0023	OSUC 553212	Y	Y
Telenomus podisi	G0024	OSUC 553213	Y	Y
Telenomus podisi	G0027	OSUC 553216	Y	Y
Telenomus podisi	G0072	OSUC 553293	Y	Y
Telenomus podisi	G0042	OSUC 553263	Y	Y
Telenomus podisi	G0044	OSUC 553265	Y	Y
Telenomus podisi	G0045	OSUC 553266	Y	Y
Telenomus podisi	G0090	OSUC 553311	Y	Y
Telenomus podisi	G0094	OSUC 553315	Y	Y
Telenomus podisi	G0020	OSUC 553209	Y	Y
Telenomus podisi	G0030	OSUC 553219	Y	Y
Telenomus podisi	G0016	OSUC 553205	Y	Y
Telenomus podisi	G0032	OSUC 553221	Y	Y
Telenomus podisi	G0070	OSUC 553291	Y	Y
Telenomus podisi	G0073	OSUC 553294	Y	Y
Telenomus podisi	G0080	OSUC 553301	Y	Y
Telenomus podisi	G0081	OSUC 553302	Y	Y
Telenomus podisi	G0082	OSUC 553303	Y	Y
Telenomus podisi	G0085	OSUC 553306	Y	Y
Telenomus podisi	G0025	OSUC 553214	Y	Y

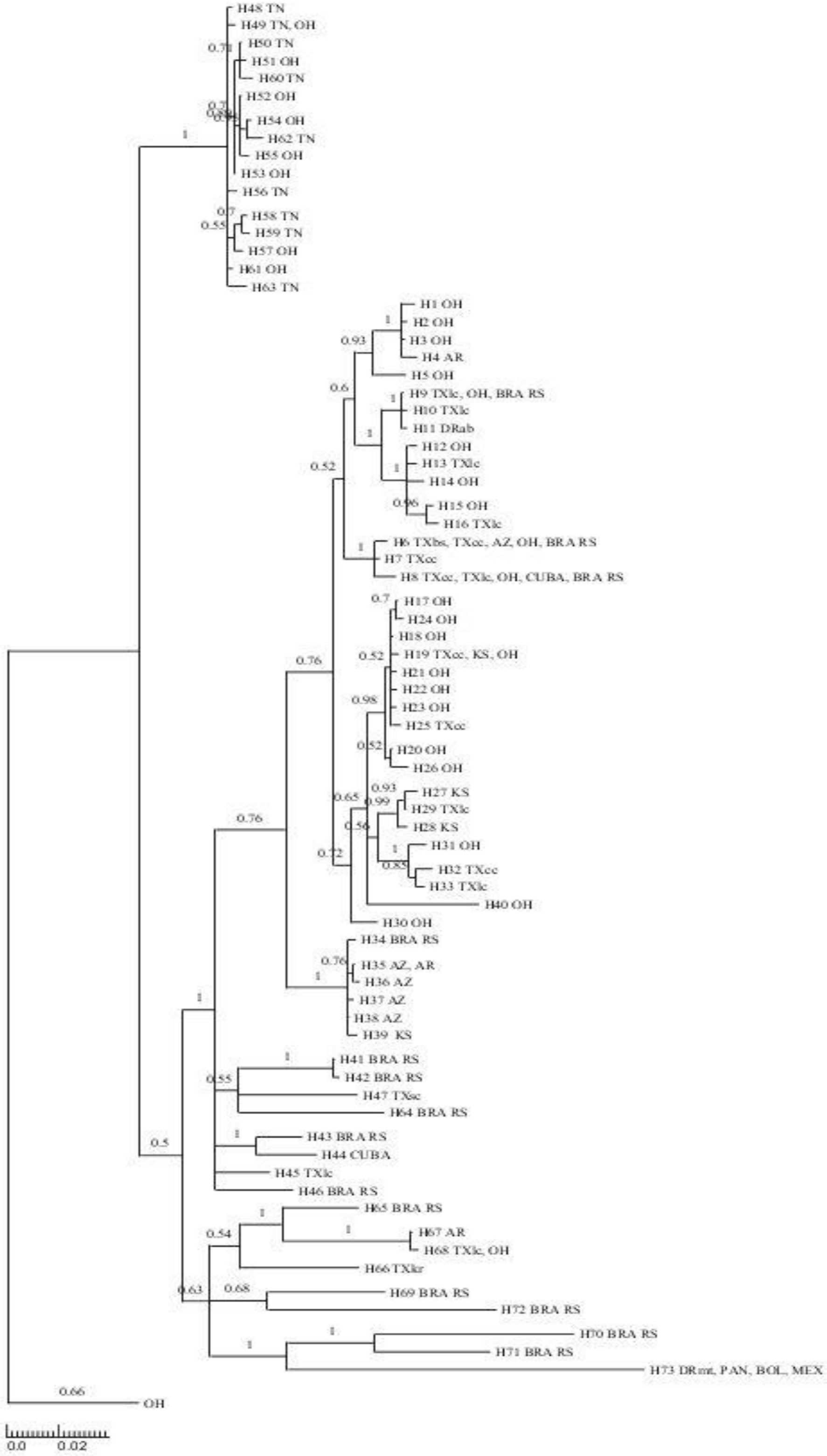
continuação APÊNDICE 1. List of specimens included in this study.

Taxa	**Lab Code**	**Voucher no.**	**COI**	**ITS2**
Telenomus podisi	G0063	OSUC 553284	Y	Y
Telenomus podisi	G0065	OSUC 553286	Y	Y
Telenomus podisi	G0071	OSUC 553292	Y	Y
Telenomus podisi	G0086	OSUC 553307	Y	Y
Telenomus podisi	G0011	OSUC 553200	Y	Y
Telenomus podisi	G0019	OSUC 553208	Y	Y
Telenomus podisi	G0052	OSUC 553273	Y	Y
Telenomus podisi	G0054	OSUC 553275	Y	Y
Telenomus podisi	G0012	OSUC 553201	Y	Y
Telenomus podisi	G0026	OSUC 553215	Y	Y
Telenomus podisi	G0028	OSUC 553217	Y	Y
Telenomus podisi	G0112	OSUC 553326	Y	Y
Telenomus podisi	G0113	OSUC 553327	Y	Y
Telenomus podisi	G0114	OSUC 553328	Y	Y
Telenomus podisi	G0156	OSUC 599344	Y	Y
Telenomus podisi	G0157	OSUC 599345	Y	Y
Telenomus podisi	G0158	OSUC 599346	Y	Y
Telenomus podisi	K0100	OSUC 372835	Y	Y
Telenomus podisi	G0159	OSUC 599347	Y	Y
Telenomus podisi	G0161	OSUC 599349	Y	Y
Telenomus podisi	G0162	OSUC 599350	Y	Y
Telenomus podisi	G0171	OSUC 599359	Y	Y
Telenomus podisi	G0172	OSUC 599360	Y	Y
Telenomus podisi	G0173	OSUC 599361	Y	Y
Telenomus podisi	G0174	OSUC 599362	Y	Y
Telenomus podisi	G0175	OSUC 599363	Y	Y
Telenomus podisi	G0176	OSUC 599364	Y	Y
Telenomus podisi	G0178	OSUC 599366	Y	Y
Telenomus podisi	G0179	OSUC 599367	Y	Y
Telenomus podisi	G0180	OSUC 599368	Y	Y
Telenomus podisi	G0181	OSUC 599369	Y	Y
Telenomus podisi	G0183	OSUC 599371	Y	Y
Telenomus podisi	G0184	OSUC 599372	Y	Y
Telenomus podisi	G0185	OSUC 599373	Y	Y
Trissolcus brochymenae	K0055	OSUC 372822	Y	Y

APÊNDICE 2. Bayesian consensus tree of the COI haplotypes with posterior probability values showed over the branches.



APÊNDICE 3. Bayesian consensus tree of the ITS2 haplotypes with posterior probability values showed over the branches.



APÊNDICE 4. Individuals number in each parasitoid family, sample spot and rice management (Organic = Org; Conventional = Conv) in both crop seasons.

	1° Crop Season										**2° Crop Season**									
Samples spots	0m (5)		100m (4)		200m (3)		300m (2)		400m (1)		0m (5)		200m (4)		400m (3)		600m (2)		800m (1)	
Families	Org	Conv	Org	Conv	Org	Conv	Org	Conv	Org	Conv	Org	Conv	Org	Conv	Org	Conv	Org	Conv	Org	Conv
Platygastridae	31	10	51	49	47	67	77	27	62	22	25	21	55	20	14	10	37	50	48	14
Mymaridae	26	3	41	57	25	42	62	30	31	13	19	19	72	18	39	20	48	18	55	5
Encyrtidae	10	7	29	58	19	48	33	63	30	33	11	7	15	4	6	7	12	9	18	6
Trichogrammatidae	9	2	27	42	30	35	31	29	36	26	7	2	13	14	7	7	15	21	10	6
Eulophidae	5	2	67	11	21	6	19	7	18	1	4	17	71	2	66	3	52	2	77	3
Ceraphronidae	5	20	4	11	11	13	3	14	4	10	8	5	5	2	3	0	1	5	4	1
Ichneumonidae	28	2	19	4	11	6	9	5	5	0	45	5	16	1	10	1	3	4	16	1
Braconidae	5	3	15	9	7	6	10	16	12	2	10	4	11	1	4	10	6	6	21	6
Figitidae	1	0	9	5	5	5	11	2	4	1	4	3	10	1	6	3	5	2	4	2
Diapriidae	0	3	4	2	5	3	3	0	2	1	2	2	4	0	1	1	1	0	1	1
Bethylidae	2	2	4	0	3	1	4	0	6	0	8	4	0	2	2	0	1	0	1	0
Chalcididae	0	0	4	7	2	0	4	0	2	0	0	1	5	0	1	0	2	1	6	2
Eupelmidae	3	0	1	2	2	1	4	1	0	0	6	2	1	0	0	0	0	0	5	0
Aphelinidae	0	0	6	0	0	2	3	0	1	0	0	0	1	0	2	0	0	0	0	1
Pteromalidae	0	3	1	2	1	0	0	0	1	2	1	0	5	0	2	0	1	1	4	0
Eurytomidae	3	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
Chrysididae	0	0	0	0	4	0	0	0	1	0	0	0	1	0	0	0	0	0	2	0
Evaniidae	4	0	0	0	1	0	0	0	0	0	0	0	1	0	1	0	1	0	0	0
Torymidae	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dryinidae	0	0	2	0	0	1	0	0	0	0	1	0	1	0	0	0	0	0	1	0
Megaspilidae	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Signiphoridae	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	2	0	1	0
Proctrotupidae	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0
Total	**135**	**57**	**285**	**261**	**194**	**236**	**273**	**195**	**217**	**111**	**126**	**74**	**233**	**45**	**150**	**52**	**150**	**69**	**226**	**34**

APÊNDICE 5. Individuals number in each parasitoid family, samples and rice management in the first crop season (2013/2014).

	CONVENTIONAL									ORGANIC							
	Vegetative					**Reproductive**				**Vegetative**					**Reproductive**		
Families	**12/12/13**	**27/12/13**	**9/1/14**	**22/1/14**	**5/2/14**	**19/2/14**	**7/3/14**	**28/3/14**	**16/4/14**	**27/12/13**	**9/1/14**	**22/1/14**	**5/2/14**	**19/2/14**	**11/3/14**	**28/3/14**	**25/4/14**
Platygastridae	14	13	30	12	12	11	30	26	27	17	49	18	30	17	64	60	13
Braconidae	6	3	6	1	0	1	2	2	15	3	10	4	3	1	14	10	4
Eulophidae	1	1	7	1	2	4	4	3	4	10	10	9	12	8	23	38	20
Trichogrammatidae	9	16	17	6	8	15	15	38	10	8	11	18	28	14	19	31	4
Aphelinidae	0	0	0	1	0	0	0	1	0	1	2	0	2	0	0	3	2
Encyrtidae	11	5	5	3	3	1	92	54	35	14	11	10	13	6	42	18	7
Mymaridae	46	6	26	6	18	7	3	28	5	14	21	21	38	12	38	31	10
Ichneumonidae	2	1	9	0	0	1	0	0	4	4	20	10	8	3	5	14	8
Ceraphronidae	2	2	5	4	5	18	21	5	6	0	2	4	5	5	4	5	2
Diapriidae	2	0	3	2	1	1	0	0	0	2	1	1	2	3	2	2	1
Chalcididae	1	1	2	0	1	0	2	0	0	1	0	0	5	2	0	3	1
Megaspilidae	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Eupelmidae	0	0	1	0	1	0	1	1	0	1	4	1	2	1	0	1	0
Bethylidae	0	0	1	0	1	0	0	1	0	2	6	3	3	2	1	2	0
Figitidae	6	2	4	1	0	0	0	0	0	2	11	1	4	1	6	5	0
Torymidae	0	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0
Dryinidae	0	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0
Chrysididae	0	0	0	0	0	0	0	0	0	0	2	0	1	1	1	0	0
Pteromalidae	2	1	1	0	1	1	0	0	1	1	1	1	0	0	0	0	0
Signiphoridae	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Evaniidae	0	0	0	0	0	0	0	0	0	1	0	0	2	0	0	2	0
Eurytomidae	1	0	0	0	0	0	0	0	0	0	0	3	0	0	2	0	0
Total	**103**	**51**	**119**	**37**	**53**	**60**	**171**	**159**	**107**	**84**	**163**	**104**	**158**	**76**	**221**	**226**	**72**

APÊNDICE 6. Individuals number in each parasitoid family, samples and rice management in the second crop season (2014/2015).

	CONVENTIONAL									ORGANIC								
	Vegetative				Reproductive					Vegetative			Reproductive					
Families	**17/12/14**	**24/12/14**	**7/1/15**	**22/1/15**	**5/2/15**	**15/2/15**	**5/3/15**	**13/3/15**	**20/3/15**	**28/11/14**	**17/12/14**	**7/1/15**	**22/1/15**	**5/2/15**	**15/2/15**	**4/3/15**	**13/3/15**	**20/3/15**
Platygastridae	10	4	22	24	1	6	10	22	16	18	11	30	21	10	40	9	36	4
Braconidae	1	2	3	14	3	4	0	0	0	2	7	7	5	2	3	6	16	4
Eulophidae	5	0	7	5	2	4	1	3	0	14	16	28	14	9	47	40	83	19
Trichogrammatidae	5	0	11	5	3	21	2	0	3	4	1	9	5	3	11	5	13	1
Aphelinidae	1	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0
Encyrtidae	1	0	12	2	4	1	9	4	0	5	3	4	6	2	14	6	21	1
Mymaridae	6	3	14	14	10	9	6	12	6	24	15	8	25	9	43	30	70	9
Ichneumonidae	2	2	1	1	0	2	1	1	2	10	13	2	5	4	4	16	24	12
Ceraphronidae	1	0	6	0	0	1	3	2	0	0	6	2	4	0	2	2	4	1
Diapriidae	2	0	1	0	0	0	1	0	0	1	1	1	1	0	0	5	0	0
Chalcididae	1	0	2	0	0	0	1	0	0	0	1	0	0	1	4	0	4	4
Eupelmidae	0	0	0	1	1	0	0	0	0	1	0	1	0	1	0	2	4	3
Bethylidae	1	0	2	1	0	1	0	0	1	6	1	0	0	0	1	1	3	0
Figitidae	0	0	6	2	1	1	0	0	1	3	5	1	2	3	6	1	6	2
Dryinidae	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	1	0
Chrysididae	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	1	0
Pteromalidae	0	0	0	0	0	0	0	0	1	1	0	3	2	1	4	0	1	1
Signiphoridae	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	2	0
Evaniidae	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	1	0
Proctrotupidae	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0
Total	**36**	**11**	**87**	**69**	**25**	**52**	**35**	**44**	**30**	**90**	**81**	**96**	**92**	**47**	**183**	**124**	**290**	**61**

APÊNDICE 7. Individuals number in each platygastroid morphospecies, sample spot and rice management (Organic = Org; Conventional = Conv) in both crop seasons.

	1° Crop Season										**2° Crop Season**									
	0 (5)		100 (4)		200 (3)		300 (2)		400 (1)		0 (5)		200 (4)		400 (3)		600 (2)		800 (1)	
Samples spots	Org	Conv	Org	Conv	Org	Conv	Org	Conv	Org	Conv	Org	Conv	Org	Conv	Org	Conv	Org	Conv	Org	Conv
Morphospecies																				
Anteris sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
Baeus sp.1	0	0	0	0	0	0	0	0	0	0	2	1	0	0	1	0	0	0	0	0
Baeus sp.2	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0
Baeus sp.3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Baeus sp.4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0
Baeus sp.5	0	1	0	3	1	2	0	1	1	1	0	0	0	0	0	0	0	0	0	1
Baryconus sp.1	1	0	0	0	4	0	1	0	2	0	1	0	1	0	0	0	0	0	0	1
Calliscelio sp.1	0	0	0	0	0	0	3	6	3	0	0	0	0	0	0	0	1	0	0	0
Calotelea sp.1	0	0	0	0	0	3	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Cremastobaeus sp.1	0	0	1	1	0	1	0	0	0	0	0	0	1	0	0	1	0	0	2	0
Cremastobaeus sp.2	0	0	0	0	0	0	1	0	0	0	0	0	2	0	1	0	0	0	3	0
Duta sp.1	0	2	1	0	0	1	3	2	6	2	0	0	1	0	0	0	0	1	1	0
Duta sp.2	0	0	0	0	0	0	1	0	0	0	0	0	3	1	0	0	1	0	1	0
Eumicrosoma sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0
Gryon sp.1	0	0	1	0	0	0	0	0	0	0	0	0	3	2	1	0	1	0	2	0
Gryon sp.2	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
Idris sp.1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Idris sp.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
Idris sp.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0
Idris sp.4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Idris sp.5	0	0	0	1	0	1	0	0	0	0	0	1	0	0	0	0	0	1	0	0
Idris sp.6	0	0	0	0	0	0	1	0	0	0	0	0	1	1	0	0	0	0	0	0
Idris sp.7	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	2	0	0	0
Idris sp.8	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0
Idris sp.10	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Idris sp.11	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Idris sp.12	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0

continuação APÊNDICE 7. Individuals number in each platygastroid morphospecies, sample spot and rice management (Organic = Org; Conventional = Conv) in both crop seasons.

	1° Crop Season										2° Crop Season									
	0 (5)		100 (4)		200 (3)		300 (2)		400 (1)		0 (5)		200 (4)		400 (3)		600 (2)		800 (1)	
Samples spots	Org	Conv	Org	Conv	Org	Conv	Org	Conv	Org	Conv	Org	Conv	Org	Conv	Org	Conv	Org	Conv	Org	Conv
Morphospecies																				
Macroteleia sp.1	0	0	4	3	0	1	3	0	4	2	0	0	1	0	0	0	1	0	0	1
Opisthacantha sp.1	1	0	0	0	2	1	1	2	2	0	2	0	2	0	0	0	1	1	0	0
Paridris sp.1	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	1	0	0	0
Phanuromyia sp.1	6	0	0	0	3	1	0	0	0	0	0	0	2	2	2	0	0	0	3	0
Probaryconus sp.1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
Probaryconus sp.2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Scelio sp.1	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
Trimorus sp.1	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	1	0
Trimorus sp.2	3	0	4	3	0	1	3	1	2	2	1	1	0	0	0	1	1	0	0	0
Trissolcus sp.1	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	0	0	0	0	0
Trissolcus sp.2	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trissolcus sp.3	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Triteleia sp.1	0	0	1	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0
Telenomus sp.1	0	1	2	2	3	6	4	1	4	1	1	2	3	6	0	1	5	7	3	1
Telenomus sp.2	1	0	2	0	0	3	7	1	2	0	0	0	2	0	1	1	3	0	8	0
Telenomus sp.3	4	0	13	3	11	11	14	6	15	6	2	1	2	2	1	0	6	3	1	0
Telenomus sp.4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	1	0
Telenomus sp.5	3	1	0	2	3	5	2	0	3	1	0	1	0	0	0	0	2	0	0	0
Telenomus podisi	8	0	14	30	19	24	30	5	13	7	1	2	22	2	3	4	3	32	7	6
Telenomus sp.7	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
Telenomus sp.8	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Xenomerus sp.1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TOTAL	**32**	**8**	**46**	**50**	**47**	**66**	**81**	**25**	**62**	**23**	**16**	**12**	**49**	**16**	**13**	**10**	**36**	**45**	**37**	**10**

APÊNDICE 8. Individuals number in each platygastroids genera, samples and rice management in the first crop season (2013/2014).

	CONVENTIONAL									**ORGANIC**							
	Vegetative					**Reproductive**				**Vegetative**					**Reproductive**		
Morphospecies	**12/12/13**	**27/12/13**	**9/1/14**	**22/1/14**	**5/2/14**	**19/2/14**	**7/3/14**	**28/3/14**	**16/4/14**	**27/12/13**	**9/1/14**	**22/1/14**	**5/2/14**	**19/2/14**	**11/3/14**	**28/3/14**	**25/4/14**
Anteris sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Baeus sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Baeus sp.2	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0
Baeus sp.3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Baeus sp.4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Baeus sp.5	0	1	1	0	0	1	1	4	0	0	0	0	0	0	2	0	0
Baryconus sp.1	0	0	0	0	0	0	0	0	0	0	3	1	1	2	0	1	0
Calliscelio sp.1	3	0	0	0	0	0	0	3	0	0	0	1	3	1	1	0	0
Calotelea sp.1	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0
Cremastobaeus sp.1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0
Cremastobaeus sp.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Duta sp.1	2	1	1	1	0	2	0	0	0	1	2	1	0	0	3	3	0
Duta sp.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Eumicrosoma sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Gryon sp.1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Gryon sp.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idris sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idris sp.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idris sp.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idris sp.4	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Idris sp.5	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
Idris sp.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Idris sp.7	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Idris sp.8	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Idris sp.10	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0
Idris sp.11	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
Idris sp.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0

continuação APÊNDICE 8. Individuals number in each platygastroids genera, samples and rice management in the first crop season (2013/2014).

	Vegetative					**Reproductive**				**Vegetative**					**Reproductive**		
Morphospecies	**12/12/13**	**27/12/13**	**9/1/14**	**22/1/14**	**5/2/14**	**19/2/14**	**7/3/14**	**28/3/14**	**16/4/14**	**27/12/13**	**9/1/14**	**22/1/14**	**5/2/14**	**19/2/14**	**11/3/14**	**28/3/14**	**25/4/14**
Macroteleia sp.1	0	0	0	2	0	0	2	1	1	2	0	1	0	0	1	7	0
Opisthacantha sp.1	0	0	1	0	0	1	0	0	1	1	0	1	0	1	2	1	0
Paridris sp.1	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
Phanuromyia sp.1	0	0	0	0	0	0	0	0	1	0	2	2	2	1	0	2	0
Probaryconus sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Probaryconus sp.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Scelio sp.1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0
Trimorus sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Trimorus sp.2	0	0	1	0	3	2	1	0	0	3	2	0	6	0	0	0	1
Trissolcus sp.1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trissolcus sp.2	1	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Trissolcus sp.3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Triteleia sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
Telenomus sp.1	1	0	2	1	1	2	0	4	0	0	5	0	3	0	0	4	1
Telenomus sp.2	0	0	2	0	1	0	0	0	1	2	5	1	1	0	2	1	0
Telenomus sp.3	1	2	1	1	5	1	6	3	6	0	3	3	4	2	25	17	3
Telenomus sp.4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Telenomus sp.5	1	0	8	0	0	0	0	0	0	0	3	0	2	0	4	2	0
Telenomus podisi	1	6	9	3	2	1	18	11	15	3	17	1	3	7	25	22	6
Telenomus sp.7	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Telenomus sp.8	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0
Xenomerus sp.1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
TOTAL	**12**	**12**	**30**	**11**	**13**	**10**	**29**	**29**	**26**	**16**	**44**	**16**	**29**	**16**	**67**	**68**	**12**

APÊNDICE 9. Individuals number in each platygastroids genera, samples and rice management in the second crop season (2014/2015).

	CONVENTIONAL									**ORGANIC**								
	Vegetative				**Reproductive**					**Vegetative**			**Reproductive**					
Morphospecies	**17/12/14**	**24/12/14**	**7/1/15**	**22/1/15**	**5/2/15**	**11/2/15**	**5/3/15**	**13/3/15**	**20/3/15**	**28/11/14**	**17/12/14**	**7/1/15**	**22/1/15**	**5/2/15**	**11/2/15**	**4/3/15**	**13/3/15**	**20/3/15**
Anteris sp.1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Baeus sp.1	1	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	1	0
Baeus sp.2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Baeus sp.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Baeus sp.4	0	0	0	0	0	0	0	0	0	0	1	0	0	0	2	0	0	0
Baeus sp.5	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Baryconus sp.1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	1	0
Calliscelio sp.1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
Calotelea sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Cremastobaeus sp.1	0	0	0	1	0	0	0	0	0	0	0	0	1	1	0	0	1	0
Cremastobaeus sp.2	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	1	1	1
Duta sp.1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0
Duta sp.2	0	0	1	0	0	0	0	0	0	0	0	1	1	1	2	0	0	0
Eumicrosoma sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0
Gryon sp.1	2	0	0	0	0	0	0	0	0	0	0	1	2	0	2	1	1	0
Gryon sp.2	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
Idris sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Idris sp.2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
Idris sp.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
Idris sp.4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Idris sp.5	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0
Idris sp.6	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0
Idris sp.7	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0
Idris sp.8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
Idris sp.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idris sp.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Idris sp.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Macroteleia sp.1	0	0	1	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
Opisthacantha sp.1	1	0	0	0	0	0	0	0	0	1	0	3	1	0	0	0	0	0

continuação APÊNDICE 9. Individuals number in each platygastroids genera, samples and rice management in the second crop season (2014/2015).

	CONVENTIONAL									ORGANIC								
	Vegetative				Reproductive					Vegetative			Reproductive					
Morphospecies	**17/12/14**	**24/12/14**	**7/1/15**	**22/1/15**	**5/2/15**	**11/2/15**	**5/3/15**	**13/3/15**	**20/3/15**	**28/11/14**	**17/12/14**	**7/1/15**	**22/1/15**	**5/2/15**	**11/2/15**	**4/3/15**	**13/3/15**	**20/3/15**
Paridris sp.1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
Phanuromyia sp.1	0	0	0	0	2	0	0	0	0	0	0	0	3	0	3	0	1	0
Probaryconus sp.1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Probaryconus sp.2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Scelio sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trimorus sp.1	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0	0
Trimorus sp.2	0	2	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
Trissolcus sp.1	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0
Trissolcus sp.2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Trissolcus sp.3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Triteleia sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Telenomus sp.1	1	0	11	2	0	0	2	1	0	2	0	3	1	1	2	0	3	0
Telenomus sp.2	0	0	1	0	0	0	0	0	0	0	0	1	2	1	6	1	3	0
Telenomus sp.3	0	0	2	3	0	0	0	1	0	4	0	3	0	0	2	1	1	1
Telenomus sp.4	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	1	0
Telenomus sp.5	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	2	0
Telenomus podisi	3	0	4	8	0	1	5	12	13	2	1	8	6	3	10	3	2	1
Telenomus sp.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Telenomus sp.8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Xenomerus sp.1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TOTAL	**9**	**4**	**20**	**16**	**2**	**3**	**8**	**16**	**15**	**15**	**3**	**28**	**20**	**9**	**37**	**12**	**21**	**6**