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Pests of Australian dairy pastures: distribution, seasonality and potential impacts on pasture production

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Abstract

The dairy industry provides an important contribution to the Australian economy, but its productivity relies on grass pastures that suffer significant damage from invertebrate pests. Managing these pests remains a challenge as information on their abundance and impact is only available for a handful of taxa in a few Australian dairy regions. In this study, we undertook an extensive survey of above and below-ground pest communities across seven dairy regions in south-eastern Australia by repeatedly sampling 57 paddocks in 2017 and 2018. We then applied energetic models to estimate the amount of metabolisable energy produced by pastures that is potentially consumed by pests. Our survey indicates dairy farmers encounter a similar composition of above-ground pests in most sampled regions, with a few pests, especially *Sminthurus viridis* (lucerne flea) and *Rhopalosiphum padi* (bird cherry-oat aphid), dominating pest communities. Below-ground pests were more variable between regions and are more likely to require region-specific control strategies. Our energetic modelling suggests pests consume a three-fold greater percentage of metabolisable energy produced by pastures during autumn than spring. *Sminthurus viridis* and *R. padi* were amongst the most economically important pests across all regions and seasons, while other pests, including several species of scarabs and the small pointed snail, *Prietocella barbara*, were predicted to be particularly damaging in specific regions. Together, our field survey and energetic modelling provide baseline information to assist dairy farmers manage invertebrate pests and help guide future research in the Australian dairy industry.

Key words

pest management, survey, metabolism, arthropods, diversity, richness, distribution, agriculture

Introduction

The dairy industry is an important contributor to the Australian economy, with an estimated farm gate value of A$4.4 billion in the 2018/19 financial year (Dairy Australia 2019). The vast majority (90%) of dairy farms are located in the four south-eastern states (Dairy Australia 2019), where cattle rely on feed produced by dryland pastures composed mostly of perennial ryegrass (*Lolium perenne*) and perennial legumes (e.g., *Medicago sativa*) (Dairy Australia 2019; Garcia et al. 2014). Since dairy productivity closely aligns with the amount and quality of pasture available to feed cattle (Garcia & Fulkerson 2005), management strategies for these pasture systems are key to safeguarding future dairy productivity. Several recent studies have considered current challenges in managing Australian dairy pastures such as stocking rates, soil types, labour cost, climate volatility, and pastoral species composition (Clark et al. 2013; Garcia et al. 2014; Pembleton et al. 2020), but far less attention has been paid to challenges posed by invertebrate pests. Invertebrate pests cause considerable economic loss to dairy pastures each year (Allen 1987; Ferguson et al. 2019), yet data is only available on the prevalence and damage caused by a handful of pest species in Australian dairy pastures. We therefore lack foundational information needed to mitigate the impact of pasture pests.

Agricultural practices, such as the introduction of new pasture species, have inadvertently created habitats that favour the survival and reproduction of several native invertebrates, which have become pests consuming foliage, stems and roots of pasture plants (Hoffmann et al. 2008; Robertson et al. 1995). A common and particularly damaging example of such a species is the redheaded pasture cockchafer (*Adoryphorus coulonii*), whose larvae live and feed in the root zone below-ground (Berg et al. 2014). The blackheaded pasture cockchafer (*Acrossidius tasmaniae*) has also become a widespread pest, with their larvae moving above-ground to sever and feed on pasture plants, often taking the foliage back down their below-ground tunnels (McQuillan et al. 2007; Wightman 1979). Similarly, common armyworm (*Mythimna convecta*), southern armyworm (*Persectania ewingii*) and inland armyworm (*Persectania dyscrita*) have become pests that thrive in improved pastures where their larvae feed on the grass component (McDonald & Smith 1986).

Several introduced invertebrate species have also become major pests in Australia due to the absence of their natural controls or lack of established management control methods (Hoffmann et al. 2008). The African black beetle (*Heteronychus arator*) was introduced into Australia around 100 years ago and has now spread to all mainland states (Allsopp & Hutchinson 2019; Beehag et al. 2016). Both adults and larvae of *H. arator* damage pastoral systems, as adults chew the stems and larvae the roots of several grass species (Bell et al. 2011; Frew et al. 2016). Other invasive species that similarly damage pastures by chewing roots and/or stems have also become problematic, such as the Argentine stem weevil (*Listronotus bonariensis*), the black field cricket (*Teleogryllus commodus*) and the lucerne flea (*Sminthurus viridis*) (Beehag et al. 2016; Carne 1957a; Pavri 2007). Introduced mites, such as redlegged earth mites (*Halotydeus destructor*) and blue oat mites (*Penthaleus* spp.), pierce and suck out the contents of plant epidermal cells and have become major pests across south-eastern Australia (Ridsdill-Smith 1997; Umina et al. 2004). Several aphid species, including the bluegreen aphid (*Acyrthosiphon kondoi*) and the bird cherry-oat aphid (*Rhopalosiphum padi*), damage plants not only through feeding on vegetation but also by acting as a vector for plant viruses (Jones 1992; Peck et al. 2012).

Pests of dairy pastures can differ in their presence and abundance due to regional differences in climate, soil, pasture composition, and management methods. For instance, the abundance and distribution of *M. convecta* in Victoria and Tasmania is limited due to winter temperatures dropping below their tolerance thresholds (Smith 1984). Similarly, the inland distribution of *Penthaleus* spp. is limited by moisture and temperature (Robinson & Hoffmann 2001). *Halotydeus destructor* are typically more prevalent in areas with high temperature seasonality, drier summers, and pasture paddocks containing a high clover component (Hill et al. 2012; Ridsdill-Smith & Pavri 2015; Umina & Hoffmann 2004). *Heteronychus arator* and *A. coulonii* populations can be supressed by high rainfall during winter and spring in south-eastern Australia (Berg et al. 2014; Frew et al. 2016; Matthiessen & Ridsdill-Smith 1991). While such past studies have provided invaluable information, they have predominately focused on a few species within relatively small or discrete regions. Consequently, we lack an understanding of how entire pest communities differ between Australian dairy regions or how dairy pastoral pest communities differ compared with pest communities in other agricultural sectors (e.g., grains). In turn, we lack fundamental baseline knowledge to design effective pest management strategies. Strikingly, this gap in knowledge on pests of Australian dairy pastures has been a long-recognized issue, and was highlighted over thirty years ago by Allen (1987).

Here, we provide a long-needed baseline survey of invertebrate pasture pest communities and estimate their impacts on the production of south-eastern Australian dairy pastures. We identified and quantified the abundance of pests in above and below-ground environments at 57 dairy farms across seven dairy regions, sampling multiple sites at each farm, with two overarching aims. First, we aimed to characterise the invertebrate pest community (e.g., pest abundance, richness and diversity) present in south-eastern Australian dairy pastures and explore what key differences in pest communities exist between regions. Notably, we paid particular attention to scarabs since this group includes taxa (e.g., *H. arator* and *A. coulonii*) that have long been considered amongst the most damaging pests to dairy pastures (Berg et al. 2014; Ferguson et al. 2019; Pauley & Miller 1993). Second, we aimed to combine our survey data with known scaling relationships between pest body-size and metabolic rate to approximate the amount of metabolisable energy that pests potentially remove from established dairy pastures. We found a high level of similarity in pest community composition between regions but identified key regional and seasonal differences in pest abundances and damage potential that will help guide future management and research priorities.

Materials and Methods

Site selection and sampling

We selected a total of 57 farms across seven distinct dairy producing regions in south-eastern Australia: Gippsland, south-west Victoria, northern Victoria, Tasmania, south coast of New South Wales, Fleurieu Peninsula of South Australia, and eastern South Australia (Fig. 1). A minimum of four and a maximum of 11 farms were selected in each region to ensure a geographic spread within each region. In selecting farms, we targeted the typical pasture type for the region. In Gippsland, south-west Victoria, Tasmania, eastern South Australia and the Fleurieu Peninsula, pastures commonly comprised perennial ryegrass (*Lolium perenne*), while in northern Victoria and the south coast of New South Wales, the pastures were more diverse and included perennial and annual species (e.g., *Lolium multiflorum* and *Pennisetum clandestinum*). At each farm, we chose a single paddock and randomly selected 10 replicate sampling sites along a transect within the paddock. This transect followed a zig-zag line, moving from one corner of each paddock inwards. The minimum distance between sampling sites was 20 m, and the maximum distance between sampling sites was 575 m. At each sampling site, location was recorded using a hand-held GPS unit, allowing us to return to the same locations at subsequent sampling periods. Paddocks were selected based on discussions with the land manager regarding the prevalence of previous pest problems, the presence of established long-term pasture, and the likely continuation of the paddock as a pasture for the survey duration. Each site was sampled on four occasions: autumn 2017, spring 2017, autumn 2018 and spring 2018. Spring and autumn sampling times were chosen because they are expected to collect the majority of pasture invertebrate pests in these regions (Bailey 2007). Further details of the climatic, botanical and soil information for each pasture paddock are provided in Table S1.

At each of the 10 sampling sites within a paddock, we used two invertebrate sampling methods; vacuum sampling to measure above-ground invertebrates and soil sampling to measure below-ground invertebrates. Specifically, above-ground sampling was undertaken by placing a 0.3 m x 0.3 m square frame with 0.25 m vertical walls on the soil surface and vacuuming invertebrates in the pasture area using a blower-vac (Stihl®, model BG 86C) modified such that the suction tube contained a removable, stainless steel sieve with a 0.2 mm mesh. The total area within each frame was vacuumed for 10 sec. All invertebrates collected from a sample were transferred to vials containing 70% ethanol for subsequent identification and counting. Below-ground sampling was undertaken by taking a core of topsoil measuring 0.2 m x 0.2 m and 0.1 m deep from the soil surface. The below-ground sample, which retained the pasture foliage, was placed on a sorting table and carefully broken down by hand until the texture of a fine crumb was achieved. All visible invertebrates were either counted *in situ* or placed in vials containing 70% ethanol for subsequent identification and counting. The two exceptions to this were mealybugs (*Pseudococcidae*) and root aphids (*Aploneura lentisci*); these were identified and counted as the total number of colonies per sample, as counting individuals was not logistically feasible. A colony was defined as a waxy clump with at least one mealybug or root aphid present. Representative samples of root aphids or mealybugs were collected into vials containing 70% ethanol for confirmation of identifications. Both sampling methods are reliable techniques routinely used to assess invertebrate densities in pastures and other agro-ecosystems (e.g., Buffington & Redak 1998; Jenkins et al. 2013; Neville & Yen 2007).

At all sampling sites within each paddock, we assessed botanical composition of the pasture using a 0.5 m x 0.5 m quadrat divided into 100 cells which was randomly placed within the sampling area. Each cell was assessed as being dominated by either pasture grass, legumes and herbs, weeds or bare ground. Botanical assessments were undertaken on all four sampling occasions. We also assessed the soil type of each paddock in spring 2019 using an Arborline® soil sampler, which extracted a 20 mm diameter core to a depth of 100 mm. Soil samples were taken at all 10 sampling sites within each paddock, pooled together per paddock, and then used to classify the soil type by using the hydrometer method to determine the proportion of sand, silt and clay in each sample (Beverwijk 1967).

Invertebrate pest identification and quantification

Morphological identification

Once in the laboratory, invertebrate samples were sorted to order using a stereomicroscope with 100x magnification. Pest invertebrates were then identified, by sorting further to family, genus and species levels, and counted. In total, we identified and counted 2,661,315 invertebrates, or invertebrate colonies, from across all samples. A large proportion of invertebrates collected were species that do not feed on pasture plants and are hence not regarded as pests for the purpose of this study. This included natural enemies (i.e., invertebrates known to predate or parasitize pest taxa, such as parasitoid wasps, lacewings and carabid beetles) and other beneficials (i.e., invertebrates that provide beneficial ecosystem services to pasture including nutrient recycling and pollination, such as bees and dung beetles). There was a small number of invertebrate taxa where the functional role within pasture systems could not be confidently assigned due to poor taxonomic resolution of these individuals.

In this study, we focused on only those invertebrates that could be confidently identified as pasture pests. For completeness, this included those taxa that feed on pasture plants, but may also provide some beneficial roles to pastures (e.g., omnivorous earwigs such as the European earwig, *Forficula auricularia*, consume pasture plants and predate on other pests) (Binns et al. 2021). Although we were able to identify the majority of taxa that were of primary interest to our study (i.e., the most abundant pests) to either species or genus level, a small number of specimens from particularly diverse taxonomic groups were only able to be classified to class, order or family. In these instances, they were pooled together into one of six groups of 'others' (Lepidoptera, Scarabaeidae, Orthoptera, slugs, snails, Curculionoidea). We classified pests as above or below-ground based on whether they were predominately collected by the above-ground sampling (i.e., vacuum sampling) or below-ground sampling (i.e., soil sampling). However, this approach meant a few pests (e.g., snails) were classified as below-ground pests when they likely spend the majority of time on soil surfaces or on plants.

In some instances, above-ground samples contained large numbers of mites that made counting every individual impractical. These samples were sub-sampled using a 13-grid cell method. The grid cell method first involved distributing the entire sample in ethanol evenly across a 25-cell gridded plate. We then identified and quantified mites from 13 cells within the plate, considering every second cell starting from the top left to bottom right. We employed this method when *H. destructor* and *Penthaleus* spp. occurred in high quantities (>75 individuals per sample). The number of individuals identified was then multiplied by 1.923 to represent the entire sample.

Scarab identification

Scarab identification was more difficult than other taxa due to the limited resources describing genera in the Scarabeidae family. Most scarabs found during our surveys were in their larval stage and the keys for scarab identification rely heavily on adult traits (Britton 1978; 1986; Britton 1957; Carne 1958; Carne 1957a; Carne 1957b; 1981; Esmonds & Halffter 1978; Houston & Weir 1992; Matthews 1971; 1974; Roberts 1968; Stebnicka & Howden 1995; Stebnicka 2009). We used Mcquillan (1985) to identify larval specimens, but this key was of limited value because it focuses on scarabs only occurring in Tasmania. While the majority of scarab specimens were able to be identified morphologically using hair patterns on the rasters, head capsule colour, texture, shape and body size, it was not possible to identify all larvae and adults to species level due to inadequate morphological keys for some taxa and/or because specimens were damaged.

To aid genus and species identification of the collected specimens, a subsample of 73 unidentified scarabs were selected for identification using standard genotyping methods. DNA was extracted destructively using whole legs (if individuals were large) or the whole specimen (if individuals were small and more than one specimen was available) using the Quick-DNA^{TM} Miniprep Plus kit (Zymo), or non-destructively (if only one specimen was available) using the method described by Paquin and Vink (2008). The 5' end of the mitochondrial cytochrome c oxidase subunit I gene (COI) was amplified using the LCO1490 and HCO2198 primers from Folmer et al. (1994). Sanger sequencing (BigDye$^{®}$v 3.1, Applied Biosystems) was conducted at Macrogen (Korea). Sequences were tidied and analysed using Geneious version Prime (Kearse et al. 2012). Sequences were compared with two online databases to find their closest match to known scarab reference sequences: (i) the Basic Local Alignment Search Tool (BLAST) in the GenBank nucleotide database (Benson *et al.* 2013), and (ii) the Identification Engine in The Barcode of Life Data Systems (BOLD) (Ratnasingham & Hebert 2007). Multiple alignments of sequences and their closest online matches were generated using the program MAFFT (Katoh & Standley 2013). The weevil, *Naupactus leucoloma* (Curculionidae), was used as the outlier. Evolutionary relationships were inferred using the UPGMA method in Mega X (Kumar et al. 2018). The robustness of the nodes in the phylogenetic tree generated was assessed by 1,000 bootstrap replication cycles.

The scarab specimens identified from our genotyping approach were subsequently used as an additional aid to resolve the taxonomic classification of the remaining unidentified scarab specimens. To do so, we thoroughly compared which morphological traits of the unidentified scarab specimens matched or mismatched with specimens identified by genotyping. In total, using a combination of morphological traits and molecular identification, we assigned 1,202 scarabs to the species or genus level; 648 scarabs remained unresolved and so remained grouped as Scarabeidae.

Statistical analysis

The invertebrate counts were scaled to reflect abundance per m^2: the above-ground counts were multiplied by 11, the below-ground counts were multiplied by 25.

Pest abundance, richness and diversity were calculated for each sampling site to assess differences in pest invertebrate communities between regions and seasons (spring and autumn). Richness was calculated using the Menhinick method which accounts for variation in sample size (Magurran 2004; Menhinick 1964; Ravera 2001). Pest diversity at each sampling site was calculated using Shannon diversity index based on Hill's number (alpha diversity), then summarized by region as a mean (gamma diversity) (de Bello et al. 2010; Jost 2006). Significant differences in abundance, richness, and diversity between regions and seasons, were each tested using separate generalised mixed models that accommodated the different distributions of these three variables. Pest abundances were analysed as negative binomial distributed responses with a log link function, to accommodate abundance being a positive integer (i.e., count) measure that was positive-skewed. Pest richness and diversity were each analysed as gamma distributed responses with a log link function, to accommodate both response variables being continuous and positive-skewed (Lindén & Mäntyniemi 2011). All three mixed models had the same linear covariates of main effects (region, season, and their interaction), and the same random effects structure (site nested within paddock) to account for spatial autocorrelation of sampling sites within the same paddock and repeated measures of sampling sites over time. All mixed models were run using glmTMB in the statistical programming language R (Brooks et al. 2017). All significant main effects were followed up with pairwise post hoc tests using the emmeans (estimated marginal means) package to conduct planned contrasts between regions and/or seasons, and final p-values were adjusted to control false discovery rates due to multiple tests (Lenth 2020; Quinn & Keough 2002).

To identify the most frequently occurring pest taxa, we characterised which taxa were ubiquitous over all regions and which were the most dominant (in terms of abundance) for each region. Ubiquitous pest taxa were identified from their presence (or absence) in each paddock. Dominant pests (i.e., those that contributed >5% of total pest abundances in one or more region) were characterised using their mean density per m^2 across sampling sites and seasons. Dominant pests were characterised separately for below and above-ground, since above-ground pests were roughly tenfold more abundant than below-ground pests.

The principal component analysis (PCA) ordination method was used as an exploratory method to compare regions and sampling sites to assess similarity in pest abundance patterns. The PCA was based on the mean abundance of pest taxa at each sampling site, and were transformed to standardized values across sites using the Hellinger method (Legendre & Gallagher 2001). The relative contribution of each sampling site and taxa was used to visualize the first two leading dimensions of the PCA.

Pest biomass and consumption of pasture

While abundance is undoubtably important, body mass influences the energetic requirements of an invertebrate and will markedly influence the magnitude of damage that any given pest taxon causes to pastures. Simply, larger pests consume more per individual than smaller pests due to the energetic requirements of their mass (Maino & Kearney 2015). The relative abundance of animal taxa typically has an inverse relationship with their relative mass (Blackburn et al. 1993) and was the case here (Fig. S1). Thus, we sought to estimate the biomass of pests in each region and the damage potentially caused by each pest taxon by accounting for both abundances and mass.

Following Ridsdill-Smith (1997), we estimated pastoral production loss attributable to pest taxa based on their average abundance (of the damaging stage only where applicable) in each region, energetic requirements due to their size, and the time spent active each year. Our approach utilises well known body-size scaling relationships that allow energetic requirements to be estimated for animals (Chown et al. 2007; Glazier 2005; Maino et al. 2014). In turn, we estimated consumption rates using allometric relationships between body mass (wet mass) and metabolic rate for arthropods (Chown et al. 2007; metabolic rate (mW) = 1.58 × mass (g)$^{0·75}$) and gastropods (Vladimirova 2001; metabolic rate (mW) = 0.73 × mass(g)$^{0.80}$), in combination with published measurements of body mass for the taxa found in our survey. When body mass estimates were unavailable, mass was calculated from body length measurements using body length-weight scaling relationships that have previously been estimated for their taxonomic group (Mercer et al. 2001; Sohlström et al. 2018). For simplicity, we used average adult body mass for all taxa except for some scarabs. Larval mass was used for *Cyclocephala signaticollis, Sericesthis* spp.*, A. coulonii,* and *A. tasmaniae* because this life-stage causes most pasture damage in these taxa (Berg et al. 2014; Jackson & Klein 2006; Matthews 1974). For *H. arator*, adult and larval mass were used for the period of time each life-stage is known to be active, since both stages cause substantial damage and have little overlap in active periods (Frew et al. 2016). We only considered taxa identified to genus or species because body mass varies too much among species in higher taxonomic groups.

Estimated pasture consumption rates for each pest taxon were converted into the percentage loss of each pasture's metabolisable energy yield. Metabolisable energy represents the amount of energy dairy cattle obtain from feed post digestion and use for maintenance, activity, pregnancy, weight gain and milk production (Moran 2005). We obtained estimates of metabolisable energy yield from Bell et al. (2013), who estimated the average monthly metabolisable energy per hectare in different regions of south-eastern Australia between 1971–2010. Bell et al. (2013) provided separate estimates of metabolisable energy yield for locations in Gippsland, south-west Victoria, northern Victoria, Tasmania, and the south coast of New South Wales, but did not consider locations in the two South Australian regions surveyed in our study. We based estimates for monthly pasture productivity and metabolisable energy in these two regions using south-west Victoria data given this region has the closest proximity and has comparable climate, soil and pasture composition (Table S1). Overall, our energetic model can be expressed as:

$$\text{Metabolisable energy yield of pasture (\%) consumed by pest } = 100 \times \frac{a \times m \times t}{e}$$

where for a given pest, *a* is their average abundance (individuals/ha), *m* is the metabolic rate of an average sized individual (joules/second/individual), and *t* is their time spent active (seconds), and for a given pasture, *e* is the metabolisable energy per area (joules/ha) in a season or year. Estimates of *t* for autumn and spring were based on the time in each season. Estimates of *t* for annual consumption were based on the number of months each taxon is expected to be active over a 12-month period. To aid future work, we provide estimates of metabolisable energy that is potentially consumed by pests in autumn and spring in kg of pastoral dry matter per hectare in Tables S2 & S3 (but these are not discussed further).

We analysed pest biomass as gamma distributed responses with a log-link function and the same linear covariates of main effects (region, season, and their interaction) and random effects as our earlier models for pest abundance, richness and diversity. However, our analysis for pest biomass is potentially anti-conservative because pests were assumed to be adults or larvae, and thus ignored finer scaled size variation between development stages, nor do our estimates account for measurement error in adult body size. As such, we did not perform statistical analysis on our estimates for pest consumption of pasture yield, and accordingly, these results should be treated with some caution.

Results

Of the 2,661,315 invertebrates, or invertebrate colonies, we identified and counted, 583,048 were pest invertebrates (Table S4). This included 40 unique taxa (Table 1).

Overall pest abundance, biomass, richness and diversity

While pests were roughly ten times more abundant in above-ground collections than below-ground collections (Fig. 2a), pest biomass was greater below than above-ground (Fig. 2b). Above-ground pests had a greater abundance (χ^2= 150.17, d.f.=1, $p<0.01$) and biomass (χ^2= 40.17, d.f.=1, $p< 0.01$) in spring compared with autumn, while below-ground pests had similar abundances (χ^2= 3.19, d.f.=1, p=0.07) and biomass (χ^2= 0.27, d.f.=1, p= 0.60) in spring and autumn (Fig. 2a & b). Pest diversity (χ^2= 37.06, d.f.=1, p<0.01) and richness (χ^2= 135.35, d.f.=1, p<0.01) were both significantly higher in spring compared with autumn (Fig. 2c & d).

Regional and seasonal differences in pest abundance, biomass, richness and diversity

Both above and below-ground pest abundances differed between regions and seasons. The interaction between season and region significantly affected above (χ^2= 267.750, d.f.=6, p<0.01) and below (χ^2= 47.83, d.f.=6, p<0.01) ground abundance. Post hoc tests suggest above-ground pest abundance significantly differed between regions during spring but not autumn (Fig. 3a). The highest above-ground pest abundances were in eastern South Australia and Tasmania during spring, and the lowest abundance was in the south coast of New South Wales during autumn (Fig. 3a). Above-ground abundances were significantly higher during spring than autumn in all regions except northern Victoria, where there was no significant difference between seasons, and the south coast of New South Wales, where abundance was significantly higher in autumn than in spring (Fig. 3a). Post hoc tests for below-ground pest abundance showed significant differences between regions in both spring and autumn (Fig. 3b). The highest below-ground pest abundance was in eastern South Australia during spring and the lowest abundance in Northern Victoria during autumn. There were significantly greater below-ground pest abundances detected in spring than autumn in the south coast of New South Wales, the Fleurieu Peninsula, eastern South Australia and Northern Victoria, but not Gippsland, south-west Victoria or Tasmania (Fig. 3b).

Seasonal changes in above and below-ground pest abundances were driven by a small number of taxa (Fig. 4). Increased above-ground pest abundances during spring in eastern South Australia, Fleurieu Peninsula, Gippsland, south-west Victoria and Tasmania were mostly attributable to *H. destructor*, *R. padi* and/or *S. viridis* (Fig. 4a). Notably, seasonal differences in above-ground pest abundances in south-west Victoria and Tasmania were driven mostly by *S. viridis,* with abundances in Tasmania increasing by ~5000 individuals per m^2 in spring compared with autumn (Fig. 4a). In the south coast of New South Wales, higher autumn above-ground abundances were mostly attributable to *Penthaleus* spp.*,* *R. padi* and *S.*

viridis (Fig. 4a). Increased below-ground pest abundances during spring in Fleurieu Peninsula, eastern South Australia and northern Victoria were predominantly due to Curculionoidea (Fig. 4b).

We estimated the average biomass for the 25 taxa identified to species or genus, which accounted for 94% of individual pests collected in our survey. We found above-ground pest biomass was higher in spring than autumn for most regions, with this shift being particularly pronounced in eastern South Australia, Fleurieu Peninsula and Tasmania (Fig. 5a). Above-ground pest biomass was consistent between autumn and spring in the south coast of New South Wales (Fig. 5a). Below-ground pest biomass estimates were similar between autumn and spring in most regions, although the average biomass was roughly ten times greater in eastern South Australia than all other regions (Fig. 5b).

Season significantly impacted pest richness (χ^2= 22.90, d.f.=1, p<0.01), but not in a consistent way across each region (χ^2= 233.90, d.f.=6, p<0.01). Pest richness was greater in autumn than spring in most regions, especially in eastern South Australia and Tasmania where pest diversity during autumn was roughly double the diversity in spring (Fig. 6). Conversely, pest richness in northern Victoria was similar across seasons, and in the south coast of New South Wales it was slightly lower in autumn than spring (Fig. 6). Across all regions and seasons, pest richness was the greatest in the Fleurieu Peninsula during autumn and lowest in eastern South Australia and Tasmania during spring.

Pest diversity was affected by season (χ^2= 6.814, d.f.=1, p=0.01), region (χ^2= 22.02, d.f.=6, p<0.01), and the interaction between these two (χ^2= 175.66, d.f.=6, p<0.01). Pest diversity significantly differed between spring and autumn for all regions. The south coast of New South Wales and northern Victoria had greater diversity in spring, while all other regions had greater pest diversity in autumn (Fig.7). Species diversity also significantly differed between regions during both spring and autumn (Fig. 7). In autumn, species diversity was the greatest in Gippsland and lowest in northern Victoria. In spring, species diversity was the greatest in the south coast of New South Wales and lowest in Tasmania (Fig. 7).

Ubiquitous and rare pest taxa

Based on occurrence data alone, the pests *R. padi* and *S. viridis* were the most ubiquitous, being recorded in all 57 paddocks (Fig. 8). *Cochlicella acuta* was the rarest taxon, being recorded from only two paddocks (both in south-west Victoria) in a single season of one year (spring 2018). *Mandalotus* spp., *Theba pisana, C. signaticollis, Cernuella virgata* and *Steriphus diversipes* were all found in less than ten paddocks over the study period (Fig. 8).

Dominant pests in each region

Of the total above-ground pest abundances within each region, at least 95% was attributable to a combination of *S. viridis*, *R. padi*, *Penthaleus* spp. and *H. destructor,* and in the case of the south coast of New South Wales, these four species and *B. medicagoense* (Fig. 9a). *Rhopalosiphum padi* and *S. viridis* were the most abundant above-ground pests in all regions (except for the Fleurieu Peninsula), accounting for more than 60% of the total above-ground pests. *Sminthurus viridis* was particularly abundant in Tasmania, averaging ~3500 per m^2 which accounted for more than 75% of the above-ground pests sampled in this region over the study period (Fig. 9a). *Halotydeus destructor* populations were highly variable between regions; this species was highly abundant (>1000 per m^2) in both South Australian regions (eastern South Australia and the Fleurieu Peninsula) but was relatively scarce or absent in the south coast of New South Wales and Tasmania (Fig. 9a). In contrast, *Penthaleus* spp. had similar abundances of ~100-200 per m^2 in all regions (Fig. 9a). *Balaustium medicagoense* had an average abundance of ~100 per m^2 in south coast of New South Wales but was rare or absent in all other regions (Fig. 9a).

Dominant below-ground pests varied far more between regions than above-ground pests (Fig. 9). Twelve below-ground pest species accounted for 95% or more of the total pest abundance across all regions. Eastern South Australia was dominated by *P. barbara,* which accounted for ~35% of below-ground pests in the region (Fig. 9b). No single taxon was clearly dominant in the Fleurieu Peninsula, but Curculionoidea, Scarabaeidae, *Sericesthis* spp. and *A. tasmaniae* were the most abundant (Fig. 9b). *Aploneura lentisci* and true wireworms (Elateridae) were the most dominant below-ground pests in south-west Victoria and Gippsland, together accounting for ~50% of the total below-ground pest abundances in each region (Fig. 9b). Taxa in the south coast of New South Wales and northern Victoria were dominated by Curculionoidea, which accounted for ~25% of the total below-ground pests in each region. In Tasmania, Pseudococcidae, *A. lentisci*, Curculionoidea and Elateridae were the most dominant taxa and collectively made up ~80% of below-ground pest abundances in the region (Fig. 9b).

Distribution maps for pest taxa from above and below-ground samples are shown in Fig. S2. In each map, the size of the circles represents the average abundance per m^2 of that taxon (calculated from the sum of their above and below-ground abundances per m^2) at each paddock where they were found present in our survey. Abundances were high and distributions were wide across much of south-eastern Australia for several pests (e.g., *Penthaleus* spp., *S. viridis, R. padi*), while for others, the abundances and distributions were low (e.g., *Mandalotus* spp.*, S. diversipes, T. pisana, C. virgata, C. acuta, C. signaticollis*), highlighting the vast differences between taxa that exist in dairy pastures in south-eastern Australia.

Scarab identification and distribution

DNA barcoding aided the identification of scarab larvae and adults that were difficult to identify using existing morphological keys, although just over half of the 73 tested specimens were able to be identified to genus or species level. All specimens belonged to the family Scarabaeidae and most (37) belonged to the subfamily Melolonthinae, with others belonging to the subfamilies Dynastinae (13), Rutelinae (9), Aphodiinae (7) and Scarabeinae (7). Based on their COI sequences, 43 specimens could be confidently assigned to one of nine genera: Anoplognathus (9), Phyllotocus (8), Sericesthis (8), Adoryphorus (7), Cyclocephala (3), Heteronychus (3), Acrossidius (2), Aphodius (2) and Onthophagus (1). Of these, 24 specimens were able to be identified to species level: *Adoryphorus coulonii* (7), *Sericesthis germinata* (6), *Cyclocephala signaticollis* (3), *Heteronychus arator* (3), *Acrossidius tasmaniae* (2), *Aphodius fimetarius* (1), *Aphodius granarius* (1) and *Onthophagus taurus* (1). The remaining specimens (30) were unable to be identified to genus or species level as there were no close sequence matches available on GenBank or BOLD (Fig. S3). All unique sequences generated in this study have been submitted to GenBank (under accession numbers

MW556490-MW556530 and MW556532-MW556563) with the sample location, season and year matching those used in Fig S3.

Scarab pest taxa had distinct differences in their distributions across south-eastern Australia (Fig. 10). *Acrossidius tasmaniae* and *Sericesthis* spp. had the widest distribution with the former occurring in all regions expect the south coast of New South Wales and the latter in all regions expect south-west Victoria. *Adoryphorus coulonii* was only found in the four most southern regions (Tasmania, Gippsland, south-west Victoria and eastern South Australia), while *H. arator* was most prevalent in the south coast of New South Wales but was found in all other regions expect Tasmania and eastern South Australia. *Cyclocephala signaticollis* had the most limited distribution, only being found in the south coast of New South Wales.

PCA of taxa abundance at each sampling site

The PCA revealed few regional differences in pest community composition, with a high level of overlap suggesting there was less variation between most regions than between paddocks within the same region (Fig. S4). However, paddocks in the Fleurieu Peninsula showed no overlap with paddocks in Tasmania and were more tightly clustered than all other regions, suggesting the Fleurieu Peninsula and Tasmania had dissimilar pest communities, and each region had less variation in pest communities relative to other regions (Fig. S4). The tight clustering of Tasmanian sites is a product of abundant *S. viridis* and Pseudococcidae since the vectors for both taxa are orientated toward the Tasmania cluster. The tight clustering of sites in the Fleurieu Peninsula is likely driven by *H. destructor* and *Penthaleus* spp., as the vectors for both species point toward the Fleurieu Peninsula cluster.

Consumption of pastures by pest species

We estimated how metabolisable energy yield of pastures was consumed by the 25 taxa identified to species or genus. Across all regions, pasture loss was estimated to be approximately three times higher in autumn (~10%) compared with spring (~3%). Pastures in eastern South Australia were predicted to suffer the greatest damage, with ~20% of pasture metabolisable energy yield lost on average during autumn and ~7% during spring, which was approximately double the amount lost in most other regions (Table 2). In eastern South Australia, *P. barbara* was estimated as the most damaging pest, consuming ~11% of pasture yield in autumn and ~1.5% in spring (Tables 2 & 3). *Sminthurus viridis* and *R. padi* were estimated as the most damaging pests when considering the entire year (Table S5), with each species estimated to consume an average of ~1.5% pasture yield annually across regions. *Sminthurus viridis* was especially damaging in Tasmania, consuming ~3% of annual pasture production. Of the scarabs, *A. tasmaniae* had the most widespread effect across the different regions, and was estimated to be particularly damaging in the Fleurieu Peninsula during autumn - predicted to consume ~6.5% of pasture yield. *Heteronychus arator* was predicted to be most damaging in the south coast of New South Wales during autumn, with an estimated pasture yield consumption of ~3.5% (Table 2).

Unsurprisingly, pests were estimated to cause far greater production losses to individual pastures during outbreaks – where they recorded their maximum abundance in a single paddock during our study. In autumn, *R. padi, A. tasmaniae, P. barbara* and *A. coulonii* were each estimated to consume above 20% of pasture yield when present in large numbers, while *S. viridis* and *H. arator* were estimated to consume above 10% of pasture yield when in large numbers (Table 2). While pest outbreaks were predicted to have less impact on pasture yield in spring, when in large numbers, *S. viridis* and *Sericesthis spp.* were estimated to consume ~10% of pasture yield (Table 3).

Discussion

Australian dairy pastures endure significant yield loss from invertebrate pests, but key knowledge gaps hinder the improvement of current pest management strategies. Here, we provide a long-needed survey of the composition and abundance pests, and estimate pasture yield losses attributable to these pests in all major Australian dairy regions. Our survey indicates that dairy farmers encounter a similar taxonomic composition of above-ground pests in most regions, with a small number of species dominating pest communities. Nevertheless, there are regional and seasonal differences in the abundances of these pests. Below-ground pests appear more variable, especially the scarabs, which have differing abundances and distributions across regions. Our energetic modelling suggests pests directly consume a three-fold greater percentage of metabolisable energy produced by pastures during autumn than spring and identifies the pest taxa most likely to cause economic damage to dairy pastures. *Rhopalosiphum padi* and *S. viridis* were consistently among the most damaging pests in all regions and seasons, however, our models did not specifically address the increased risk that pests pose to establishing pastures. For example, species such as *H. destructor*, *Penthaleus* spp. and *A. tasmaniae* can cause significant losses to legume and grass seedlings, which are particularly vulnerable to feeding damage (Ferguson et al. 2019; Ridsdill-Smith et al. 2008). Other pests were identified as economically important in specific regions, particularly the scarabs *Sericesthis* spp. and *A. tasmaniae* in the Fleurieu Peninsula, *A. coulonii* in Gippsland, and *H. arator* in the south coast of New South Wales, along with the snail *P. barbara* in eastern South Australia. Our survey and energetic models provide baseline information that provides direction for future research and can be immediately utilised to develop pest management strategies.

The two most common and consistently damaging pasture pests over regions and seasons identified here, *S. viridis* and *R. padi*, are widespread agricultural pests with existing management strategies available (Arthur et al. 2020; Kirkland et al. 2018). *Sminthurus viridis* is highly polyphagous, attacking broadleaf plants, canola, cereals and legumes (Bishop et al. 2001). This wide host plant range has aided *S. viridis* spread throughout southern Australia, where it is active from autumn to spring and endures hot summer months by producing diapause eggs (Roberts et al. 2011; Wallace 1968). *Rhopalosiphum padi* is a major pest of cereals and grasses worldwide (Edwards et al. 2008), and not only damages plants through direct feeding but also through the transmission of plant viruses (Valenzuela & Hoffmann 2015). Current control strategies for *S. viridis* and *R. padi* are reported to be effective but are heavily reliant on insecticide sprays and seed treatments (Clouston et al. 2016; Kirkland et al. 2018). Continued reliance on insecticides will accelerate the evolution of insecticide resistance, which is occurring with increasing frequency in Australian pests (Umina et al. 2019). Employing more diverse control strategies for *S. viridis* and *R. padi* is important. Non-insecticide control strategies have shown encouraging results through the utilisation of natural enemies such as predatory mites for *S. viridis* (Ireson et al. 2002) and parasitoid wasps for *R.*

padi (Entling et al. 2003), although continued work is needed to facilitate their application in dairy pastures.

The findings of our energetic modelling support previous research indicating scarabs are among the most economically important pests to Australian dairy pastures (Ferguson et al. 2019; Pauley & Miller 1993), and suggests control strategies should be tailored to address differences in scarab community composition and damage. For instance, *A. coulonii* was abundant and damaging in cooler southern regions (Tasmania, south-west Victoria and Gippsland) and absent in warmer northern regions (northern Victoria, the south coast of New South Wales and the Fleurieu Peninsula). This is consistent with research suggesting *A. coulonii* favours cooler climates with average temperatures between 12-15°C (Berg et al. 2014). Conversely, *H. arator* was most abundant in the south coast of New South Wales in our study, which is congruous with previous findings suggesting optimal conditions for larval development are relatively warm (20-25°C) conditions over the late spring to autumn period (Bell et al. 2011; King et al. 1981). *Acrossidius tasmaniae* was the most consistently sampled scarab in our survey, found in all dairy regions in south-eastern Australia except the south coast of New South Wales, suggesting this species may have a broader environmental tolerance compared with *A. coulonii*, *H. arator, C. signaticollis* and *Sericesthis* spp.

The ability to effectively manage scarabs in Australia dairy pastures is hindered by the soil-dwelling nature of their larvae. Most scarab species spend the majority of their life underground, where chemical controls are less effective (e.g., Berg et al. 2014). However, chemical control is effective on *A. tasmaniae* because larvae move above-ground to feed (McQuillan et al. 2007). While biological controls offer a promising alternative to manage scarabs (e.g., parasitic nematodes and pathogenic fungi can suppress scarab populations; Grewal et al. 2005; Rath & Bullard 1997), a lack of awareness and prohibitive costs of commercial entomopathogens remain barriers to their use (Baker et al. 2020). Furthermore, efforts to manage pest scarabs are also hindered by the difficulty of identification using current taxonomic keys which are largely based on adults even though scarabs are typically most damaging to pastures during their larval stages (Berg et al. 2014; Jackson & Klein 2006). Even with the DNA approaches applied here, only half of the tested specimens could be successfully identified to species or genus due to a paucity of sequences associated with verified voucher specimens. Investment is needed to develop morphological keys for larval stages and to expand the public databases of DNA sequences associated with morphologically identified scarab adults in GenBank and BOLD. These actions will provide tools that enable identification and improved development of management strategies for pasture scarabs.

The small pointed (or conical) snail, *P. barbara,* was highly abundant and estimated to cause considerable losses to pasture production during autumn in eastern South Australia. Originating from the Mediterranean region, this snail is well suited to climatic conditions in southern Australia; it is typically most abundant in higher rainfall areas with alkaline (calcareous) soils, where it aestivates over summer months (Jourdan et al. 2019; Leonard et al. 2003). Although a pest of pasture plants, *P. barbara* also feeds on dead organic matter above and below the soil surface (Leonard et al. 2003). Several control strategies, including cultural, chemical and biological, have been trialled on *P. barbara* and related conical snails (Baker et al. 2012; Coupland & Baker 2007; Leonard et al. 2003), but a highly effective strategy remains elusive (Jourdan et al. 2019). Molluscicide baits are regularly used but are not a particularly attractive food source for snails and are costly for famers (Baker et al. 2012; Leonard et al. 2003). Cultural controls methods (e.g., burning paddocks prior to sowing) are also practised but incur environmental damage in the process (Jourdan et al. 2019).

The large seasonal fluctuations in pest abundance and biomass identified in our study are expected since the phenology of different species enables them to maximise feeding and reproductive efforts during periods of the year when conditions are most favourable (Logan et al. 2006). Here, both above and below-ground pests showed seasonal changes in abundance and biomass; the magnitude of these changes was far greater in above than below-ground pests. Most of the seasonal change in abundance and biomass in above-ground pests was driven by a combination of *S. viridis, R. padi* and *H. destructor.* All three species have a shorter generation time (Gu et al. 2007; Rispe et al. 1999; Wang et al. 2018) compared with the dominant below-ground pests (i.e., scarabs) which are often univoltine (Candy & McQuillan 1998; Frew et al. 2016; Matthiessen & Ridsdill-Smith 1991). The ability to develop and reproduce faster during favourable conditions leads to large responses to seasonal environments (e.g., variable temperature and rainfall). On the other hand, below-ground pests inhabit a more stable environment, buffered from climatic extremes and access to a more stable food source in plant roots (Hooper et al. 2000). Seasonal expansions of pest abundance were typically driven by a few species, and consequently tended to correspond with lower pest diversity and richness. These seasonal changes were far more pronounced in Tasmania and eastern South Australia compared with other dairy regions. Seasonal changes in Tasmanian pest communities were driven mostly by a ten-fold increase in *S. viridis* abundances. Such vast seasonal shifts in *S. viridis* populations during our study were likely related to the high moisture requirement of this species (Roberts et al. 2011; Wallace 1967). High winter and spring rainfall in Tasmania provides *S. viridis* with near-optimum conditions for development (Hennessy et al. 1999). The cause of similarly pronounced seasonal changes in eastern South Australia are less clear, as differences were mostly driven by a combination of three species (*S. viridis, R. padi* and *H. destructor*). However, *R. padi* seasonality in eastern South Australia is potentially due to their migration into pastures in spring and to other plant hosts in autumn (Barro & Wallwork 2008).

In addition to seasonal shifts in pest communities, dairy farmers need to manage changes in pasture productivity over time. Our energetic modelling suggests that pests consume, on average, a three-fold greater percentage of the metabolisable energy produced by pastures during autumn than in spring; this is despite more pests being present during spring than autumn. Seasonal changes in estimated pasture consumption were particularly evident in the south coast of New South Wales, where pests were predicted to consume a five-fold greater percentage of autumn pasture production compared with spring pasture production. Pasture productivity in south-eastern Australia during spring is often surplus to the nutritional requirements of dairy cattle, and farms are therefore typically able to sustain greater amounts of pasture loss before suffering economic losses (Chapman et al. 2011; Lewis et al. 2020). In contrast, pasture productivity during autumn is lower and far more likely to be a limiting factor in dairy production systems (Nie et al. 2004; Wales & Kolver 2017). Accordingly, any pasture lost to pests will likely cause greater economic loss because supplementary feed will need to be provided (Lewis et al. 2020). Strategies that supress autumn pest populations are therefore likely to be a higher priority for dairy farmers.

The taxonomic composition of species was found to be similar among the seven dairy regions, indicating many pasture pests can withstand environmental differences across south-eastern Australia. Our findings suggest that greater variation in pest community composition exists within, rather than between, regions. As such, differences in management practices between farms within each region seem to be shaping pest composition more than broad-scale differences (e.g., climate) between regions. Our findings are consistent with Tozer et al. (2014), who found few differences in above and below-ground pest communities between multiple New Zealand dairy regions. Similarities between regions are, to some extent, expected since improved pastures create similar habitats that will favour a similar cohort of taxa. Moreover, many of the dominant pests have effective dispersal strategies, which have enabled them to spread over a broad range. For instance, *R. padi* and several below-ground coleopteran pests, have winged morphs or life stages that provide them with a ready means of dispersal (Delmotte et al. 2002; Jackson & Klein 2006). Other pests, such as *S. viridis* and *H. destructor*, produce robust eggs that can disperse between farms passively via wind or by accidental human-facilitated transport in animal fodder, seeds and soil (Ridsdill-Smith 1997; Roberts & Weeks 2011).

This study provides useful new knowledge of pests in Australian dairy pastures but is not without limitations. Our data is based on four snapshots at each paddock over two years which is unlikely to have fully captured the temporal variation in pests, or pests that have invaded Australia but not established in dairy regions (e.g., Allsopp & Hutchinson 2019). Sampling over only two years also restricted our ability to accurately survey sporadic pests, such as the armyworms, *M. convecta*, *P. ewingii* and *P. dyscrita*, which are highly migratory and invade pastures in south-eastern Australia irregularly (Farrow & McDonald 1987; Hoffmann et al. 2008). Our collections may have also missed peak periods of abundance in seasonal taxa such as *H. destructor*, which we found at lower abundances than previous studies in Australian pastures (Ridsdill-Smith et al. 2013). More frequent sampling and the inclusion of winter and summer sampling periods was beyond our capacity but would provide increased information on seasonal pest variation. The inclusion of additional sampling techniques (e.g., refuge traps, pitfall traps and sticky traps) may have also enabled us to detect pest species not readily collected by the vacuum and soil samples undertaken here. One such group are the slugs; although we detected several hundred slugs (most notably *Milax gagates* and *Deroceras reticulatum*), abundances are likely to have been much greater if refuge traps were employed (see Nash et al. 2007). Our energetic modelling relied on assumptions that led to conservative estimates of pasture metabolisable energy yield losses; indeed our estimates are typically less than those based on alternative approaches (e.g., Ferguson et al. 2019; Pauley & Miller 1993). For example, we assumed a constant metabolic rate within each species, although metabolic rate will vary between individuals of each species and periods of dispersal, feeding, warmer temperature, and reproduction will increase metabolic (and hence consumption) rate (Chown & Nicolson 2004; Pettersen et al. 2018). Furthermore, our models quantified metabolisable energy yield losses from direct consumption; they did not account for pasture plant loss from root or stem damage, from insect-vectored transmission of damaging plant viruses, or any indirect damage caused from partial plant consumption on future pasture productivity. Additionally, pasture productivity within each region was based on the monthly averages predicted between 1971–2010 by Bell et al. (2013), which may not accurately reflect yield potential during our 2017-18 surveys when rainfall was below average. Furthermore, our models were unable to place a financial value on pest consumption levels. Further research that can estimate the value of replacement feed, accounting for variation in market values between regions, seasons, and years, would be a valuable next step.

In conclusion, our study provides fundamental information on the composition of pest taxa and the potential losses to metabolisable energy yield in Australian dairy pastures. While our surveys and energetic modelling were able to identify pests of most concern in each region, many of these species (e.g., *P. barbara* and *A. coulonii*) currently lack effective management strategies. For other pests where management strategies are available (e.g., *S. viridis, R. padi, Penthaleus* spp.) these are heavily reliant on broad-spectrum chemical measures, which negatively impacts beneficial invertebrates and places these pests at risk of evolving insecticide resistance. Future research is needed to build upon the foundations provided here.

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Tables

Table 1. List of the 40 pest taxa sampled from south-eastern Australian dairy pastures and the lowest taxonomic level to which they were identified in this study.

Taxa	**Scientific name**	**Taxonomic level**
African black beetle	*Heteronychus arator*	Species
Argentine scarab	*Cyclocephala signaticollis*	Species
Argentine stem weevil	*Listronotus bonariensis*	Species
armyworm	Noctuidae	Family
Auchenorrhyncha	*Auchenorrhyncha*	Sub Order
balaustium mite	*Balaustium medicagoense*	Species
bird cherry-oat aphid	*Rhopalosiphum padi*	Species
black field cricket	*Teleogryllus commodus*	Species
black field earwig	*Nala lividipes*	Species
black keeled slug	*Milax gagates*	Species
black Portuguese millipede	*Ommatoiulus moreletii*	Species
blackheaded pasture cockchafer	*Acrossidius tasmaniae*	Species
blue oat mite	*Penthaleus* spp.	Genus
bryobia mite	*Bryobia* spp.	Genus
Coccoidea	Coccoidea	Super Family
European earwig	*Forficula auricularia*	Species
false wireworm	Tenebrionidae	Family
grey field slug	*Deroceras reticulatum*	Species
lucerne flea	*Sminthurus viridis*	Species
mandalotus weevil	*Mandalotus* spp.	Genus
mealybug (colony)	Pseudococcidae	Family
other Lepidoptera	Lepidoptera	Order
other Scarabaeidae	Scarabaeidae	Family

other Orthoptera	Orthoptera	Order
other slugs	Gastropoda (slugs)	Class
other snails	Gastropoda (snails)	Class
other Curculionoidea	Curculionoidea	Super Family
pest thrips	Thysanoptera	Order
pointed snail	*Cochlicella acuta*	Species
redheaded pasture cockchafer	*Adoryphorus coulonii*	Species
redlegged earth mite	*Halotydeus destructor*	Species
root aphid (colony)	*Aploneura lentisci*	Species
small pointed snail	*Prietocella barbara*	Species
spider mite	Tetranychidae	Family
spotted alfalfa aphid	*Therioaphis trifolii*	Species
spotted vegetable weevil	*Steriphus diversipes*	Species
true wireworm	Elateridae	Family
vineyard snail	*Cernuella virgata*	Species
white Italian snail	*Theba pisana*	Species
yellowheaded cockchafer	*Sericesthis* spp.	Genus

Table 2. Percentage of metabolisable energy produced by pastures that is lost during autumn due to pest consumption based on predicted energetic requirements of each taxon. Values show the average estimates for each region, the average over all regions, and the maximum (Max) lost (based on the highest recorded abundance in a single paddock for each taxon). Standard errors for each estimate are based on observed variation in pest abundances within each region. For simplicity, the table here shows the ten most damaging pests and the remaining taxa are reported in Table S2. ESA = eastern South Australia, FSA = Fleurieu Peninsula, GIP = Gippsland, NSW = south coast of New South Wales, NVC = northern Victoria, SWVC = south-west Victoria, TAS = Tasmania.

Scientific name	**ESA**	**FSA**	**GIP**	**NSW**	**NVC**	**SWVC**	**TAS**	**All regions**	**Max**
Rhopalosiphum padi	1.60 ±0.97	0.39 ±0.29	0.75 ±0.18	4.21 ±2.29	4.98 ±1.39	1.46 ±0.54	1.13 ±0.22	2.07 ±0.84	38.9
Acrossidius tasmaniae	2.44 ±2.24	6.64 ±3.64	1.83 ±1.12	0.00 ±0.00	0.00 ±0.00	0.70 ±0.28	1.72 ±0.73	1.90 ±1.14	23.62
Prietocella barbara	11.35 ±3.24	0.58 ±0.37	0.05 ±0.02	0.08 ±0.05	0.00 ±0.00	0.44 ±0.21	0.19 ±0.14	1.81 ±0.58	22.01
Sminthurus viridis	0.94 ±0.4	0.33 ±0.21	1.20 ±0.39	2.47 ±0.84	2.79 ±0.92	0.79 ±0.41	1.52 ±0.21	1.43 ±0.48	16.24
Heteronychus arator	0.00 ±0.00	0.53 ±0.23	0.77 ±0.43	3.48 ±1.02	0.19 ±0.09	0.06 ±0.06	0.00 ±0.00	0.72 ±0.26	10.42
Adoryphorus coulonii	0.00 ±0.00	0.00 ±0.00	2.41 ±1.26	0.00 ±0.00	0.00 ±0.00	0.86 ±0.53	0.80 ±0.54	0.58 ±0.33	23.15
Penthaleus spp.	0.35 ±0.32	0.4 ±0.21	0.17 ±0.06	0.75 ±0.26	0.27 ±0.11	0.38 ±0.11	0.03 ±0.01	0.34 ±0.15	3.35
Deroceras reticulatum	0.89 ±0.52	0.11 ±0.06	0.08 ±0.06	0.23 ±0.14	0.00 ±0.00	0.29 ±0.11	0.23 ±0.07	0.26 ±0.14	4.00
Teleogryllus commodus	0.85 ±0.85	0.00 ±0.00	0.00 ±0.00	0.00 ±0.00	0.07 ±0.07	0.49 ±0.23	0.09 ±0.05	0.21 ±0.17	6.79

Halotydeus destructor	0.23 ±0.23	0.57 ±0.4	0.05 ±0.03	0.04 ±0.04	0.15 ±0.12	0.36 ±0.19	0.00 ±0.00	0.20 ±0.14	2.91
All taxa*	19.11 ±4.23	10.05 ±3.71	7.46 ±1.79	12.23 ±2.7	8.88 ±1.68	6.16 ±0.99	6.04 ±0.99	9.99[†] ±6.85	46.60

** includes all 25 taxa identified to species or genus; [†] max combined consumption of all 25 taxa.*

Table 3. Percentage of metabolisable energy produced by pastures that is lost during spring due to pest consumption based on predicted energetic requirements of each taxon. Values show the average estimates for each region, the average over all regions, and the maximum (Max) lost (based on the highest recorded abundance in a single paddock for each taxon). Standard errors for each estimate are based on observed variation in pest abundances within each region. For simplicity, the table here shows the ten most damaging pests and the remaining taxa are reported in Table S3. ESA = eastern South Australia, FSA = Fleurieu Peninsula, GIP = Gippsland, NSW = south coast of New South Wales, NVC = northern Victoria, SWVC = south-west Victoria, TAS = Tasmania.

Scientific name	**ESA**	**FSA**	**GIP**	**NSW**	**NVC**	**SWVC**	**TAS**	**All regions**	**Max**
Sminthurus viridis	1.38 ±0.46	0.10 ±0.06	0.82 ±0.24	0.24 ±0.08	0.64 ±0.33	0.95 ±0.32	2.96 ±0.41	1.01 ±0.27	8.82
Rhopalosiphum padi	1.9 ±0.43	0.48 ±0.17	0.43 ±0.10	0.41 ±0.11	0.87 ±0.34	0.22 ±0.07	0.46 ±0.07	0.68 ±0.18	4.69
Prietocella barbara	1.63 ±0.59	0.45 ±0.25	0.03 ±0.01	0.07± 0.04	0.00 ±0.00	0.12 ±0.05	0.30 ±0.26	0.37 ±0.17	3.90
Sericesthis spp.	0.00 ±0.00	1.31 ±1.31	0.06 ±0.02	0.12 ±0.06	0.19 ±0.11	0.00 ±0.00	0.02 ±0.01	0.24 ±0.22	10.46
Milax gagates	0.52 ±0.22	0.08 ±0.08	0.02 ±0.02	0.00 ±0.00	0.04 ±0.03	0.33 ±0.08	0.27 ±0.12	0.18 ±0.08	2.50
Halotydeus destructor	0.45 ±0.38	0.33 ±0.23	0.06 ±0.03	0.00 ±0.00	0.26 ±0.18	0.06 ±0.03	0.00 ±0.00	0.17 ±0.12	3.55
Heteronychus arator	0.00 ±0.00	0.04 ±0.04	0.07 ±0.04	0.75± 0.19	0.04±0.02	0.00 ±0.00	0.00 ±0.00	0.13 ±0.04	3.42

Adoryphorus coulonii	0.01 ±0.01	0.00 ±0.00	0.56 ±0.26	0.00 ±0.00	0.00 ±0.00	0.06 ±0.02	0.09 ±0.05	0.10 ±0.05	3.82
Theba pisana	0.50 ±0.4	0.00 ±0.00	0.00 ±0.00	0.00 ±0.00	0.00 ±0.00	0.00 ±0.00	0.00 ±0.00	0.07 ±0.06	3.34
Acrossidius tasmaniae	0.11 ±0.11	0.17 ±0.11	0.06 ±0.02	0.00 ±0.00	0.02 ±0.02	0.02 ±0.01	0.01 ±0.01	0.06 ±0.04	0.86
All taxa*	6.85 ±4.23	3.32 ±3.71	2.32 ±1.79	2.17 ±2.70	2.20 ±1.68	1.86 ±0.99	4.27 ±0.99	3.28† ±2.00	15.90

** includes all 25 taxa identified to species or genus; † max combined consumption of all 25 taxa.*

Figures

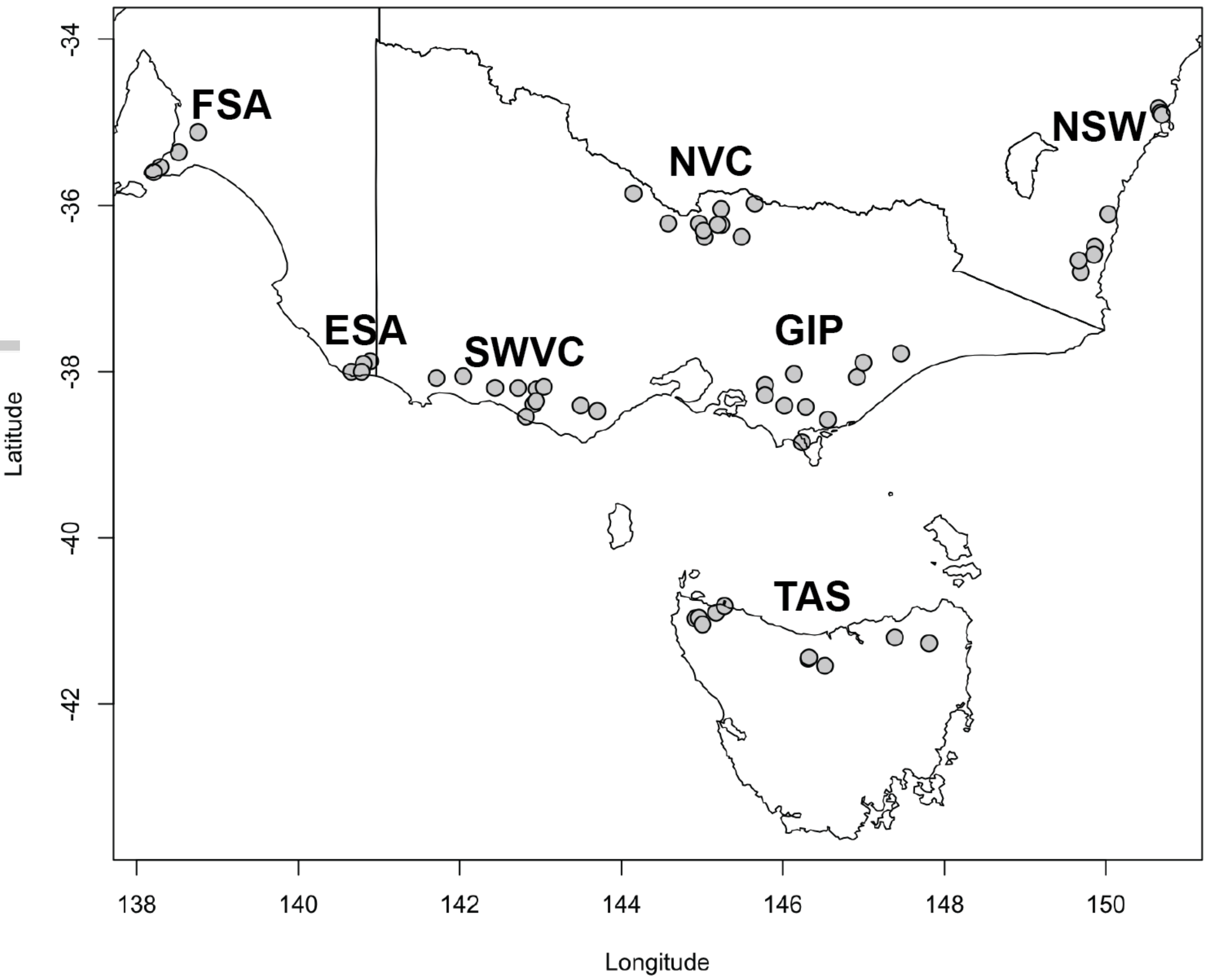

Figure 1. Locations of the 57 paddocks surveyed across seven dairy regions in south-eastern Australia. ESA = eastern South Australia, FSA = Fleurieu Peninsula, GIP = Gippsland, NSW = south coast of New South Wales, NVC = northern Victoria, SWVC = south-west Victoria, TAS = Tasmania.

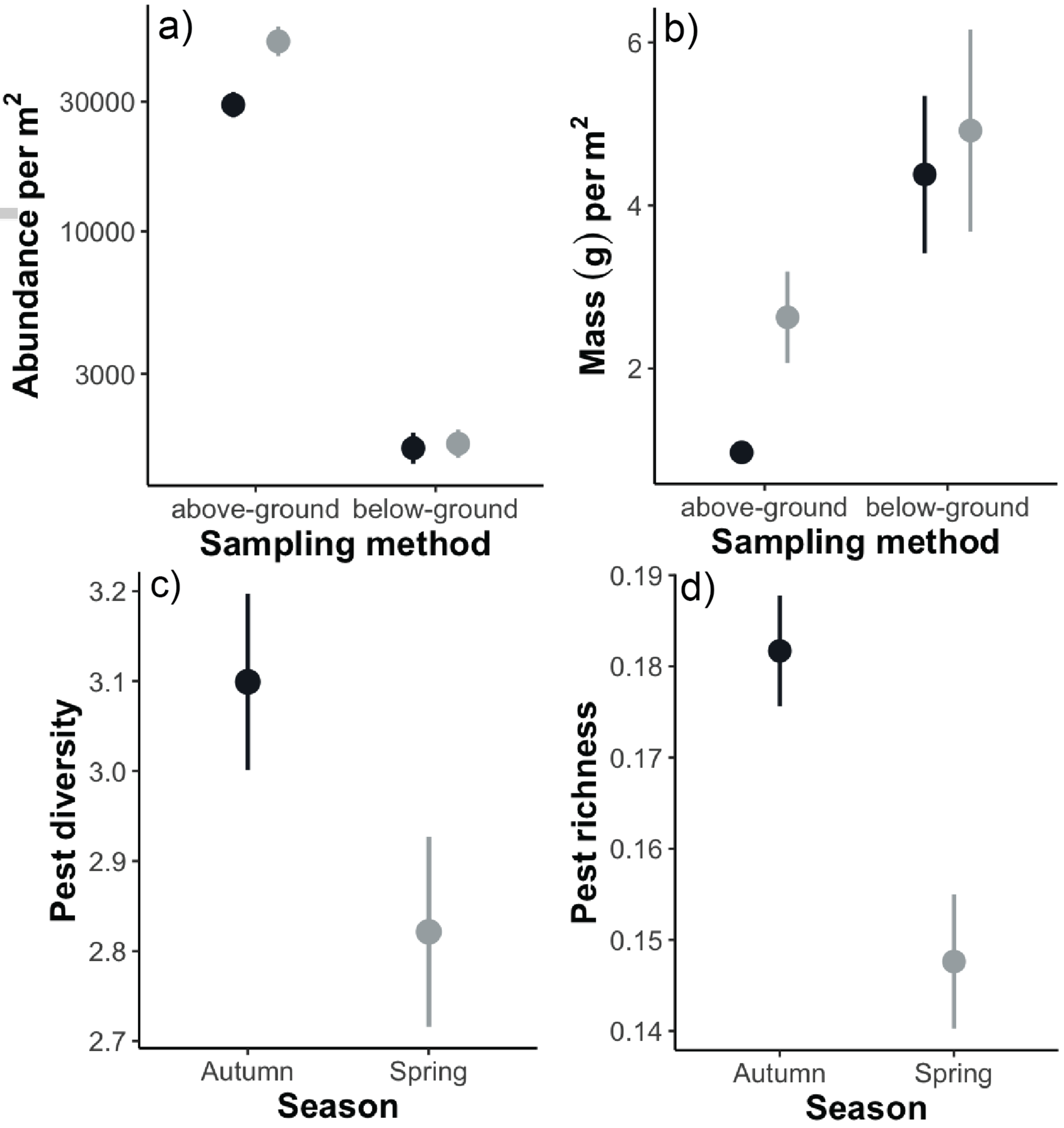

Figure 2. Average pest abundance (a), biomass (b), diversity (c), and richness (d) (± standard error) for pest communities across all regions during autumn (black colour) and spring (grey colour). Abundance and biomass were estimated separately for above and below-ground samples. Note: biomass estimates only account for the 25 taxa identified to species or genus, and standard errors for biomass estimates do not account for intra-specific variation in mass.

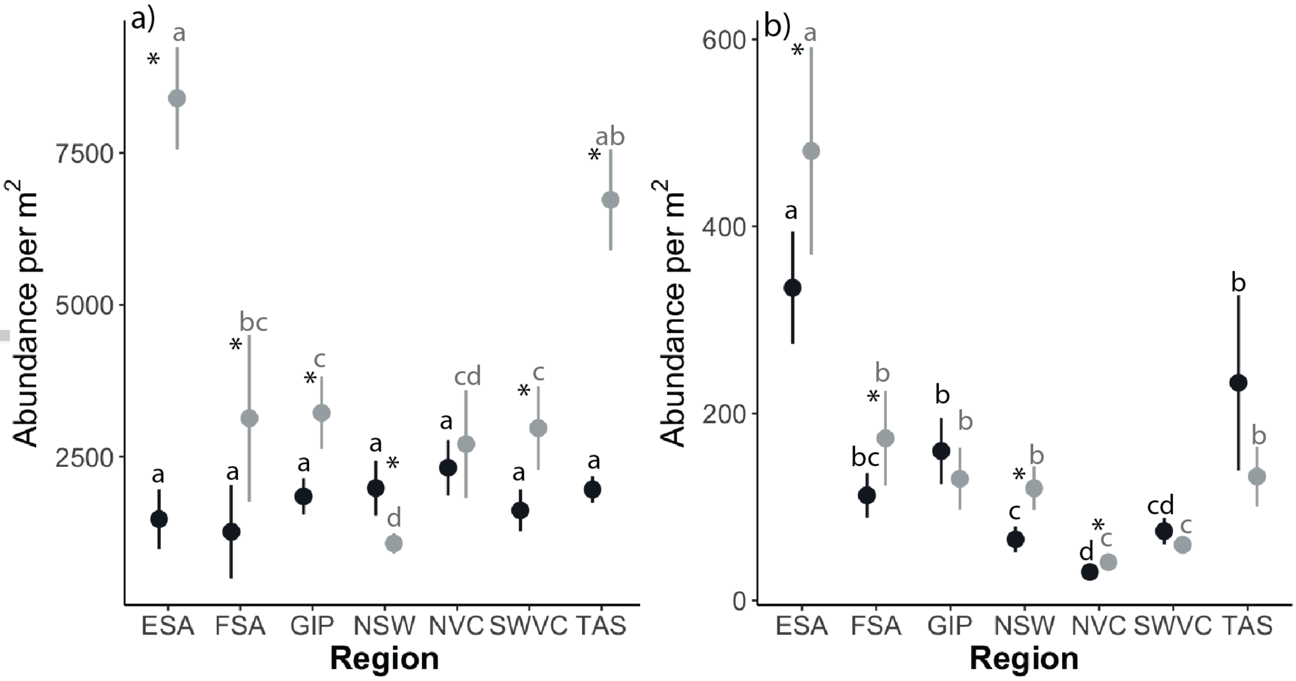

Figure 3. Average abundance of pests above-ground (a) and below-ground (b) in each region during autumn (black colour) and spring (grey colour). Circles show the mean abundance per sampling occasion in each region (± standard error). Asterisks indicate instances where season had a significant impact within a region. Grey coloured letters indicate significant differences between regions in spring and black letters indicate significant differences between regions in autumn. ESA = eastern South Australia, FSA = Fleurieu Peninsula, GIP = Gippsland, NSW = south coast of New South Wales, NVC = northern Victoria, SWVC = south-west Victoria, TAS = Tasmania.

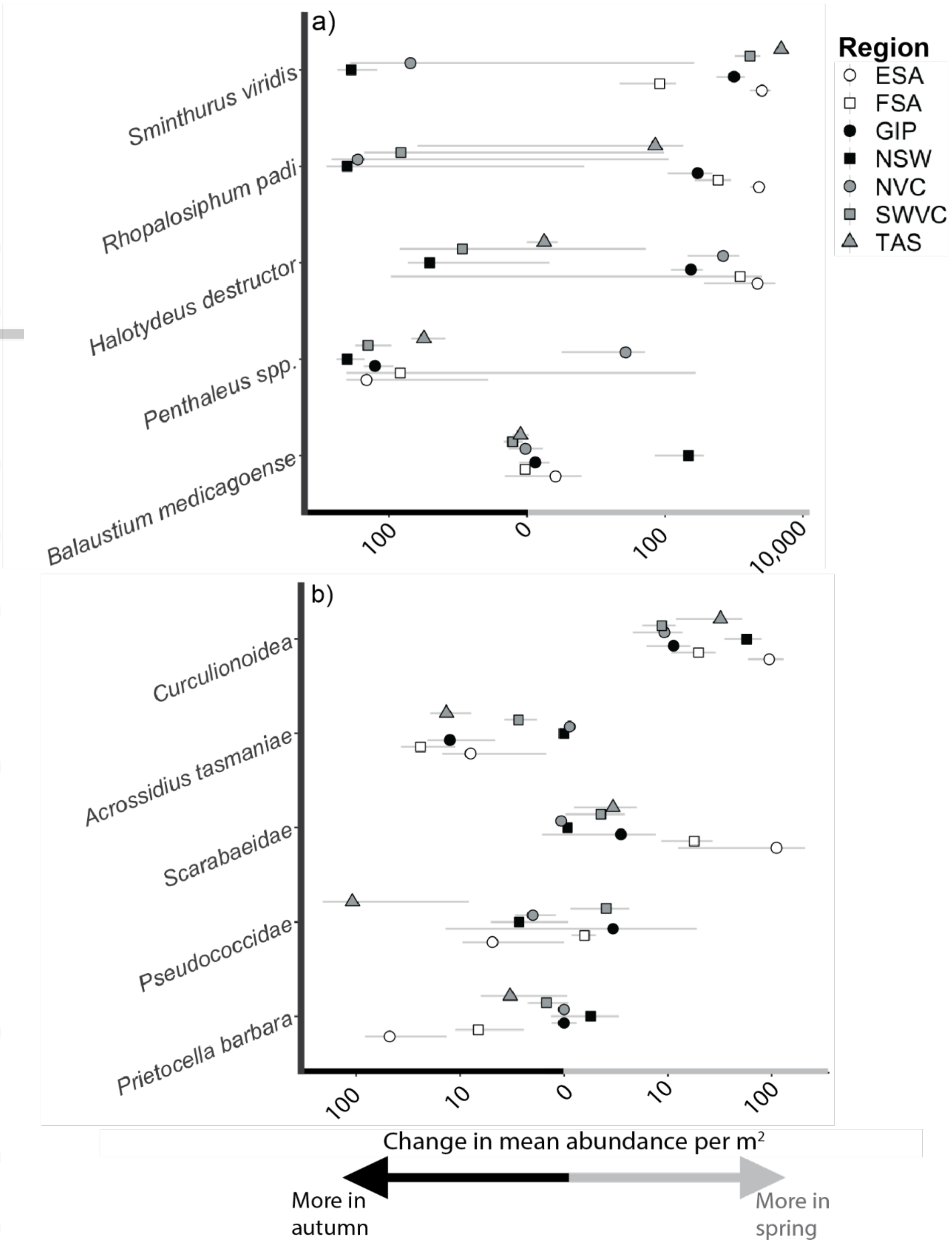

Figure 4. Seasonal changes in average abundance (± standard error) of above-ground (a) and below-ground (b) pest taxa in each region during autumn (black colour) and spring (grey colour). For simplicity, the figure only shows the five taxa that experienced the greatest changes in seasonal abundance. ESA =

eastern South Australia, FSA = Fleurieu Peninsula, GIP = Gippsland, NSW = south coast of New South Wales, NVC = northern Victoria, SWVC = south-west Victoria, TAS = Tasmania.

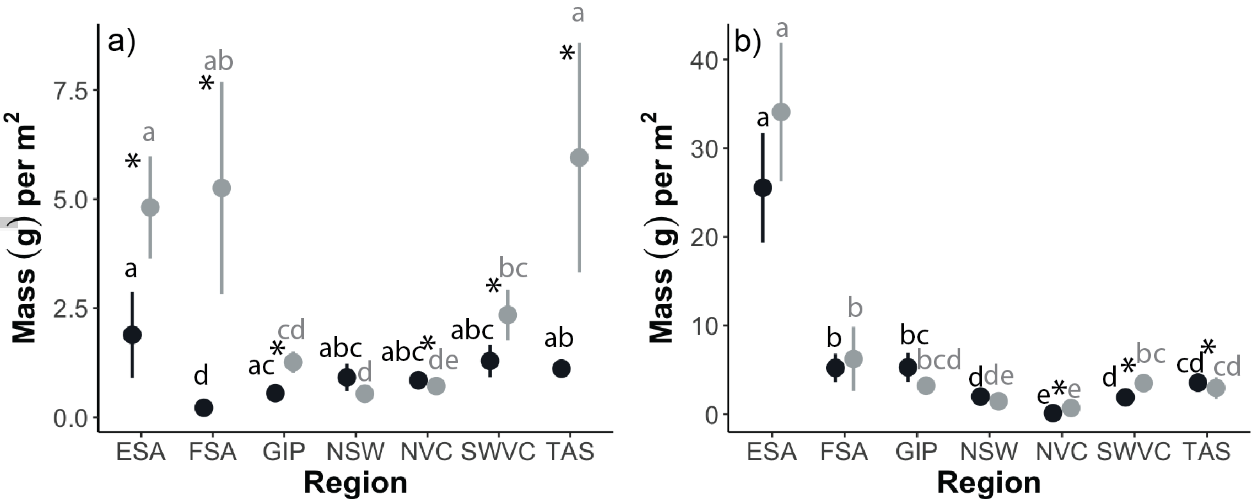

Figure 5. Average biomass (± standard error) of pests above-ground (a) and below-ground (b) in each region during autumn (black colour) and spring (grey colour). Biomass only accounts for the 25 taxa identified to species or genus and are based on previous estimates of body mass/size for these taxa. Asterisks indicate instances where season had a significant impact within a region. Grey coloured letters indicate significant differences between regions in spring and black letters indicate significant differences between regions in autumn. ESA = eastern South Australia, FSA = Fleurieu Peninsula, GIP = Gippsland, NSW = south coast of New South Wales, NVC = northern Victoria, SWVC = south-west Victoria, TAS = Tasmania.

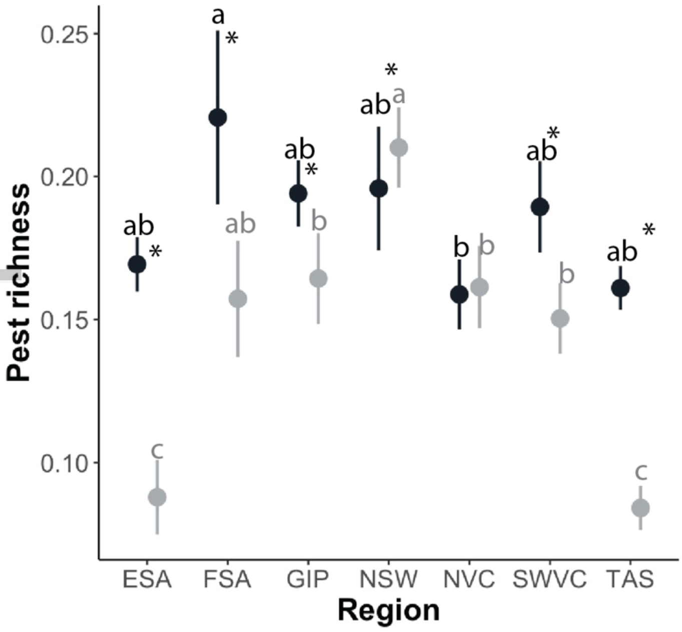

Figure 6. Average richness (± standard error) of pests in each region during autumn (black colour) and spring (grey colour). Above and below-ground pests are combined. Asterisks indicate instances where season had a significant impact within a region. Grey coloured letters indicate significant differences between regions in spring and black letters indicate significant differences between regions in autumn. ESA = eastern South Australia, FSA = Fleurieu Peninsula, GIP = Gippsland, NSW = south coast of New South Wales, NVC = northern Victoria, SWVC = south-west Victoria, TAS = Tasmania.

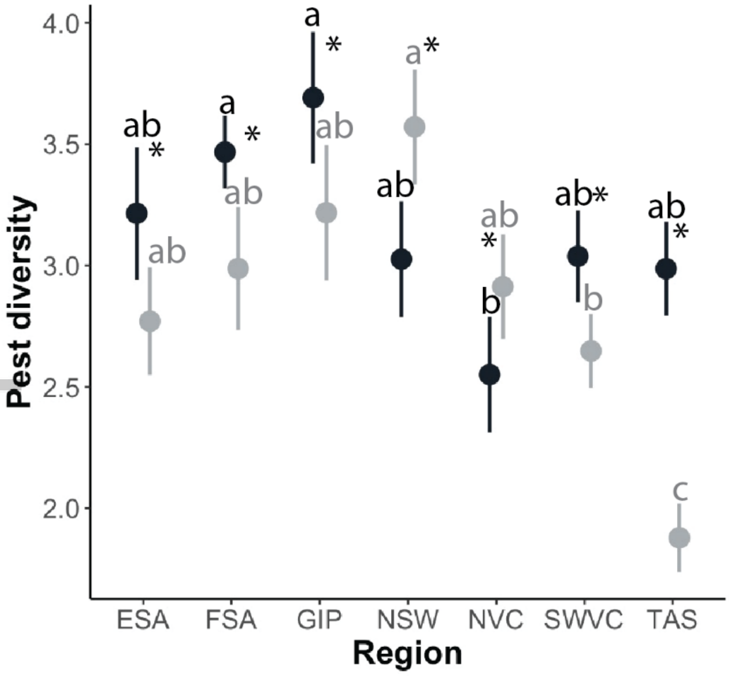

Figure 7. Average diversity (± standard error) of pests in each region during autumn (black colour) and spring (grey colour). Above and below-ground pests are combined. Asterisks indicate instances where season had a significant impact within a region. Grey coloured letters indicate significant differences between regions in spring and black letters indicate significant differences between regions in autumn. ESA = eastern South Australia, FSA = Fleurieu Peninsula, GIP = Gippsland, NSW = south coast of New South Wales, NVC = northern Victoria, SWVC = south-west Victoria, TAS = Tasmania.

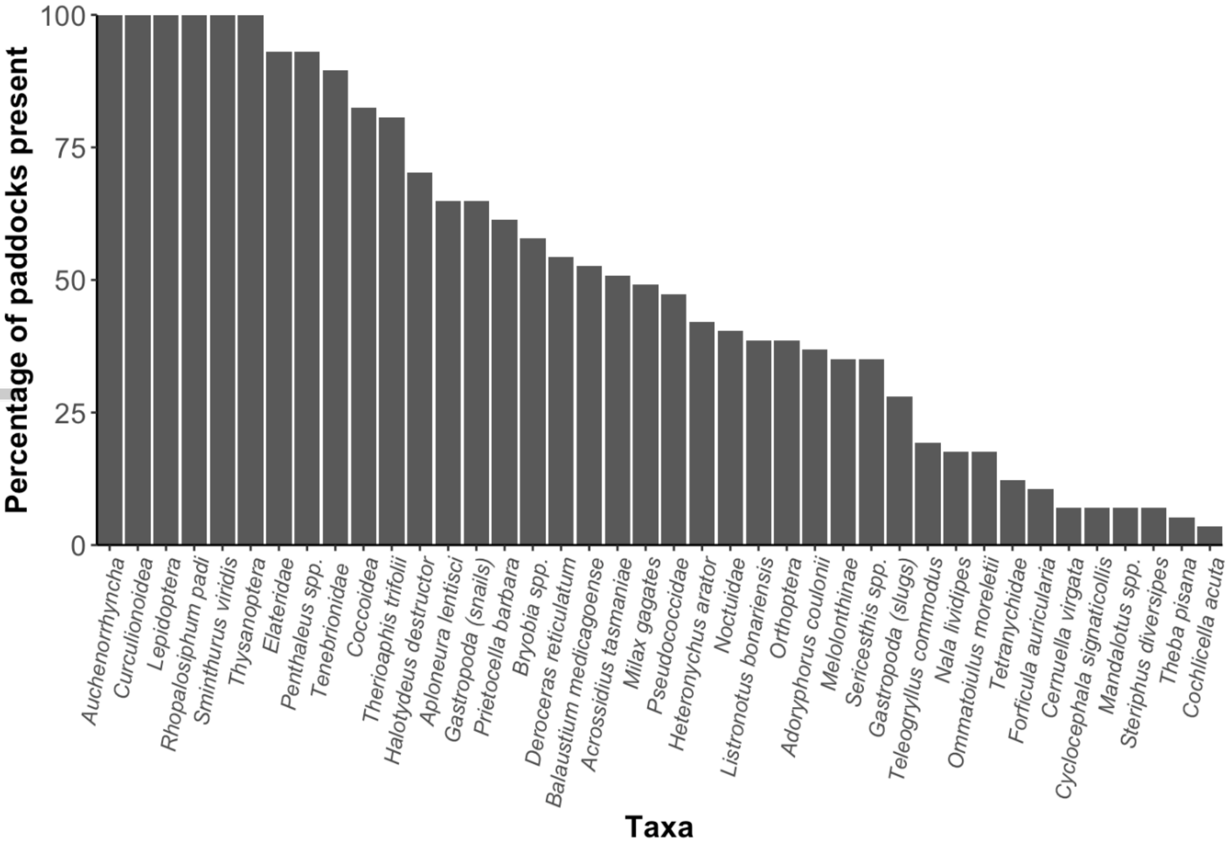

Figure 8. Percentage of paddocks where each pest taxon was found to be present in south-eastern Australian dairy pastures during our survey.

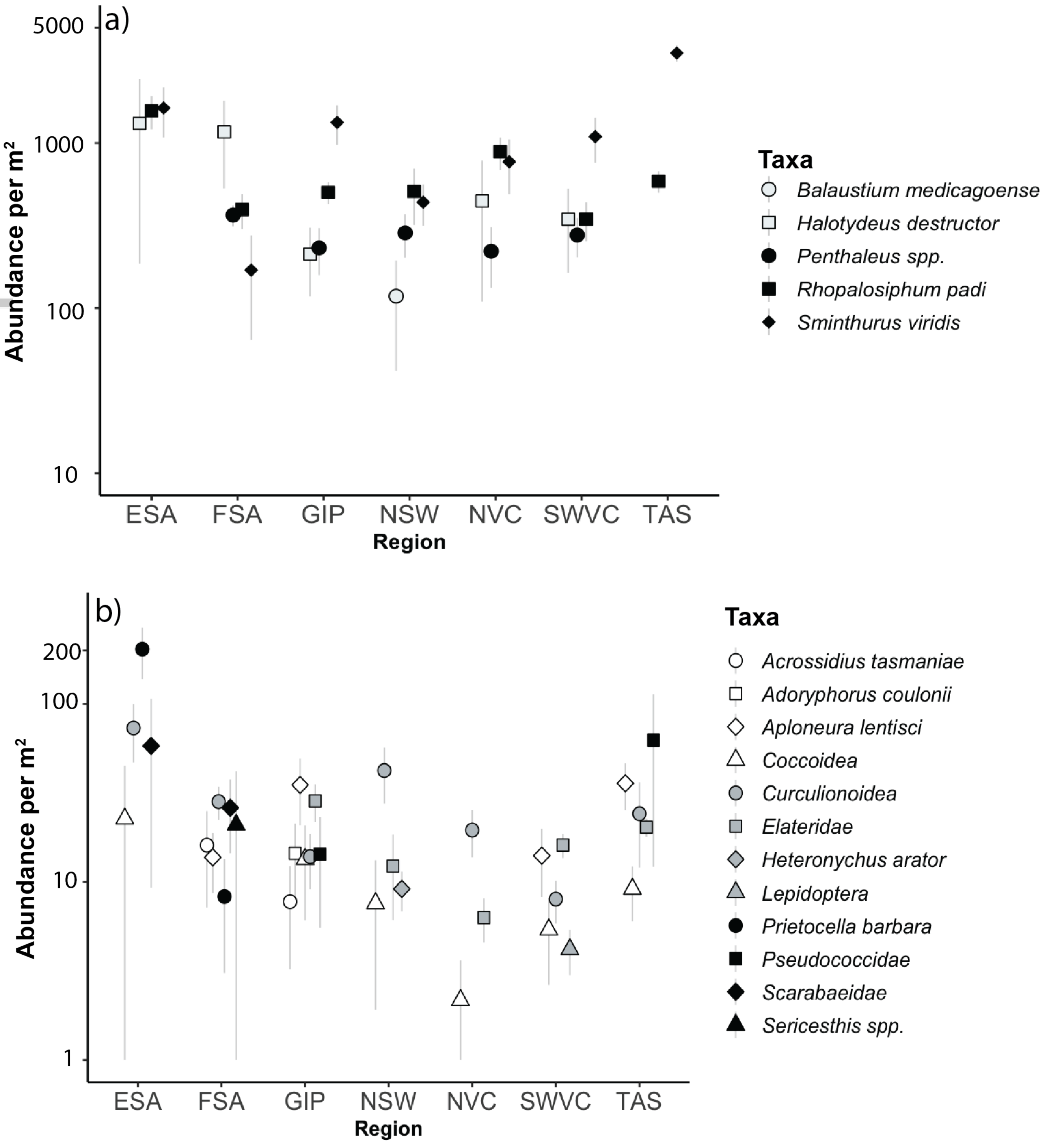

Figure 9. Average abundance (± standard error) above-ground (a) and below-ground (b) of dominant pest taxa in each region (i.e. those that contribute >5% of total pest abundance in each region). ESA = eastern

South Australia, FSA = Fleurieu Peninsula, GIP = Gippsland, NSW = south coast of New South Wales, NVC = northern Victoria, SWVC = south-west Victoria, TAS = Tasmania.

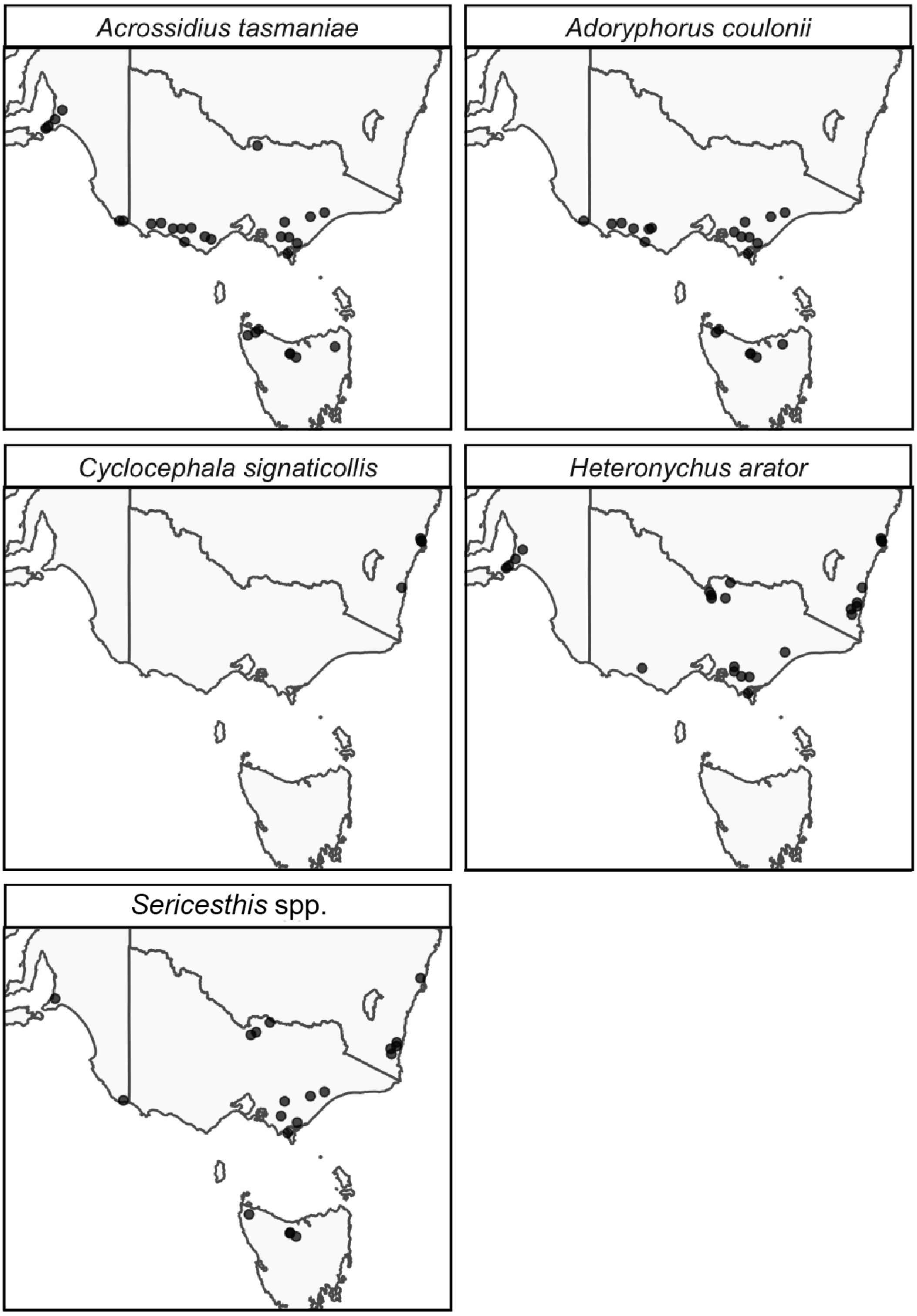
Acrossidius tasmaniae
Adoryphorus coulonii
Cyclocephala signaticollis
Heteronychus arator
Sericesthis spp.

Figure 10. Distribution of pest scarab species found in our survey of south-eastern Australian dairy pastures. Black dots indicate paddocks where each taxon was found.