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Characterization of pyrethroid resistance in the western corn rootworm Diabrotica *virgifera virgifera* LeConte

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Characterization of pyrethroid resistance in the western corn rootworm *Diabrotica virgifera virgifera* LeConte

by

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Characterization of pyrethroid resistance in the western corn rootworm *Diabrotica virgifera virgifera* LeConte

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The western corn rootworm (WCR), *Diabrotica virgifera virgifera* Le Conte (Coleoptera: Chrysomelidae), is a major pest of maize (*Zea mays* L.) in the United States and has continuously challenged our ability to develop sustainable pest management solutions. Resistance to chemical insecticides, crop rotation, and most recently transgenic plants that express toxins derived from *Bacillus thuringiensis* Berliner (*Bt*) have been well documented among WCR populations. Furthermore, US regulatory insecticide prohibitions and the lack of new active ingredients have reduced the options for WCR control. Pyrethroid insecticides are one of the few remaining chemical options. Therefore, the recent confirmation of WCR field-evolved resistance to pyrethroids in the US western Corn Belt is a major concern. The present research aimed to characterize WCR pyrethroid resistance.

The initial objective was to evaluate the field performance of formulated pyrethroids on pyrethroid-resistant WCR populations. An aerial application simulation method was developed to evaluate the performance of foliar adulticides whereas soil insecticides targeting WCR larvae were tested in field plots with representative WCR populations. Laboratory bioassays estimated the susceptibility of tested WCR populations against the active ingredients of formulated insecticides. Results indicated that relatively low levels of WCR pyrethroid resistance are enough to significantly impact the performance of pyrethroid products commonly used for either adult or larval control.

A second objective was to artificially select a pyrethroid-resistant WCR population to be used along with field populations for pyrethroid resistance characterization. A population was selected in the laboratory with a diagnostic bifenthrin concentration for several generations reaching levels of pyrethroid resistance observed in field-collected WCR populations. A pilot heritability investigation suggested that a major portion of WCR bifenthrin resistance phenotypic variance may be due to genetic variation, and that a substantial increase in resistance could be expected after <10 generations of insecticide exposure.

Finally, the third objective was to identify WCR pyrethroid resistance mechanisms. Biochemical assays and High-Throughput RNA Sequencing results revealed that insecticide-related metabolism in pyrethroid-resistant WCR populations was significantly enhanced compared to pyrethroid-susceptible populations. The relevance of results is discussed within the context of WCR pyrethroid resistance monitoring and management.

Dedication

To my parents and grandmother for your unconditional love.

To my husband who lights up my every day.

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CHAPTER 1. INTRODUCTION AND LITERATURE REVIEW

Introduction

The western corn rootworm (WCR), *Diabrotica virgifera virgifera* LeConte, is one of the main insect threats to maize (*Zea mays* L.) production in the United States (US). Depending on the maize hybrid, pest infestation level, degree of abiotic stresses, and control strategies used, root damage by larval feeding may cause significant yield losses (Metcalf, 1986; Spike and Tollefson 1991; Davis 1994; Urías-López et al. 2000; Urías-López and Meinke 2001; Sappington et al. 2006; Tinsley et al. 2013, 2015). This insect pest also became a major concern for European countries after it was first found in 1992 close to Surcin International Airport in Belgrade (Berger 2001, Miller et al. 2005). Since this first report, WCR has spread to more than 15 countries in Europe and has placed many others at risk of biological invasion (Aragón et al. 2010, Wesseler and Fall 2010, Lemic et al. 2015, Mrganić et al. 2018).

For decades, WCR management history in the US has been a repetitive sequence of ephemeral success, rapid resistance evolution, and control failure. Soil broadcast application of organochlorine insecticides commonly used in the 1950s became rapidly ineffective with high levels of WCR resistance documented by 1962 (Ball and Weekman 1962, 1963). Carbamate and organophosphate aerial applications used for adult WCR control selected for significant levels of resistance by the 1990s (Meinke et al. 1998; Scharf et al. 1999; Wright et al. 2000). Finally, field-evolved resistance of WCR to transgenic maize, that expresses rootworm-specific Cry toxins, was reported for Cry3Bb1 in 2009, mCry3a in 2011, and Cry34/35Ab1 in 2016

(Gassmann et al. 2011, 2014, 2016, Gassmann 2012, Wangila et al. 2015, Reinders et al. 2018).

The efficacy of current options available to control WCR is a major concern. Many growers have adopted rotation of maize with a nonhost crop and/or transgenic maize as first-line defense against this insect pest in the US (Wilson et al. 2005). However, insecticides are still used as a complementary tool. Particularly in the western Corn Belt, where consecutive planting of maize for ≥ two years is a norm (continuous maize), aerial applications of pyrethroids are frequently used to manage high population densities of WCR and other maize pests such as western bean cutworm, *Striacosta albicosta* (Smith) (Levine and Oloumi-Sadeghi 1991, Chandler 2003, Pereira et al. 2015, Archibald et al. 2018). However, the repeated use of this practice has placed significant selection pressure on local pest populations, recently resulting in WCR field-evolved resistance to pyrethroids (Pereira et al. 2015, 2017).

The goal of this research project was to characterize the WCR pyrethroid resistance detected in the US western Corn Belt, by not only identifying the resistance mechanisms involved, but also by evaluating the impact of pyrethroid resistance levels found in the lab on the field performance of commercial formulations. Additionally, laboratory selection of a pyrethroid-resistant WCR population was performed providing a pilot estimation of the resistance trait heritability. Results obtained from this research will inform WCR resistance management programs and contribute to the development of protocols to detect and confirm field resistant individuals.

Literature review

Pest management concepts

After the World War II, insecticides were heavily developed and deployed to manage insect pests. Insecticides were relatively cheap, broad-spectrum, relatively easy to use, and provided significant control of many pest species. However, this almost universal reliance on chemical pesticides triggered many adverse effects. Problems such as pesticide resistance, destruction of natural enemies, resurgence of secondary pests, destruction of pollinators, contamination of food webs (bioaccumulation), and environmental contamination led to social pressure against pesticides, new environmental legislation, and development of ecological pest management strategies (Carson and Darling 1962, Perkins 1982).

In the 1970's, the US government started to significantly implement policies and funding to support research in pest management to enhance environmental quality, e.g. implementation of the Environmental Protection Agency (EPA). This facilitated the shift from unilateral reliance on chemical control to a more naturalistic focus that evolved into the concept of Integrated Pest Management (IPM) (Perkins 1982, Flint and Gouveia 2001). In few words, IPM is a paradigm for managing pests within an ecological framework based on cost/benefit analyses that consider the interests of and impacts on society and the environment. The IPM system considers the pest as part of a complex ecosystem and supports sustainable decision making and use of multiple tactics to maintain pest populations at levels below those causing economic injury while minimizing adverse environmental, economic, and safety consequences (Kogan 1998).

The theory surrounding selection pressure that naturally occurs in the environment was also applied to the IPM philosophy. It is accepted that there is a natural evolutionary process where organisms better adapted to their environmental conditions tend to survive and reproduce, which is called natural selection (Gregory 2009). By changing the environment and imposing artificial selection pressures, agriculture is also shaping the evolutionary process of associated living species (Georghiou and Taylor 1977). Pest control measures are recognized as selection pressure factors to which pests can evolve resistance, thus Insect Resistance Management (IRM) strategies were developed in association with IPM to slow that process (Georghiou 1983). Mathematical models and statistics were developed to estimate the initial frequency of resistant pests and their evolution over time under different control tactic regimens. The concept of rotation was applied to avoid the evolution of pest resistance based on the theory that the initial frequency of pests resistant to multiple control strategies is extremely rare, and that by rotating strategies the evolution of resistance will be significantly delayed (Roush and McKenzie 1987, Roush and Daly 1990). Not only rotation of strategies but also rotation of modes of action within a strategy, e.g. insecticides, were incorporated into the IPM paradigm (Sparks and Nauen 2015).

WCR bio-ecology

During an expedition in Kansas in 1867, the North American entomologist John Lawrence LeConte found a new species of Coleoptera: Chrysomelidae, which he classified and named as *Diabrotica virgifera* (LeConte 1868). Later, this species was recognized as a maize pest and was divided into two subspecies: the WCR *Diabrotica virgifera virgifera* LeConte, and the Mexican corn rootworm *Diabrotica virgifera zeae* Krysan and Smith (Gillette 1912, Krysan 1986). For over a century, the WCR was primarily confined to North America with its center of origin believed to be in Central America (Webster 1895, Krysan 1982, Lombaert et al. 2018). However, in 1992 it was found in Serbia, and has been spreading through Europe since then (Berger 2001, Miller et al. 2005, Wesseler and Fall 2010, Lemic et al. 2015, Mrganić et al. 2018).

The total life cycle of WCR occurs only once a year in the field, which means it is a univoltine species (Ball 1957). The eggs overwinter in the soil and hatch in late spring with larval host range limited to specific grasses (Branson and Krysan 1981, Clark and Hibbard 2004, Moeser and Vidal 2004, Oyediran et al. 2004, Wilson and Hibbard 2004). The larval stage is comprised of three instars with an average development time at 20°C of 11 days for the first instar, 14 days for the second, 27 days for the third instar, and 15 days for the pupa stage (George and Hintz 1966). Adult longevity averages 50 days for females and 40 days for males (Ball 1957). Each WCR female oviposits an average of 400 eggs in soil (Ball 1957, Elliott et al. 1990, Fisher et al. 1991, Boetel and Fuller 1997, Toepfer and Kuhlmann 2006). However, the number of viable eggs laid by each female can reach more than one thousand in the lab if diet is supplemented (Hill 1975).

WCR beetles can be very mobile, and are attracted by maize fields containing good sources of food like pollen, maize silks, and maize kernels (Ball 1957, Hill and Mayo 1980, Grant and Seevers 1989, Naranjo 1991, Darnell et al. 2000). WCR males emerge before females, and reach sexual maturity a few days after emergence (Guss

1976, Branson 1987, Kang and Krupke 2009a, 2009b, Marquardt and Krupke 2009). Conversely, adult females are receptive for mating as soon as they emerge (Ball 1957, Hammack 1995). Although males emerge first, there is an overlap in emergence time of most males and females (Quiring and Timmins 1990, Meinke et al. 2009). Most mating occurs in mid-late summer with a variable frequency between eight and 15 times for each male, whereas females rarely mate more than once in their lives (Branson et al. 1977, Kang and Krupke 2009a, 2009b, Spencer et al. 2009). The adult preoviposition period is typically 10-14 days after mating when suitable food is available (Ball 1957, Elliott et al. 1990).

More than 80% of WCR eggs are laid within 20 cm soil depth next to a maize plant base (Ball 1957, Kirk 1979, Gray et al. 1992). After approximately one month, egg embryos enter diapause and, in temperate climates, hatch 4-5 months later in spring (Krysan 1982, Meinke et al. 2009). After egg hatch, neonate larvae move in the soil attracted to CO_2 released by roots of maize plants growing in the field (Strnad et al. 1986, Strnad and Bergman 1987, Bernklau and Bjostad 1998, Bernklau et al. 2004). Several compounds released by germinating maize have been associated with larval feeding acceptance and stimulation, especially a combination of sugars and lipids (Bernklau and Bjostad 2008). Larvae can feed on the root hair and outer cortical tissue of maize plants, as well as bore inside roots moving from root to root and plant to plant as the larvae grow larger (Chiang 1973, Strnad and Bergman 1987, Hibbard et al. 2003, Spencer et al. 2009).

The WCR was first recognized as a maize pest in 1912 after root damage was reported in Colorado, US (Gillette 1912). Silk clipping by adult WCR may in some cases interfere with pollination (Meinke 2014), but the most significant damage is caused by WCR larval feeding on maize roots (Levine and Oloumi-Sadeghi 1991). Larval injury has been associated with root pruning, plant lodging, disturbance of plant nutrient content and water relationships, plus reduction of leaf area, plant height and photosynthetic rate, and finally grain yield loss (Kahler et al. 1985, Riedell 1990, Spike and Tollefson 1991, Godfrey et al. 1993a, 1993b, Roth et al. 1995, Hou et al. 1997, Urías-López et al. 2000, Urías-López and Meinke 2001, Tinsley et al. 2013, 2015). This insect has become a major threat for US maize production costing up to 2 billion dollars a year in yield losses and control costs (Sappington et al. 2006, Tinsley et al. 2013, 2015, Wechsler and Smith 2018).

WCR control strategies

Rotation of maize with a nonhost crop is the main recommendation available for WCR management. WCR oviposition occurs mainly in maize fields and larvae cannot survive on nonhost roots after egg hatch the following season (Rondon and Gray 2004). In 1995, crop rotation failed in nine counties in east central Illinois and 15 counties in northwestern Indiana causing severe root injury in first-year maize (Levine et al. 2002, Gray et al. 2009). After investigation, it was found that annual crop rotation in the US eastern Corn Belt had selected some local WCR populations for behavioral resistance. Studies suggested that WCR females leaving maize fields to oviposit in nonhost crops were provided a selective advantage in an annual maize-soybean (*Glycine max* (L.) Merr.) rotation system, which over time resulted in some economically damaging WCR larval infestation the following year in maize (Sammons et al. 1997, Rondon and Gray

2003, Schroeder et al. 2005, Pierce and Gray 2006, Spencer et al. 2009). WCR behavioral resistance did not widely spread, thus rotation of maize fields with nonhost crops is still a good management tactic in most of the US Corn Belt (Levine et al. 2002, Wilson et al. 2005, Gray et al. 2009, Meinke et al. 2009).

Biological control is still little explored and applied for WCR. Studies have shown a good control opportunity by using entomopathogenic bacterial and fungal products, like *Bacillus thuringiensis* Berliner, *Metarhizium anisopliae* (Metchnikoff) Sorokin, and *Beauveria bassiana* (Bals.-Criv.) Vuill. (Pilz et al. 2009, 2011, Rudeen et al. 2013, Balog et al. 2014, Oliveira-Hofman 2018). The use of predators and parasitoids have been also explored (Toepfer et al. 2008, 2009, Lundgren et al. 2009, Prischmann et al. 2011). The use of entomopathogenic nematodes like *Heterorhabditis* and *Steinernema* species have been the most promising WCR biological control so far (Ellsbury et al. 1996, Pilz et al. 2009, 2014, Hiltpold et al. 2010, 2012, Toepfer et al. 2010, 2014, Kahrer et al. 2014, Geisert et al. 2018). However, many of these techniques, performed either in the laboratory or in small plots, have not been cost effective when compared to insecticides or transgenic maize on a large commercial field scale.

Insecticides are commonly used for WCR control and can be deployed through seed treatments, soil applications, or foliar spraying. Although seed treatments can provide maize root protection and WCR control, they are usually effective only with low-moderate insect pressure (Furlan et al. 2006, Obopile et al. 2013, Petzold-Maxwell et al. 2013). The most commonly used insecticide seed treatments in the US are the neonicotinoids, i.e., thiamethoxam and clothianidin (Van Rozen and Ester 2010). Bifenthrin, tefluthrin (pyrethroids), carbofuran (carbamate), chlorpyrifos, chlorethoxyfos, ethoprophos, phorate, terbufos (organophosphates), fipronil (fiprole), and a mix of tebupirimiphos (organophosphate) with cyfluthrin (pyrethroid) are examples of soil insecticides that have historically been applied in furrow or in narrow bands over the row at planting for WCR control in the US (Mayo and Peters 1978, Van Rozen and Ester 2010). However, because of new pesticide legislation (i.e., 1996 Food Quality Protection Act) the US Environmental Protection Agency (EPA) has been restricting the use of many of the carbamate and organophosphate compounds (Zager et al. 2003).

Whereas seed treatments and soil insecticides target WCR larvae to prevent maize root damage, foliar insecticides target the adults to prevent silk clipping and further oviposition (Tollefson 1991, Meinke 1995, 2014). At one time, many organophosphate and carbamate foliar insecticides were registered in the US for WCR adult control (Van Rozen and Ester 2010). However, after EPA enforcement of new pesticide legislation, key compounds were no longer allowed and options for foliar spraying were significantly reduced. Most foliar insecticides currently used for WCR adult control are pyrethroids and organophosphates applied either aerially or through irrigation systems (chemigation). The extensive use of this strategy is not recommended as it can place high selection pressure on local insect populations (Meinke 1995). In the last decades, the repeated use of foliar formulations has selected for WCR field-evolved resistance to carbamates, organophosphates and pyrethroids (Chio et al. 1978, Miota et al. 1998, Scharf et al. 1999, 2000, Zhu et al. 2001, Elzen and Hardee 2003, Parimi et al. 2003, Stebbing 2003, Siegfried et al. 2004, Gray et al. 2009, Pereira et al. 2015).

A more recent WCR management strategy has been the development and use of transgenic plants expressing Cry insecticidal proteins of soil bacterium *Bacillus* *thuringiensis* Berliner (*Bt*) for larval control (Schnepf et al. 1985, Vaeck et al. 1987, Narva et al. 2013). So far, there are four genetically modified *Bt* traits commercialized for WCR control in the US: Cry3Bb1; Cry34Ab1/Cry35Ab1 double protein; mCry3A; and eCry3.1Ab pyramided with mCry3A (Wangila et al. 2015). Consecutive planting of *Bt* maize is commonly observed in parts of the US, which has resulted in multiple cases of WCR field-evolved resistance to this technology (Gassmann et al. 2011, 2014, 2016, Wangila et al. 2015, Reinders et al. 2018).

Transgenic maize plants have also been engineered to express WCR double-stranded RNAs (dsRNAs) aiming to control the pest by RNA interference (RNAi) mechanisms (Baum et al. 2007, Rangasamy and Siegfried 2012, Chu et al. 2014, Fishilevich et al. 2016, Vélez and Fishilevich 2018). The first commercial use of this technology was approved by the EPA in mid-2017 and is expected to be a valuable tool for WCR control (US-EPA 2017). However, for every new insect control technology there is a risk of insect resistance evolution. If resistance management practices are not proactively adopted for RNAi-based technologies, WCR populations might also be selected for dsRNA resistance in the future (Khajuria et al. 2018).

Overall, WCR control has always been accompanied by cases of technology overuse and resistance evolution. However, rotation of crops and control strategies are recommended to delay WCR resistance evolution (Wright et al. 1996, Tabashnik 2008, Huang et al. 2011, Gassmann 2012, Andow et al. 2015). The adoption of IPM and IRM programs is key to prolong the efficacy of available WCR control technologies (Wright et al. 1996, Devos et al. 2012, Reinders et al. 2018).

WCR insecticide resistance history

The revolution of insecticide use occurred just after World War II with the development of DDT (dichloro-diphenyl-trichloroethane), cyclodienes and benzene hexachloride. The low cost, persistence, versatility and high efficacy made organochlorines popular for insect control in the 1950's. In 1959, DDT usage alone reached a peak of 80 million pounds a year (US-EPA 1975). Broadcast (total area) application of organochlorine insecticides was commonly used for WCR control (Hill et al. 1948, Lilly 1956). However, cases of WCR resistance started to be reported for this insecticide class within a few years of use (Ball and Weekman 1963, Bigger 1963). At the same time, public concern regarding non-target toxicity and environmental contamination led the EPA to ban the use of organochlorine in the US during the late 1970's. Although organochlorines were banned in the US almost 50 years ago, recent monitoring studies confirm that some WCR populations still have high levels of resistance to these compounds (Parimi et al. 2006)

Carbamate and organophosphate insecticide technologies were also inherited from World War II research and became the major insecticide classes for WCR control after the organochlorine banishment (Ball 1969, Ball and Su 1979). Areas adopting infurrow soil applications of these insecticides in combination with crop rotation for WCR larval control were able to circumvent insecticide resistance for a number of years (Parimi et al. 2003). However, areas in the US western Corn Belt relying on consecutive planting of maize and multiple insecticide aerial applications observed a different outcome. In Nebraska, for example, broadcast aerial application of organophosphates and carbamates were repetitively used for more than 30 years to suppress WCR adult populations (Meinke 1995). As a result of this intense adult selection pressure, multiple reports of WCR resistance to methyl-parathion and carbaryl began to occur (Meinke et al. 1998, Scharf et al. 1999, Wright et al. 2000, Zhu et al. 2001, Siegfried et al. 2004).

Pyrethroids were the most effective insecticides available to replace some organophosphates and carbamates in the late 1990's (Elliott et al. 1978, Bradbury and Coats 1989). This insecticide class became popular for WCR control in both soil and foliar formulations (Van Rozen and Ester 2010). Particularly in the US western Corn Belt, where crop rotation has been historically less frequent than eastern counterparts, broadcast aerial applications of pyrethroids have been the method to manage high population densities of maize pests (Chandler 2003, Archibald et al. 2018). Repeated use over time has led to field-evolved resistance of WCR to pyrethroids in populations from southwestern areas of both Nebraska and Kansas (Pereira et al. 2015, 2017). Most insecticides currently used in maize production belong to the pyrethroid class and resistance to these compounds significantly restricts WCR management options in the US western Corn Belt.

Pyrethroids

The Dalmatian pyrethrum flower *Tanacetum cinerariifolium* (Trevir.) Sch. Bip. grown mainly in Kenya, Tanzania, Rwanda, and Ecuador, is the natural source of insecticidal compounds called pyrethrins (Casida 1980, Casida et al. 1983, Katsuda 1999). The insecticidal properties of these plants were first recognized around 1800 by Caucasian tribes in Persia who originally used powders or dusts from the dried flowers (Casida 1980). However, through successive chemical modifications of pyrethrins, it was possible to synthesize some analogues called pyrethroids, that are more potent and photostable for agricultural use (Elliott et al. 1973, 1978, Elliott 1980, Katsuda 1999). Pyrethroids retain many favorable pyrethrin properties like relative low mammalian toxicity and lipophilicity that facilitates both insect cuticle penetration and retention on plant surfaces (Casida 1980).

Pyrethroids are neurotoxins generally classified in two groups based on the symptoms produced by acutely toxic doses in poisoned animals, and also by the presence or absence of an α-cyano group in the molecule. Type I compounds are characterized cause restlessness, incoordination, and prostration, whereas Type II, which contains an α-cyano group in the molecule, cause incoordination, convulsions, and intense hyperactivity (Gammon et al. 1981, Lawrence and Casida 1982). Some pyrethroids exhibit properties intermediate between the two groups (Gammon et al. 1981, Lawrence and Casida 1983, Scott and Matsumura 1983, Soderlund et al. 2002).

The toxicity of pyrethroids depends mainly on the level of exposure and their ability to bind and disrupt voltage-gated sodium channels of animal nerves, although information has been published on secondary targets like voltage-gated calcium and chloride channels (Ray et al. 1996, Hildebrand et al. 2004, Symington and Clark 2005, Breckenridge et al. 2009, Soderlund 2011). Pyrethroids bind to sodium channels causing a delay in channel closing, and prolonged sodium inactivation (Yu 2014). Thus, repetitive discharges are generated across the nerve finally disrupting the normal flow of nerve impulses.

Insect resistance to pyrethroids

Metabolic resistance

Several processes can contribute to pyrethroid inefficiency, but the most important factor might be the ability of insects to detoxify them. It is well known that insects possess an elaborate system of enzymes involved in the metabolism and detoxification of toxic compounds (Yu 2014). Perhaps the most important detoxification systems are the cytochrome P450 microsomal monooxygenases. In fact, many cases of pyrethroid resistance are related to overexpression of P450 *Cyp* genes and consequent higher levels of detoxification (Lee and Scott 1989, Pittendrigh 1997, Kasai and Scott 2000, Nikou et al. 2003, Zhu and Snodgrass 2003, Yang et al. 2006, Djouaka et al. 2008, Bariami et al. 2012, Stevenson et al. 2012, Chigure et al. 2018). Other important enzymes for pyrethroid detoxification in insects are the glutathione S-transferases and esterases that facilitate insecticide excretion by transforming the insecticide parental compound into more water soluble metabolites (Yu 2014). High activities of these enzymes have been commonly found in pyrethroid resistant insects (Dowd et al. 1987, Sogorb and Vilanova 2002, Enayati et al. 2003, Fragoso et al. 2003, 2007, Young et al. 2005, 2006, Lumjuan et al. 2011, Kamita et al. 2016).

Insecticides sharing similar molecule components can be detoxified by similar metabolic processes. For example, pyrethroid, carbamate, and organophosphate molecules contain ester bonds and can be metabolized by same hydrolytic enzyme groups, such as carboxylesterases and other esterases (Sogorb and Vilanova 2002, Montella et al. 2012). Furthermore, some enzymes such as P450s provide broad detoxification specificity and can metabolize a variety of insecticides (Scott 1999).

Therefore, it is common to find pyrethroid-resistant insects showing metabolic cross-resistance to other compounds (Devonshire and Moores 1982, Harris et al. 1982, Miller 1988, Bisset et al. 1997, Scharf et al. 1999, Rodríguez et al. 2002, Sogorb and Vilanova 2002, Carvalho et al. 2013, Mutunga et al. 2015, Xi et al. 2015).

Treating insects with enzyme inhibitors prior to insecticide exposure is a common method to verify if pyrethroid resistance is due to metabolic enhancement. Under the presence of enzyme inhibitors (insecticide synergists), resistant insects with enhanced metabolism may respond as susceptible (Brindley and Selim 1984). Piperonyl butoxide (PBO) is a chemical compound commonly used to suppress cytochrome P450 monooxygenases, and tribufos (DEF) inhibits hydrolytic enzymes like esterases (Enayati et al. 2003, Yang et al. 2004, Young et al. 2005, 2006). Strong synergism of pyrethroids by these enzyme inhibitors suggested that enhanced metabolism could be involved in the mechanism of WCR pyrethroid resistance (Pereira et al. 2017). WCR populations developed resistance to carbamates and organophosphates in the past by metabolic mechanisms (Miota et al. 1998, Scharf et al. 1999, Wright et al. 2000, Parimi et al. 2003, Coates et al. 2016).

Microplate kinetic bioassays are also used for *in vitro* quantification of insect enzyme activity and can be a useful method to identify insecticide-resistant and -susceptible individuals (Cleland 1967, Stitt and Gibon 2014). In these bioassays, chemical substrates with targeted specificity are mixed with insect tissue homogenates and the correspondent enzyme activity is measured by spectrophotometry or fluorimetry (Rose et al. 1995, Zhao et al. 1996, Scharf et al. 2000, Wright et al. 2000, Yang et al. 2004). Application of antibody techniques (e.g. ELISA) and more complex enzyme kinetic analyses providing functional information about proteins (e.g. k_{cat}, K_m and V_{max} values) can be further used to determine if differences in enzyme activity are due to properties of the enzyme itself or due to differing amounts of enzyme produced by insect populations (Schilder et al. 2011, Stitt and Gibon 2014).

Gene duplications and point mutations are the main sources of variation subject to selection in insect populations (Ranson et al. 2002). Multiple gene copies, up-regulation of gene expression and mutations in coding regions result in overexpression of detoxification enzymes and/or more efficient detoxification processes (Hemingway et al. 1998). New enzymatic functions achieved by just one or few amino acid substitutions in protein structure were reported to confer insecticide resistance (Newcomb et al. 1997, Oakeshott et al. 1999, 2005, Amichot et al. 2004). Duplication and altered expression of genes belonging to the three main families of detoxification enzymes (esterases, glutathione S-transferases and cytochrome P450 monooxygenases) have been also implicated in insect resistance to insecticides (Bass and Field 2011, Jugulam and Gill 2018).

Biochemical and toxicological results are often complemented and confirmed with molecular investigations. Molecular biological techniques such as polymerase chain reaction (PCR), DNA Sanger sequencing and more recently high-throughput RNA-sequencing can provide useful information regarding differential expression of metabolism-related genes as well as identity of genetic mutations in resistant insects (ffrench-Constant et al. 2004, ffrench-Constant 2013, Stitt and Gibon 2014, Coates et al. 2016). However, not all cases of insecticide resistance are related to enhanced metabolism. Resistance can occur also by modifications in the insecticide target site preventing effective binding of the insecticide. For example, as discussed below, mutations in the insect voltage-gated sodium channels are known to reduce sensitivity of the nervous system to pyrethroid insecticides, leading to what is called knockdown resistance (*kdr*) (Soderlund and Knipple 2003).

Kdr **resistance**

Kdr insect resistance is not a metabolic resistance which means it is not affected by the use of enzyme inhibitors like PBO and DEF. Instead, it is caused by a reduction in the sensitivity of the insect nervous system through mutations in the voltage-gated sodium channels. Insect voltage-gated sodium channels are only found in neurons, and consist of large pseudotetramer protein α-subunits (~260kDa) that contain four internally homologous domains (I-IV) (Yu 2014). Each domain has six hydrophobic helical transmembrane segments (S1-S6) that contribute to the formation of the ion pore (Soderlund and Knipple 2003). Each S4 segment contains repeated motifs of amino acids that serve as a voltage sensor of the sodium channel; it moves outward in response to membrane depolarization leading to pore opening and consequent activation of sodium channels (Dong et al. 2014). Fast-inactivation by pore occlusion is accomplished by the movement of an inactivation gate made of three hydrophobic amino acids – methionine, phenylalanine and methionine (MFM) - connecting domains III and IV of insect sodium channels (McPhee et al. 1995, Dong et al. 2014).

In 1989, it was discovered that a single gene is responsible for encoding sodium channels in the fruit-fly *Drosophila melanogaster* Meigen, called *para* gene and later *DmNa*$_V$ gene (Loughney et al. 1989, Hong and Ganetzky 1994, Dong et al. 2014).

Analysis of *para* locus cDNAs revealed a minimum of 24 exons within 60 kb of genomic DNA (Loughney et al. 1989). The sequencing of the fruit fly *para* gene also led to the isolation of orthologous genes in other insect species (Doyle and Knipple 1991, Knipple et al. 1991). Gene sequencing allowed tests of the hypothesis that pyrethroid resistance is linked to sodium channel gene mutations. In fact, more than 50 sodium channel mutation combinations have been associated with knockdown resistance to pyrethroids in various arthropod pests (Dong et al. 2014). These mutations are identified usually by comparisons of nucleotide sequences between resistant and susceptible insects. A single amino acid substitution can be associated with pyrethroid resistance (Dong 1997, Vais et al. 2000).

New resistance-associated gene mutations are rare and the frequency in which they arise is dictated by a combination of deleterious effects of encoded protein and the mutation rate (Drake et al. 1998, Fu and Huai 2003, ffrench-Constant 2013). Mutations are usually derived from premutagenic damage of DNA, misreplication, and recombination (Maki 2002, Ohnishi et al. 2009). Changes in DNA are the ultimate source of all genetic variation in the form of deletions, insertions, duplications, and translocations of DNA sequences (Lewin 2004, Hamilton 2009). The same mutation could have multiple origins within and between insect species given the large effective population sizes of insects (Thompson et al. 1993, Andreev et al. 1999, Pinto et al. 2007, ffrench-Constant 2013). Also, the frequency of a given mutation may vary between populations (Song et al. 2007, Zhu et al. 2010, Alvarez et al. 2015).

Many studies employing site-directed mutagenesis and expression in big unfertilized oocytes of the frog *Xenopus laevis* Daudin have led to the identification of many sodium channel point mutations or combinations of mutations that modify the sensitivity of insect sodium channels to pyrethroids (Dong et al. 2014). Nucleotide substitutions that occur within coding genes may or may not alter the protein function (Hamilton 2009). However, *kdr* resistance is frequently caused by nonsynonymous or missense mutations in the voltage-gated sodium channel gene that does change the resulting amino acid sequence reducing pyrethroid binding at the target site (Alvarez et al. 2015).

The majority of insect *kdr* point mutations are associated with sodium channel intracellular linkers between transmembrane segments S4 and S5, or S5 and S6 (Soderlund 2011). The most common amino acid substitutions occur at sites V410 in IS6, M918 in the linker connecting S4 and S5 in domain II, T929 in IIS5, F1534C in IIIS6, and L1014, I1011, V1016 in IIS6 (Dong et al. 2014). In the Colorado potato beetle *Leptinotarsa decemlineata* (Say), a chrysomelid like WCR, mutations in both sites L1014 and T929 were identified as the major mechanism of pyrethroid resistance (Rinkevich et al. 2012). However, different substitutions could confer different levels of resistance. For example, L1014F, L1014H and L1014S mutations provide variable levels of protection to Type I or Type II pyrethroids, whereas F1534C confers sodium channel resistance to Type I, but not Type II pyrethroids (Burton et al. 2011, Hu et al. 2011). Also, when the rate of sodium channel inactivation is beyond that of *kdr*, it is common to call it a *super-kdr* mutation (Zimmer et al. 2014).

Another important factor to consider about pyrethroid *kdr* resistance is that it can originate from or lead to resistance to other insecticides, which is called *kdr* cross-resistance. Organochlorines like DDT and oxadiazines like indoxacarb also target the insect voltage-gated sodium channels (Yu 2014). In fact, there are many cases of *kdr* cross resistance among insect pests (Williamson et al. 1993, Chandre et al. 1998, Schuler et al. 1998, Brengues et al. 2003, Enayati et al. 2003, Rodríguez et al. 2005). Furthermore, some studies suggest that there might be different levels of *kdr* cross-resistance in insects. For example, it seems that the mutation M918T provides extremely high levels of resistance against permethrin and deltamethrin but does not provide resistance to DDT (Vais et al. 2000, Usherwood et al. 2005). Also, DDT-induced *kdr* resistance appears to have cross-resistance only to Type I pyrethroids (Scott and Matsumura 1983). Cross-resistance between pyrethroids and DDT suggested that *kdr* mutations could be involved in the mechanism of WCR pyrethroid resistance (Pereira et al. 2017).

Insects can produce functional diversity of sodium channels from a single gene by two post-transcriptional mechanisms that could also affect pyrethroid sensitivity: alternative splicing and RNA editing. Alternative splicing of mRNA precursors is a crucial mechanism for gene regulation and contributes to genomic diversity and tissue specificity of many organisms (Chen and Manley 2009). Through this mechanism, a single gene can be translated into multiple distinct proteins with diverse functions in the organism. After production of the primary transcript, the introns are usually trimmed out while exons are linked together to form a final version of the transcript, known as mature messenger RNA (mRNA) (Smith and Valcárcel 2000, Park et al. 2004). However, the cell splicing regulatory proteins can produce a different mature RNA sequence by trimming out an exon, leaving in an intron, or combinations of both in the final mRNA transcript (Graveley 2001, Modrek and Lee 2002). RNA editing results in conversion, insertion, and deletion of one nucleotide to another leading to amino acid substitutions, splice site variations or alteration in the level of transcripts (Nishikura 2010).

The *para* gene transcript appears to go through alternative splicing to produce several distinct subtypes of insect sodium channels by removing or including some exons (Loughney et al. 1989, Thackeray and Ganetzky 1995, Park et al. 1999, Tan et al. 2002, Sonoda et al. 2006, Chang et al. 2009). Also, extensive RNA editing is found in the insect sodium channel transcript, which is an important mechanism that generates tissue-/cell type-specific variants (Song et al. 2004, Olson et al. 2008). Five sites of alternative splicing in the sodium channel *para* locus could generate at least 48 different splice variants by differential exon usage in *Drosophila* (Thackeray and Ganetzky 1994). Also, the range of splice types differed between insect stages, which suggests that this mechanism could be developmentally regulated (Thackeray and Ganetzky 1994, Lee et al. 2002). Splicing may also influence sodium channel kinetics not only through changes in the protein structure, but also by allowing other modifications like phosphorylation, binding of cofactors, etc. (Lin et al. 2009). Although there is a strong conservation of alternative exon location and structure between species, some marked interspecific differences appear to occur as well (Lee et al. 2002).

Justification and research objectives

It has become increasingly apparent that single tactic approaches to managing insect populations are unlikely to be sustainable and that integration of crop rotation, biotechnological approaches such as the use of *Bt* maize and traditional insecticides are necessary to increase durability of WCR management strategies. However, the increased usage of pyrethroid insecticides and the potential for resistance evolution threaten the future use of this important insecticide class and the potential to integrate these compounds with other approaches for WCR management. The confirmation of WCR pyrethroid resistance in the US western Corn Belt may significantly impact pest management strategies in affected areas. Lab bioassays with pyrethroid active ingredients estimated that pyrethroid resistance levels in question were relatively low and that multiple mechanisms of resistance could be involved. However, the impact of the low resistance levels on practical control with formulated products was unclear and the molecular basis for the resistance trait was unknown. Characterizing the resistance mechanisms involved would provide critical information to refine predictive models for estimating WCR resistance evolution and to recommend effective resistance management strategies. Therefore, the research described in this doctoral dissertation aimed to characterize WCR pyrethroid resistance. The three specific objectives and correspondent hypotheses are as follows:

1) Characterize pyrethroid efficacy in the field as a western corn rootworm control agent. *Hypothesis:* Resistance levels reported for WCR populations in laboratory bioassays are affecting the field efficacy of formulated pyrethroids in both adult and larval stages (Chapter 2 and Chapter 3);
2) Select a pyrethroid-resistant WCR population for use in objectives 1 and 3 plus use it to obtain a preliminary estimate of the heritability of the resistance trait. *Hypothesis:* WCR pyrethroid-resistance is a genetic characteristic substantially inheritable (Chapter 4); and

3) Identify resistance mechanisms. *Hypothesis:* Multiple mechanisms are involved in WCR pyrethroid resistance (Chapter 4 and Chapter 5).

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CHAPTER 2. WESTERN CORN ROOTWORM PYRETHROID RESISTANCE CONFIRMED BY AERIAL APPLICATION SIMULATIONS OF COMMERCIAL INSECTICIDES

Introduction

The western corn rootworm (WCR) *Diabrotica virgifera virgifera* LeConte (Coleoptera: Chrysomelidae) is a major pest of corn *Zea mays* L. in the United States (US) and has adapted over time to many management tactics (Gray et al. 2009, Miller et al. 2009). Broadcast application of organochlorine soil insecticides starting in the late 1940's became rapidly ineffective with control issues apparent by late 1950's (Ball and Weekman 1962). Aerial applications of carbamates and organophosphates selected adult WCR for significant levels of resistance in the 1990's (Meinke et al. 1998, Scharf et al. 1999, Wright et al. 2000). Resistance to transgenic corn producing rootworm-specific Cry toxins from the soil bacterium *Bacillus thuringiensis* (*Bt*) was initially reported for Cry3Bb1 in 2009, mCry3a in 2011, and Cry34/35Ab1 in 2016 (Gassmann et al. 2011, 2014, 2016, Wangila et al. 2015). Furthermore, the cultural practice of corn rotation with a nonhost crop was circumvented in areas of the US eastern Corn Belt by WCR oviposition in nonhost crops indicating the evolution of behavioral resistance (Levine et al. 2002, Gray et al. 2009, Meinke et al. 2009). These events collectively have made WCR management exceedingly difficult.

Although crop rotation is the most recommended tactic to manage the WCR, continuous corn (consecutive planting of corn for ≥ two years) is a common agronomic practice in the US western Corn Belt because under irrigation, continuous corn production is often the most profitable, and corn demand is high for confined livestock and ethanol production (Meinke et al. 2009, Wangila et al. 2015). However, this intensive system of continuous corn production facilitates build-up of WCR densities over time making WCR management an annual challenge (Meinke et al. 2009, Pereira et al. 2015, 2017). Consequently, aerial applications of pyrethroid and organophosphate insecticides are often used to reduce WCR densities and complement other management tactics (Levine and Oloumi-Sadeghi 1991, Pereira et al. 2015, 2017). In this system, other corn pests like western bean cutworm *Striacosta albicosta* (Smith) and two-spotted spider-mite *Tetranychus urticae* Koch are also managed with the same insecticide classes used to manage rootworms, so WCR adults can be exposed to aerial applications as nontarget insects as well (Bynum et al. 1990, Michel et al. 2010, Archibald et al. 2018). These practices have placed annual selection pressure on WCR populations which has led to field-evolved resistance to pyrethroids in southwestern areas of Nebraska and Kansas (Pereira et al. 2015).

Laboratory bioassays conducted with WCR populations collected across the US Corn Belt have shown that populations from west of the Missouri River were consistently more tolerant to the active ingredient bifenthrin than eastern populations (Pereira et al. 2015). Furthermore, cross-resistance and synergism studies performed with field collected bifenthrin-resistant populations suggested that multiple mechanisms of resistance could be involved such as target-site insensitivity and higher activity of detoxification enzymes (Pereira et al. 2017). Although the levels of bifenthrin resistance found were relatively low, resistance levels were highest in the adult stage (Pereira et al. 2015, 2017). Despite having laboratory bioassay data documenting resistance, the efficacy of formulated bifenthrin commonly used in aerial applications to control WCR adults had not been formally evaluated.

Field efficacy of foliar insecticides depends on a combination of several factors such as target susceptibility, exposure, and application technique efficiency. For example, aerial application of insecticides can provide uneven coverage in the corn canopy resulting in insect sublethal exposure and reduced control (Bynum et al. 1991). Some parameters such as spray carrier volumes, droplet size distribution, crop canopy, and environmental conditions often influence the coverage and uniformity of insecticide deposition which can confound field trial results (Fritz 2006, Fritz et al. 2009, Martin et al. 2010, Garcerá et al. 2014, Creech et al. 2015). Carrying out consistent field trials to evaluate the efficacy of insecticide aerial applications on adult rootworms is even more challenging considering the potential interaction of population density and pest movement that may occur in the field (Grant and Seevers 1989, Naranjo 1991, Isard et al. 2000, Meinke et al. 2009). Thus, methods that minimize factors influencing aerial application performance are necessary to evaluate the impact of WCR pyrethroid resistance on the efficacy of recommended foliar insecticides.

Pyrethroid and organophosphate classes contain many of the insecticides recommended for WCR control. However, enhanced metabolism can confer cross-resistance to structurally related insecticides, which has been observed between pyrethroids and organophosphates for different insect species (Devonshire and Moores 1982, Elzen et al. 1992, Cahill et al. 1995, Bisset et al. 1997, Sayyed et al. 2010, Couso-Ferrer et al. 2011). Thus, the likely involvement of detoxification enzymes in the mechanism of WCR bifenthrin-resistance could impact organophosphate efficacy, which needs further investigation (Pereira et al. 2017). The past use of organophosphates (e.g. dimethoate) may also contribute to selection of WCR adults with increased detoxification enzyme activity. Resistance to both insecticide classes would greatly reduce alternative insecticide options and impact the integration of these compounds with other management tactics. Indoxacarb represents an insecticide class i.e., the oxadiazines, with unique mode of action that was recently registered by the US Environmental Protection Agency (EPA) for use to control WCR adults in field corn (McCann et al. 2001, US-EPA 2018). This product was reported to reduce adult WCR populations in the field and may provide a tool to help manage WCR pyrethroid resistance (DeVries and Wright 2016). However, the susceptibility of pyrethroid-resistant WCR to the indoxacarb active ingredient needs to be evaluated.

Therefore, as part of a larger project to characterize WCR pyrethroid resistance (Pereira et al. 2015, 2017) and to optimize WCR resistance management and integrated pest management (IPM) programs, the objectives of this study were: (1) to develop a method of simulated aerial application that uniformly reproduces insecticide field deposition; (2) use the simulated aerial application method to assess the performance of bifenthrin and dimethoate commercial formulations against pyrethroid-resistant WCR populations; and (3) to conduct dose-response lab bioassays to estimate and compare the susceptibility of pyrethroid-resistant WCR populations to bifenthrin, dimethoate and indoxacarb active ingredients.

Methods

Western corn rootworm populations

Six WCR adult populations were tested during this study. Two non-diapausing populations purchased in 2016 and 2017 from Crop Characteristics, Inc., Farmington, MN (S-Lab1) and French Agricultural Research, Lamberton, MN (S-Lab2), and one field population collected from Saunders County, NE (S-Field) in 2016 were used as pyrethroid-susceptible controls given their high susceptibility to bifenthrin measured in prior bioassays (Pereira et al. 2015). The Saunders Co. field was located at the University of Nebraska Eastern Nebraska Research and Extension Center, which is surrounded by a large area of continuous corn that had not received insecticide aerial applications for over ten years. Bifenthrin had only been used in that area for soil applications in a few small-plot trials. In 2016, two field populations (R-Field1 and R-Field2) previously confirmed to have field-evolved resistance to bifenthrin (Pereira et al. 2015) were collected from commercial fields 18 Km apart in Keith County, NE. Each field was in continuous corn production plus annual soil- and aerial bifenthrin applications had been made for at least five consecutive years prior to this study. A third bifenthrin-resistant population tested in 2017 bioassays (R-Lab) was collected from Perkins County, NE in 2014 and then reared in a non-diapause background for nine generations under adult selection with a pre-established bifenthrin diagnostic concentration (LC_{99}) (Pereira et al. 2015). Populations were maintained in the Department of Entomology, University of Nebraska-Lincoln, Lincoln, NE using standard lab rearing procedures and temperature profiles to facilitate egg diapause development and termination (Wangila et al. 2015).

Aerial application simulation

Cornfield spray deposition

A series of aerial spray applications were performed in a late season cornfield (R5) located just south of Snook, TX (30°28'37.1"N, 96°27'58.7"W) in order to document deposition characteristics that would be expected under typical aerial application conditions. Applications were made using an airplane (AirTractor 402B, Olney, TX) equipped with 40º 10-orifice flat fan nozzles at spray application rates of 18.7 and 46.8 L/ha (Fritz and Hoffmann 2015). The spray solution consisted of water and a 90% non-ionic surfactant (R-11, Wilbur-Ellis Company LLC, Tukwila, WA) at 0.25% v/v. At the 18.7 L/ha application rate, a total of 36 nozzles were used, where nozzles were deflected 15 degrees downward and operated at 317 kPa at an airspeed of 225 Km/h. At the 46.8 L/ha rate, a total of 68 nozzles were used with nozzles deflected at 30 degrees and operated at 413 kPa and at an airspeed of 209 Km/h.

During the applications wind speeds were steady at 4 m/s with a temperature of 30 ºC and relative humidity of 75%. Water sensitive papers (WSP) (Syngenta Crop Protection AG, Basel, Switzerland) were placed in the field canopy at three locations denoted as Top, Middle, and Bottom. The Top position was located near the uppermost fully extended leaf with the Bottom near the lowermost extended leaf and the Middle located midway between Top and Bottom positions. WSPs were attached to plants spaced 2 m apart covering a full 20 m application swath using binder clips such that the surface was horizontal to the ground. Applications were performed in two sampling lines (blocks), each with ten WSP (replicates) for each canopy and application rate treatment combination.

After each spray pass replication, WSPs were collected and stored in labeled film negative sleeves. WSPs were digitally scanned at 600 dpi (EPSON Perfection V600) and analyzed for droplet size characteristics using Dropletscan (WRK of Arkansas, LLC., Lonoke, AR), an image processing software package designed for WSP analysis (Wolf 2003, Cunha et al. 2012). Spray deposition rate (L/ha) and droplet size diameters at which 10, 50, and 90% of the total spray volume is contained in droplets of the specified size or less ($DV_{0.1}$, $DV_{0.5}$, and $DV_{0.9}$, respectively) were measured and reported (Hoffmann and Hewitt 2004).

Wind tunnel and spray-chamber calibration

In 2016, a low-speed wind tunnel at the Pesticide Application Technology Laboratory (PAT-Lab, University of Nebraska–Lincoln, West Central Research and Extension Center, North Platte, NE) was used to identify ground application nozzles and operating pressures that could effectively simulate the spray deposition collected from the cornfield aerial application. This system has been used for droplet sizing of different nozzle designs, tank solutions and pesticide application scenarios (Creech et al. 2015, Vieira et al. 2018, Butts et al. 2019). Droplet size distribution data collected at Middle corn canopy position were targeted since this would include the major feeding and activity zone for WCR adults in the field (Spencer et al. 2009). Tap water solutions of Brigade 2EC (bifenthrin 25.1%, FMC Corporation, Philadelphia, PA) were prepared using the highest label rate recommended for rootworm control (112.1 g ai/ha) at the lowest and highest recommended carrier volume rates (18.7 and 46.8 L/ha respectively). The application of the insecticide solutions was then performed in the wind tunnel with a TT110015 ground spray nozzle (TeeJet Technologies, Spraying Systems Co., Wheaton, IL) at different spray pressures until targeted droplet size parameters were achieved. Droplet size distribution data were evaluated by a Sympatec Helos/Vario KR laser diffraction system (Sympatec Inc., Clausthal, Germany) placed at 0.3 m from the nozzle tip to ensure full spray atomization prior to measurement. The system was equipped with an R7 lens that detects droplets in a range from 9 to 3700 µm. Nozzles were attached to an actuator and traversed vertically at a constant speed (0.2 m/s) to ensure that the entire spray plume crossed the laser diffraction system. Volumetric droplet size distribution parameters $DV_{0.1}$, $DV_{0.5}$, and $DV_{0.9}$ were reported. The wind tunnel insecticide applications and respective droplet size distribution measurements were carried out with three replications under controlled conditions of 20 ± 1 °C and 60-70% relative air humidity. Once the best spray pressure for the TT110015 ground spray nozzle was found, the timed output volume per nozzle was measured three times with a graduated glass cylinder (Fisherbrand™, Thermo Fisher Scientific Inc., Waltham, MA, Cat. No. S63461). A customized multi-nozzle research track spray chamber (DeVries, Hollandale, MN) (Rodrigues et al. 2018) was then calibrated to simulate aerial applications of commercial insecticides recommended for adult WCR control. Two TT110015 nozzles spaced 0.76 m apart and 0.56 m above the target were used and the travel speed calculated according to the formula (Matthews et al. 2014, TeeJet 2014):

$$Output\ per\ nozzle\ (L/min) = \frac{Volume\ application\ rate\ (L/ha) \text{ x } speed\ (km/h) \text{ x } nozzle\ spacing\ (m)}{600\ (correction\ factor\ for\ unit\ conversion)}$$

Efficacy of commercial insecticides

The aerial application simulation previously described was used to evaluate the performance of two commercial insecticides recommended for adult WCR control. Replicated experiments were repeated twice within a two-year period (2016 / 2017) in the research track spray chamber available in the PAT-Lab, North Platte, NE. The pyrethroid Brigade 2EC (bifenthrin 25.1%, FMC Corporation, Philadelphia, PA) was tested at the lowest and highest label rates recommended for rootworm control, 36.8 and 112.1 g a.i./ha respectively. The organophosphate Dimethoate 4EC (dimethoate 43.5%, Drexel Chemical Company, Memphis, TN) was tested at the lowest label rate of 369.9 g a.i./ha, which has been the common recommendation to provide WCR adult control in the US western Corn Belt. Insecticide solutions were prepared in tap water at the lowest and highest carrier volumes recommended for aerial application rates (18.7 and 46.8 L/ha, respectively).

The aerial spray coverage obtained in the cornfield at the Middle position was reproduced on 100 mm-diameter x 15 mm-height Petri dishes (Thermo Fisher Scientific Inc., Waltham, MA, Cat. No. FB0875713) that were pre-labeled and evenly distributed in the spray chamber to receive the insecticide applied to internal surfaces of dish bottoms and lids. Treatments were combinations of insecticide rate, carrier volume rate and WCR population. A total of four Petri dishes were used as replicates for each treatment, which were sprayed separately during four different rounds. Treated dishes were left opened for 30 min to ensure complete drying, then closed and transferred to cardboard boxes where they were kept in darkness at 23 ± 1 °C for a maximum of 16 h until use for WCR bioassays.

The WCR bioassays were conducted at the University of Nebraska-Lincoln, Lincoln, NE. In 2016, field-collected beetles were provisioned with ears of sweet corn for one week prior to testing whereas in 2017, the F_1 generations of 2016 field-collected beetles already under lab rearing procedure were used. In both years, each Petri dish was infested with a group of 20 mixed-age beetles of even sex ratio. Active beetles were collected from rearing cages with a mouth aspirator and each group placed individually in 15 ml centrifuge tubes (VWR®, Radnor, PA - Cat. No. 76176-950). Beetles were anesthetized (1.5 minute inside a -20°C freezer) and transferred to treated dishes. Four untreated dishes were used as controls for each WCR population tested and infested dishes were maintained under laboratory conditions of 23 ± 1 °C and 13 ± 1h photophase. Mortality of beetles at each treatment combination was recorded after 24 h. Insects that did not respond to prodding or were unable to walk consistently when placed ventral side down were considered dead.

Susceptibility of adult WCR populations to insecticide active ingredients

Chemicals

Analytical standards of bifenthrin, dimethoate and indoxacarb were used. Bifenthrin 98% was obtained from Chem Service Inc., West Chester, PA (Cat. No. N-11203-100MG/CAS: 82657-04-3). Dimethoate 99.5% and indoxacarb ≥95.0% were purchased from Sigma-Aldrich Corp., St. Louis, MO (Cat. No. 45449-100MG/CAS: 60-51-5 and 33969-25MG-R/CAS: 144171-61-9, respectively). The insecticides were dissolved and diluted in acetone ≥99.9% supplied by Sigma-Aldrich Corp (Cat. No. 650501/CAS: 67-64-1).

Bioassays

The susceptibility of adult WCR to insecticide active ingredients was estimated in 2017 when the F_1 generation of beetles that were field-collected in 2016 started to emerge. The vial bioassay method previously adapted for WCR (Scharf et al. 1999, Pereira et al. 2015) was used. The evaluation time and procedure were modified for this study as described below. Wheaton™ Glass 20 ml scintillation vials (Thermo Fisher Scientific Inc., Waltham, MA, Cat. No. 03-340-25N) were treated with 500 µl each of increasing concentrations of bifenthrin, dimethoate and indoxacarb diluted in acetone. For control, vials were treated with acetone only. The number of insecticide concentrations used to test each population varied from 5 to 7 depending on the number of insects available at the time. Insecticide concentrations were replicated three times for each WCR population tested. Vials were homogeneously coated internally and allowed to dry under a fume hood by rolling for 30 minutes at room temperature on a commercial roller machine (Nemco 8045SXW Hot Dog Roller Grill, Nemco Food Equipment Inc., Hicksville, OH). Each treated vial was infested with a group of ten 48h-old adults of even sex ratio. Vial caps were loosely closed to allow air exchange inside the vials while preventing beetle escape. After 24h, one kernel of sweet corn was added to each vial to allow beetle feeding and at 48h after infestation the mortality of beetles was recorded. Insects that did not respond to prodding or were unable to walk consistently when placed ventral side down were considered dead. All treatments were maintained at 23 ± 1 °C and 13 ± 1h photophase.

Statistical analysis

Corn canopy spray deposition rate and droplet size parameters reported from WSPs were subjected to analysis of variance in SAS 9.4 software (SAS Institute, Cary, NC) at significance level α=0.05. The treatment design was a factorial arrangement with spray application rates (18.7 and 46.8 L/ha) and corn canopy position (Bottom, Middle, and Top) as factors in a randomized complete block experimental design (RCBD) where application lines were considered blocks.

To analyze the performance of commercial insecticides on adult rootworm populations under simulated aerial application conditions, insect mortality data collected from each treatment combination was corrected by Abbott's formula for mean mortality in the respective untreated controls (Abbott 1925). The corrected proportion mortality that has a continuous distribution within the restricted interval of [0,1] was analyzed with a Beta-binomial distribution using a logit link function with a generalized mixed model in SAS 9.4 software (Ferrari and Cribari-Neto 2004, Stroup 2015). A completely randomized experimental design and factorial treatment design were used. Multiple comparison of treatment means was performed using Fisher’s least significant difference procedure at significance level α=0.05.

The susceptibility of adult WCR populations to insecticide active ingredients was evaluated by analyzing the relationship between insecticide concentrations tested and mortality responses obtained. Data were corrected by Abbot’s formula for natural control mortality and analyzed with a probit link function with Normal distribution in POLOPlus-PC software (LeOra Software LLC) (Finney 1971, Russell and Robertson 1979, LeOra 1987). The probit procedure also estimated a Pearson goodness-of-fit chi-square value

(χ^2) testing the null hypothesis that the expected regression model adequately fits the data. Resistance ratios (RR_{50}) with correspondent 95% confidence intervals (95%CI) were calculated by dividing the estimated LC_{50}s of resistant populations by the estimated LC_{50} of each susceptible population of reference (Robertson et al. 2007).

Results

Aerial application simulation

Cornfield spray deposition

The spray deposition rates and droplet size characteristics obtained by aerial applications across corn canopies were considerably variable (Fig. 1). The WSP results indicated that the interaction between corn canopy position and application rate did not influence spray deposition rate ($F_{2,113}$=0.11; p = 0.8999). Therefore, the interaction term was removed from the model. Application rate influenced spray deposition rate ($F_{1,115}$=5.72; p = 0.0184), whereas corn canopy position did not ($F_{2,115}$=1.42; p = 0.2450). The average deposition rate across the three corn canopy positions (Bottom, Middle, and Top) was within a 2.9 - 15.7 L/ha 95%CI for the aerial application performed at 18.7 L/ha, whereas the one performed at 46.8 L/ha resulted in average deposition values within a 7.3 - 20.1 L/ha 95%CI. The average deposition rates at Middle canopy position (used later for the spray-chamber calibration) were 10.9 and 16.5 L/ha for the lowest and highest aerial application rates evaluated, respectively.

The droplet size distribution reported in the WSP analysis indicated that the $DV_{0.5}$ was not influenced by the interaction between corn canopy and application rate ($F_{2,113}$=0.37; p=0.6947), therefore the interaction term was removed from the model.

Corn canopy alone influenced the $DV_{0.5}$ of the spray deposition ($F_{2,115}$=3.62; p=0.0298), whereas application rate did not ($F_{1,115}$=0.55; p=0.4602). Estimated 95%CI for droplets deposited on the Top canopy position had greater $DV_{0.5}$ (334 - 382 µm) when compared to Middle (299 - 346 µm) and Bottom (291 - 339 µm) canopy positions. The interaction between corn canopy position and application rate did not influence the $DV_{0.1}$ ($F_{2,113}$=0.32; p=0.7279) or the $DV_{0.9}$ ($F_{2,113}$=0.31; p=0.7356) of the spray deposition. Furthermore, both $DV_{0.1}$ and $DV_{0.9}$ were not affected by either application rate ($F_{1,115}$=0.16; p=0.6864 and $F_{1,115}$=0.01; p=0.9400, respectively) or corn canopy position ($F_{2,115}$=2.73; p=0.0696 and $F_{2,115}$=1.34; p=0.2659, respectively).

Wind tunnel and spray-chamber calibration

The wind tunnel test conducted in 2016 identified combinations of TT110015 nozzle and operating pressures compatible with the spray deposition data collected at Middle canopy position of corn (Fig 1). The resultant spray-chamber calibration parameters and droplet size distribution for each chosen spray pressure combination are available in Table 1.

Efficacy of commercial insecticides

Overall, there were no significant two- and three-way interaction effects of carrier volume on the performance of bifenthrin and dimethoate rates tested (p >0.05), so this factor was excluded from the statistical model used. In both years, bifenthrin efficacy was significantly affected by the interaction of WCR populations and insecticide rates (Fig. 2). Mortality of resistant WCR populations was lower than susceptible populations over two rates of bifenthrin tested with a mean mortality range of 40-82% in 2016 and 34-76% in 2017. The highest label rate of bifenthrin was more effective against pyrethroid-resistant WCR than the lowest label rate tested. However, mortality of laboratory-selected resistant WCR (R-Lab) tested in 2017 was higher than mortality observed for field collected resistant WCR at both label rates of bifenthrin. In dimethoate bioassays, the lowest label rate (369.9 g a.i./ha) provided >99% mortality across all populations tested in the first run without statistical difference among treatments ($F_{4,35}$=0.22, p=0.9283) and 100% mortality in all treatments during the second run.

Susceptibility of adult WCR populations to insecticide active ingredients

Probit regressions were obtained for WCR populations exposed to bifenthrin, dimethoate and indoxacarb active ingredients (Table 2). Values of χ^2 obtained suggest that observed mortality data of tested populations fitted the expected probit regression model. Field populations tested that were considered resistant to pyrethroids (R-Field1, R-Field2 and R-Lab) exhibited reduced susceptibility to both bifenthrin and dimethoate active ingredients. Confidence intervals of resistance ratios (RRs) estimated for pyrethroid-resistant WCR populations overlapped for each insecticide tested and were different than those estimated for pyrethroid-susceptible populations (Table 2). However, RRs of pyrethroid-resistant WCR varied depending on the population used as the susceptible reference in the calculation. In general, higher RRs were obtained when using a non-diapausing lab susceptible population (S-Lab1 and S-Lab2) versus the field-collected susceptible population (S-Field). Compared to S-Lab2, RRs of pyrethroid-resistant populations ranged from 22.86- to 33.18-fold for bifenthrin and from 14.36- to

22.60-fold for dimethoate. Furthermore, compared to S-Lab2 and S-Field, pyrethroid-resistant WCR populations showed increased susceptibility to indoxacarb with RRs ranging from 0.32- to 0.35-fold (Table 2).

Discussion

The method of aerial application simulation used in this study accurately reproduced aerial application parameters such as the combination of spray carrier volumes and droplet size distribution compatible to what is deposited on corn leaves in a field situation. This allowed a more realistic representation of aerial application than could be obtained with more traditional spray techniques often used in laboratory studies (Potter 1952, Tang et al. 2015, Little et al. 2017). Although the wind tunnel calibration was performed with only one rate of formulated bifenthrin, droplet size deposition obtained could practically be used for other rates and insecticides. Previous research has shown that nozzle type has more influence on spray droplet size distribution than active ingredient and carrier solution (Creech et al. 2015). Therefore, the droplet size distribution data collected worked as a useful baseline for the insecticide treatments tested in this study.

When used to evaluate the efficacy of formulated bifenthrin against WCR populations, the aerial application simulation consistently captured differences in performance among the rates tested. The significant difference in mortality between pyrethroid-resistant and control populations at both the lowest and highest label rates of formulated bifenthrin confirmed resistance to bifenthrin revealed in active ingredient bioassays and was consistent with anecdotal reports of reduced WCR adult control received from farmers and local crop consultants (Pereira et al. 2015, 2017). Conversely, the lowest label rate of formulated dimethoate provided optimal control of both pyrethroid-resistant and -susceptible WCR populations under simulated aerial application conditions despite the low level of dimethoate resistance that had been revealed when pyrethroid-resistant populations were bioassayed with active ingredients. Results suggest that the observed shift in dimethoate susceptibility of pyrethroid-resistant WCR populations did not reach a level that would lead to “practical resistance” defined as field-evolved resistance that reduces field efficacy of a pesticide with practical consequences for pest control (Tabashnik et al. 2014). This same phenomenon has been reported in other insect pest systems suggesting that the relationship between levels of resistance confirmed in dose-response bioassays and actual efficacy of formulated product in the field needs to be explored in order to understand the practical impact of resistance (Siegfried et al. 2007, Tabashnik et al. 2009, 2013, Luttrell and Jackson 2012).

The simulated aerial application method used was a conservative approach since it tested one model of spray deposition compatible with mid-canopy of corn plants of a given stage and beetles could not escape from treated surfaces. In the field there is a considerable interaction of environmental conditions, beetle movement behavior, and different levels of insecticide coverage within the corn canopy that could lead to differential adult exposure to insecticides. In fact, the spray deposition we collected in the field was fairly variable confirming the uneven canopy coverage previously observed for aerial applications (Bynum et al. 1991). Variable levels of WCR exposure to insecticide applications could potentially lead to greater survival of WCR beetles in the field than measured in the aerial application simulation method, which may contribute to evolution of insecticide resistance and increase resistance levels measured in the lab over time (Georghiou and Taylor 1977, Guedes and Cutler 2013).

Effective insecticide resistance management strategies include the integration of different control strategies and rotation of insecticide modes of action to reduce selection pressure and potential evolution of resistance (Georghiou 1972, Sparks and Nauen 2015). However, compliance with management strategies depends on several social-economic aspects such as compatibility with growers' tradition and past experiences, technology complexity, visibility of results, as well as technology cost and associated profitability (Hurley and Mitchell 2014). Price and convenience often drive growers' choice of pest management practices, which may lead to continued use of a specific insecticide (Wirtz et al. 2009, Dewar 2016). The increase in off-patent generic bifenthrin formulations has lowered pricing of this insecticide often leading to grower preference over other products and frequent inclusion in tank mixtures with other pesticides. Also, regulatory action such as the Food Quality Protection Act has led to reevaluation and cancellation of many insecticides uses in agriculture so fewer modes of action remain available to manage WCR . Collectively, these factors probably have facilitated ongoing selection pressure and contributed to the evolution of WCR resistance to pyrethroids. Educational and incentive programs often fail to consider sociopolitical perspectives for effective resistance management and could be better improved by considering the farmers perception, the potential support of networked communities, and the compatibility between industry interests and federal policies (Gould et al. 2018).

The recent EPA registration of indoxacarb for adult rootworm control in field corn (US-EPA 2018) provides a different mode of action that may be useful in WCR pyrethroid-resistance management programs. In this study, LC_{50}'s from dose-response bioassays performed with indoxacarb active ingredient were lower for pyrethroid-resistant than -susceptible WCR populations. Also, calculated resistance ratios were <1.00, which suggests that pyrethroid-resistant WCR populations tested were more sensitive to indoxacarb than pyrethroid-susceptible populations. Indoxacarb is considered a pro-insecticide that needs bioactivation by esterase/amidase enzymes present in the target to become a more toxic compound (Wing et al. 2000). Therefore, insecticide resistance mechanisms that involve increased activity of hydrolytic enzymes can result in a higher activation rate of indoxacarb in a negative cross-resistance relationship (Gunning and Devonshire 2003, Ramasubramanian and Regupathy 2004), which could be further explored to manage pyrethroid-resistant WCR populations with enhanced metabolism. Our bioassay results suggest that the previously reported likely involvement of enhanced metabolism as part of the WCR pyrethroid-resistance mechanism (Pereira et al. 2017) may be contributing to increased susceptibility to indoxacarb.

In summary, we conclude that the simulated aerial application method used to evaluate the performance of formulated insecticides in corn effectively confirmed bifenthrin resistance and could be useful to evaluate the efficacy of various aerially-applied insecticides for other pest insects. Many of the insecticides still used in the US western Corn Belt belong to the pyrethroid class, so WCR resistance to bifenthrin and potential cross-resistance with other compounds significantly restricts control options in affected areas. Dimethoate and indoxacarb could be useful compounds to manage bifenthrin WCR resistance using rotation-based approaches. However, because of potential cross-resistance between structurally related pyrethroids and organophosphates (Devonshire and Moores 1982, Elzen et al. 1992, Cahill et al. 1995, Bisset et al. 1997, Sayyed et al. 2010, Couso-Ferrer et al. 2011), dimethoate and other organophosphate insecticides should be used with caution in areas where WCR pyrethroid-resistance has been confirmed. In the western Corn Belt, WCR resistance evolution to rootworm-active *Bt* traits has increased the importance of aerially-applied insecticides and crop rotation as tactics to manage densities and mitigate resistance (Reinders et al. 2018). To develop more sustainable WCR management strategies, additional field research and modeling is needed to determine the biological and economical value of short- and long-term best management practices and specifically the optimal role of insecticides in the system. Because of the highly adaptable nature of WCR populations to selection pressure we reinforce the importance of using insect resistance management within an IPM framework to delay the evolution of WCR resistance and prolong the efficacy of formulated insecticide products and plant-incorporated traits.

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Tables and Figures

Table 1. Research track spray chamber application parameters used for aerial application simulations of commercial insecticides. Output per nozzle and droplet size distribution data are mean values ±SE obtained from combinations of TT110015 nozzle and spray pressures that best replicated the cornfield aerial application deposition on the Middle canopy of corn.

Application rate (L/ha)	Spray pressure (kPa)	Output per nozzle (L/min)	Application speed (Km/h)	Droplet size distribution (μm)		
				$DV_{0.1}$	$DV_{0.5}$	$DV_{0.9}$
10.89	110.32	0.38±0.003	27.25	188±0.249	348±0.358	528±1.843
16.50	131.00	0.41±0.003	19.68	178±0.391	333±0.745	506±1.163

Table 2. Western corn rootworm adult susceptibility of pyrethroid-resistant (R-) and pyrethroid-susceptible (S-) populations estimated in 2017 for insecticide active ingredients.

Insecticide	Population	N[a]	Slope±SE	LC_{50} (95% CI) [b]	χ^2 (d.f.)	RR_{50} (95% CI)[c]		
Bifenthrin	S-Lab1	120	3.30±0.53	0.19 (0.14-0.24)	1.19 (2)	1	-	-
	S-Lab2	180	1.57±0.23	0.32 (0.19-0.47)	2.86 (4)	1.66 (1.00-2.76)	1	-
	S-Field	151	2.21±0.36	2.49 (1.85-3.31)	0.42 (3)	13.08 (9.05-18.91)	7.89 (4.64-13.41)	1
	R-Lab	151	4.79±1.21	7.23 (5.00-8.86)	1.65 (3)	37.92 (26.98-53.29)	22.86 (13.70-38.12)	2.90 (2.00-4.20)
	R-Field1	121	2.97±0.53	7.55 (5.46-9.63)	0.33 (2)	39.60 (27.66-56.69)	23.87 (14.13-40.31)	3.03 (2.05-4.46)
	R-Field2	121	1.74±0.40	10.49 (6.14-17.18)	0.79 (2)	55.05 (32.53-93.14)	33.18 (17.32-63.55)	4.21 (2.44-7.27)
Dimethoate	S-Lab2	150	3.29±0.58	0.20 (0.15-0.24)	2.72 (3)	1	-	-
	S-Lab1	150	6.58±1.82	0.37 (0.30-0.42)	1.57 (3)	1.87 (1.46-2.41)	1	-
	S-Field	120	11.75±1.94	0.98 (0.92-1.05)	1.61 (2)	4.95 (3.96-6.18)	2.64 (2.28-3.06)	1
	R-Field1	181	3.09±0.37	2.85 (2.33-3.47)	2.97 (4)	14.36 (10.74-19.21)	7.67 (6.05-9.72)	2.90 (2.36-3.57)
	R-Field2	153	3.41±0.62	3.23 (2.36-4.06)	2.69 (3)	16.30 (11.68-22.76)	8.70 (6.52-11.61)	3.30 (2.53-4.29)
	R-Lab	121	2.57±0.43	4.48 (3.44-5.64)	1.57 (2)	22.60 (16.40-31.15)	12.07 (9.18-15.86)	4.57 (3.57-5.85)
Indoxacarb	S-Lab2	152	2.66±0.41	7.40 (3.90-11.19)	3.78 (3)		1	-
	S-Field	150	3.14±0.58	7.62 (5.79-9.93)	0.28 (3)		1.03 (0.72-1.47)	1
	R-Field1	150	1.66±0.31	2.47 (1.14-4.00)	2.81 (3)		0.33 (0.18-0.63)	0.32 (0.17-0.61)
	R-Lab	151	1.76±0.27	2.58 (1.80-3.53)	1.66 (3)		0.35 (0.23-0.52)	0.34 (0.22-0.51)

[a] number of insects tested; [b] µg a.i./vial; [c] resistance ratios relative to each S- population

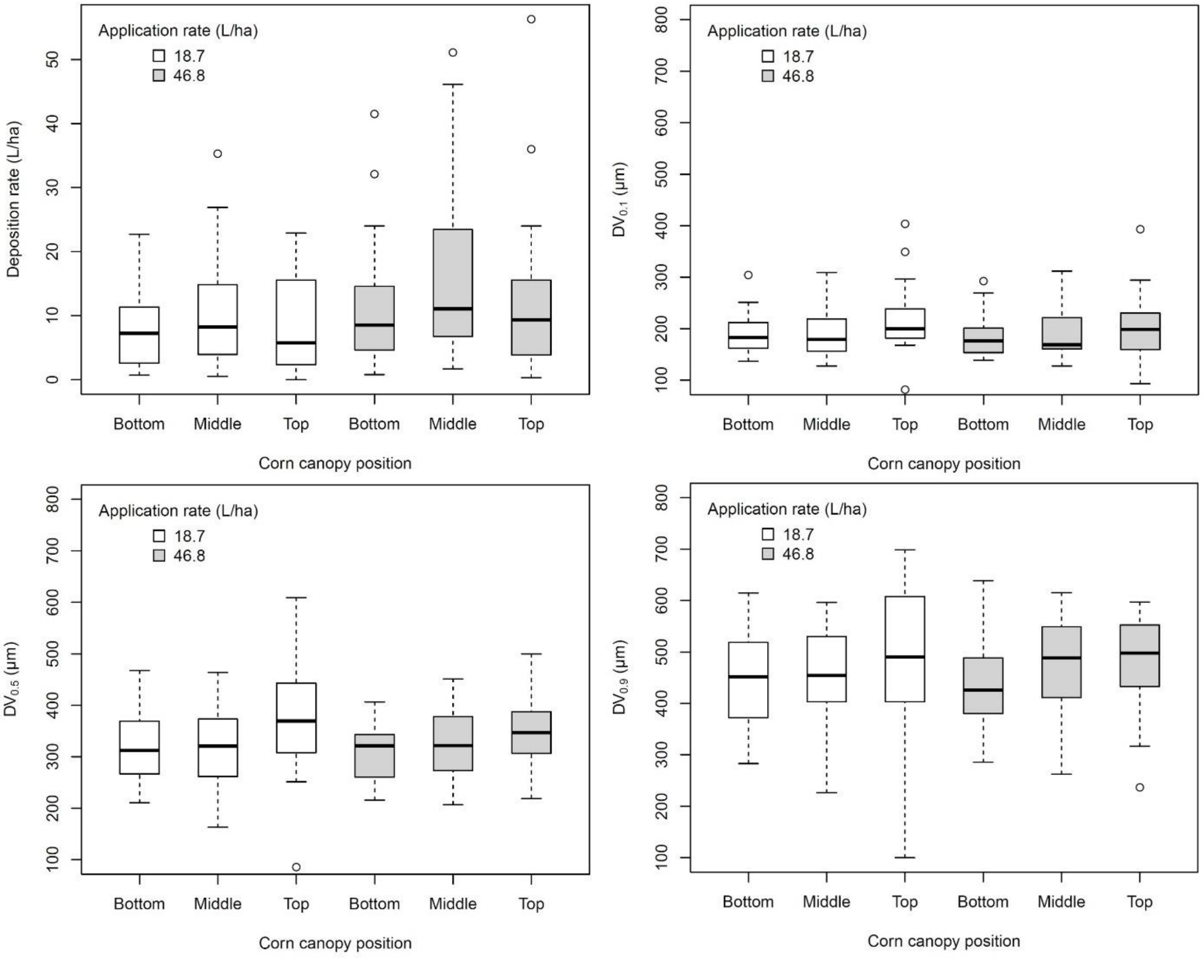

Figure 1. Field spray deposition rate and droplet size parameters ($DV_{0.1}$, $DV_{0.5}$, and $DV_{0.9}$) collected from WSPs placed in the corn canopy at three positions denoted as Top, Middle, and Bottom prior to aerial application.

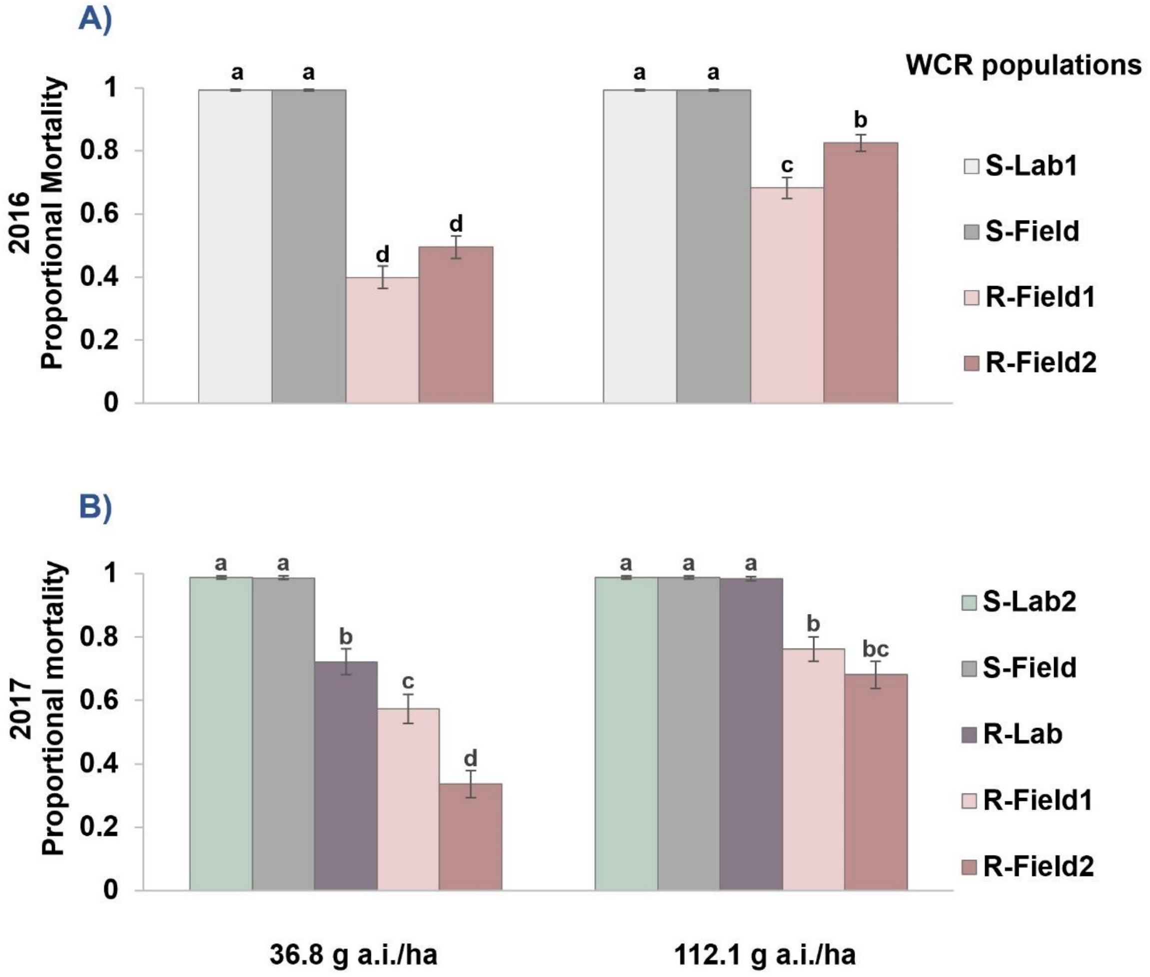

Figure 2. Efficacy of Brigade 2EC (25.1% bifenthrin) against pyrethroid-resistant (R-) and pyrethroid-susceptible (S-) western corn rootworm populations in simulated aerial application bioassays; **A)** 2016 ($F_{3,56}$=4.66, p=0.0056), **B)** 2017 ($F_{4,70}$=8.48, p <0.0001). Data are inverted link proportional mortality means ±SE. Within year and across two bifenthrin rates, treatment combination means followed by the same lower-case letter were not statistically different (Fisher's LSD Test, p >0.05).

CHAPTER 3. FIELD EFFICACY OF SOIL INSECTICIDES ON PYRETHROID-RESISTANT WESTERN CORN ROOTWORMS (*DIABROTICA VIRGIFERA VIRGIFERA* LECONTE)

Introduction

The western corn rootworm (WCR), *Diabrotica virgifera virgifera* LeConte, (Coleoptera: Chrysomelidae) is a major pest of maize, *Zea mays* L., in the United States (US) (Gray et al. 2009, Andow et al. 2016, Wechsler and Smith 2018). Although adult WCR may adversely affect maize pollination by severe silk clipping (Meinke 2014), the most significant damage is caused by larvae feeding on maize roots (Levine and Oloumi-Sadeghi 1991, Hou et al. 1997). Yield loss from root injury or from subsequent plant lodging is highly variable and influenced by a number of biotic and abiotic factors such as maize hybrid, soil moisture, rootworm density, and management practices (Sutter et al. 1989, Gray and Steffey 1998, Urías-López and Meinke 2001). Root injury equivalent to one node of roots pruned was associated with a 9.7-12.2% yield reduction across hybrids tested under irrigation in Nebraska (Urías-López and Meinke 2001). For non-irrigated corn in Illinois, studies suggest that 15.2-17.9% yield loss can be expected for each node of roots pruned by WCR larvae (Dun et al. 2010, Tinsley et al. 2013).

Current methods to protect maize from rootworm injury include maize rotation with a nonhost crop, transgenic maize producing rootworm-specific Cry toxins, and soil- or aerial-applied insecticides (Levine and Oloumi-Sadeghi 1991, Petzold-Maxwell et al. 2013, Wangila et al. 2015). However, local socioeconomic conditions may dictate that some methods are not practical to implement. For example, in the US western Corn

Belt, maize production under irrigation has often been more profitable than other available crops, which discourages the adoption of crop rotation. The demand for maize is high for livestock operations and ethanol production leading to a higher adoption of continuous maize planting (maize planted consecutively for two or more years) (Wangila et al. 2015, Reinders et al. 2018, Souza 2019). This can lead to build-up of WCR densities making the annual management of this pest a considerable challenge. Furthermore, changing of pesticide regulations and field-evolved WCR resistance to control tactics has restricted options to manage this important pest in the US.

In the late 1940s, organochlorines were introduced in the US and became very popular as soil broadcast applications for rootworm larval control (Ball and Weekman 1963, Levine and Oloumi-Sadeghi 1991, Fernandez-Cornejo et al. 2014). However, widespread use of this insecticide class, which remains active in the soil for long periods of time, selected for high levels of WCR resistance to aldrin and heptachlor in parts of the US Corn Belt (Ball and Weekman 1962, 1963, Chio et al. 1978). In the 1970s, broadcast soil application of organochlorines was replaced by in-furrow or banded application of either carbamate or organophosphate insecticides that were less persistent in the field and primarily protected the root zone close to the plant stem from rootworm injury (Mayo 1986, Felsot 1989, Sutter et al. 1991, Parimi et al. 2006). The combination of insecticide chemistry and application placement provided a natural refuge as maize roots that grew outside of the treated zone produced WCR that had not been exposed to the insecticide, which helped maintain population susceptibility to soil applied carbamates and organophosphates over time (Gray et al. 1992, Parimi et al. 2006). An alternative WCR management approach was also adopted in the western

Corn Belt from the 1960s to the 1990s, in which aerial application of either carbamate or organophosphates insecticides was used to suppress adult WCR populations (Meinke et al. 1998, Van Rozen and Ester 2010). This was a stand-alone management strategy that targeted gravid WCR females to reduce egg density to a level that would not lead to economic loss in maize the following season (Meinke 1995).

In Nebraska, aerial application of carbaryl or methyl parathion was common in continuous maize. Methyl parathion use reached approximately 30% of total insecticide use per weight by 1995 (NASS-USDA 2018). At that time, parts of Nebraska had been using the adult management strategy for up to 20-30 years (Meinke 1995, Meinke et al. 1998). This practice placed annual selection pressure on adult WCR populations which led to field-evolved carbaryl and methyl parathion cross-resistance (Meinke et al. 1998, Scharf et al. 1999, Zhu et al. 2001) and significantly impacted the performance of some soil insecticides (Wright et al. 2000). In 1996, the Food Quality Protection Act (FQPA) altered the regulation of pesticides and pushed the US Environmental Protection Agency (EPA) to cancel uses of a number of organophosphate and carbamate insecticides leaving fewer options for WCR control (Zager et al. 2003).

Soil insecticides were largely replaced in the 2000s by genetically engineered maize expressing one or more rootworm-active proteins derived from *Bacillus thuringiensis* (*Bt*) (Tabashnik 2008, Fernandez-Cornejo et al. 2014, Andow et al. 2016). However, WCR field-evolved resistance to commercially available *Bt* events has been documented in some areas of the US Corn Belt since 2009 (Gassmann et al. 2011, 2014, 2016, Wangila et al. 2015). Consequently, the use of soil- and aerially-applied insecticides has increased (Fernandez-Cornejo et al. 2014) to complement *Bt* traits, to reduce high WCR densities and to mitigate resistance (Wangila et al. 2015). However, because many carbamates and organophosphates had been removed from the market, there was a shift in insecticide class usage to pyrethroids such as bifenthrin (Pereira et al. 2015, Atwood and Paisley-Jones 2017).

From 2002 to 2014, there was a 40% increase in bifenthrin use on maize in Nebraska. (NASS-USDA 2018) This included soil and foliar applications for WCR control, and foliar applications for spider mites *Tetranychus urticae* Koch and western bean cutworm *Striacosta albicosta* Smith (Michel et al. 2010, Pereira et al. 2015, Archibald et al. 2018). The selection pressure imposed on maize pests from up to four aerial applications of bifenthrin per crop season led to field-evolved resistance of WCR to bifenthrin in some populations by 2015 (Pereira et al. 2015). Cross-resistance to tefluthrin and DDT was then observed in laboratory bioassays supporting enhanced metabolism and target site insensitivity as possible mechanisms of WCR bifenthrin-resistance (Pereira et al. 2017). Although the estimated resistance ratios to pyrethroids were relatively low, they were higher in the adult stage (Pereira et al. 2017) and high enough to cause bifenthrin control failure of resistant adult WCR under simulated aerial application of bifenthrin commercial product (Souza 2019). However, the impact of pyrethroid resistance levels observed in the larval bioassays on the field performance of formulated pyrethroid soil insecticides commonly used to protect maize roots from rootworm injury had not been evaluated. Therefore, in order to complement a larger project to characterize WCR pyrethroid resistance (Pereira et al. 2015, 2017, Souza 2019) and to inform WCR management strategies, the present study was designed to 1) evaluate the efficacy of some commonly used formulated soil insecticides against WCR in fields with different levels WCR pyrethroid resistance, and 2) estimate in the laboratory current susceptibility levels of WCR larvae to the soil insecticide active ingredients.

Methods

Field performance of formulated soil insecticides

In 2016 and 2017, replicated field trials were conducted to evaluate the performance of soil insecticides on maize root protection at three different geographic locations in Nebraska, US where different levels of WCR susceptibility to pyrethroids had been reported (Pereira et al. 2015). A Saunders County field site was selected to test a pyrethroid-susceptible WCR population, whereas Clay and Keith County field sites were selected to test populations that exhibited moderate and high levels of WCR pyrethroid resistance, respectively. Keith Co. locations in 2016 (Keith1) and 2017 (Keith2) were different commercial farms, 18 Km apart, where annual soil- and aerial bifenthrin applications had been made for five years prior to this study. The same field locations at Saunders and Clay Counties were used each year and are referred to in this study as Saunders and Clay, respectively. The Saunders Co. site was at the University of Nebraska Eastern Nebraska Research and Extension Center, and the Clay Co. site was on the University of Nebraska South Central Agricultural Lab farm. The Saunders Co. site was surrounded by a large area of continuous maize that had not received insecticide applications for over ten years. Bifenthrin had only been included previously as a soil application in a few small-plot trials. Bifenthrin had only been used at the Clay Co. site in small plot trials but the small farm was near commercial farms where soil– and aerial –applied bifenthrin had been used over the last decade

The maize hybrid N65Z-3220 (Agrisure® Viptera™, Syngenta Seeds Inc., Minnetonka, MN) was provided by the manufacturer and was used in all trials in both years. Seeds contained three *Bt* genes for controlling above-ground lepidopteran species (Cry1Ab/Cry1F/Vip3A) and came treated with Avicta® Complete Corn 250 (Syngenta Crop Protection LLC, Greensboro, NC) that included thiamethoxam (0.25 mg a.i./seed) and abamectin (0.22 mg a.i./seed). Seeds were glyphosate tolerant and did not contain genetically engineered traits to control rootworms. Standard tillage, irrigation, nitrogenous fertilizer and weed control programs were used each year in all field locations.

Four treatments were tested: 1) Untreated control; 2) 1.17 L/ha of liquid Capture LFR (bifenthrin 17.15%, FMC, Philadelphia, PA); 3) 0.73 L/ha of liquid Force CS (tefluthrin 23.4%, Syngenta Crop Protection LLC, Greensboro, NC); and 4) 8.20 Kg/ha of granular Aztec 2.1G (cyfluthrin 0.1% + tebupirimphos 2.0%, AMVAC, Newport Beach, CA). The fourth treatment was included as a positive control due to the presence of an organophosphate (OP) in the formulation. Liquid insecticides were prepared in tap water for 46.77 L/ha carrier volume rate. All insecticides were applied in-furrow at planting with four replicates randomized in four blocks. Each replicate consisted of a four-row plot of 10 m long and 0.76 m row spacing (74-79 000 seeds/ha). After peak larval feeding, five plants were randomly dug from the central two rows of each plot, labeled and taken to the laboratory. In 2016, roots were dug on July 20 (Saunders), July 15 (Clay) and July 27 (Keith1), whereas in 2017 they were collected on July 18 (Saunders), July 12 (Clay) and July 25 (Keith2). Roots were washed and rated for rootworm injury using the 0-3 node injury scale (NIS) (Oleson et al. 2005). In 2016, single-plant emergence cages (Pierce and Gray 2007) were placed in all field locations to evaluate the impact of rootworm larval control obtained from each insecticide treatment on adult emergence. Three emergence cages were placed in the central two rows of each plot. Once WCR emergence started, cages were checked on a weekly basis and beetles counted until the emergence had ended. Adult emergence periods in 2016 were: June 28 – August 22 (Saunders); June 27 – August 11 (Clay); and July 6 – October 10 (Keith1).

Larval laboratory bioassays with insecticide active ingredients

Chemicals

Analytical standards of bifenthrin, tefluthrin, cyfluthrin and tebupirimphos were used, which were the active ingredients in formulated soil insecticides tested in the field. Bifenthrin 98%, cyfluthrin 99.2% and tebupirimphos 97% were obtained from Chem Service Inc., West Chester, PA (Cat. No. N-11203/ CAS: 82657-04-3, N-11130/CAS: 68359-37-5 and N-13503/ CAS: 96182-53-5, respectively). Tefluthrin ≥ 95% was provided by Santa Cruz Biotechnology, Inc., Dallas, TX. (Cat. No. sc-236965/ CAS: 79538-32-2). All insecticides were dissolved in acetone ≥99.9% supplied by Sigma-Aldrich Corp., St. Louis, MO (Cat. No. 650501/CAS: 67-64-1) for stock solution preparation.

WCR populations

Four WCR populations were tested in the laboratory at neonate larval stage (<36 hours old). One pyrethroid-susceptible non-diapausing lab population (Lab) provided in 2017 by Crop Characteristics, Inc., Farmington, MN, and three populations originally collected in 2016 at the adult stage from fields in Nebraska-US were used. The population from Saunders Co. (Saunders) was pyrethroid-susceptible, whereas populations from Keith Co. (Keith1 and Keith2 described earlier) were pyrethroid-resistant. Adults collected in 2016 were taken to the Department of Entomology at the University of Nebraska-Lincoln, Lincoln, NE and maintained there under standard rearing procedures (Wangila et al. 2015). Eggs obtained from field-collected populations were maintained in a growth chamber at 8º±1°C in diapause for 4-5 months and then transferred to 25±1°C to facilitate post-diapause egg development. All field collections were allowed by the property owners.

Bioassays

In 2017, dose-response bioassays were performed with insecticide analytical standards to estimate the susceptibility of WCR larvae to the active ingredients of commercial soil insecticides. Filter papers obtained from Thermo Fisher Scientific Inc, Waltham, MA (Whatman™ grade 1, circles 42.5mm, Cat. No. 1001-042), were placed inside sterile petri dishes purchased from VWR International, Radnor, PA (9.0 mm height × 50.0 mm diameter, Pall Corporation, Port Washington, NY Cat. No. 25388-606) and treated with increasing concentrations of bifenthrin, tefluthrin, cyfluthrin and tebupirimphos following methods described in previous research (Magalhaes et al.

2007). For a negative control, filter papers were treated with purified water only. Insecticide stock solutions prepared in acetone were diluted in purified water into 5-8 concentrations. The number of insecticide concentrations used to test each population varied depending on the number of WCR larvae available. A volume of 150 µl insecticide solution was homogeneously applied on each filter paper with a pipette and each concentration was replicated three times. Treated filter papers were allowed to dry at room temperature for 15 minutes to prevent condensation on the petri dishes once closed. A group of 20 WCR larvae were then carefully transferred to each petri dish using a fine camel hair paintbrush. Petri dishes were closed and maintained in the dark at a temperature of 23 ± 1 °C. Larval mortality was recorded at 24h after infestation. Larvae that did not respond to gentle prodding or were unable to move around the filter paper area consistently were considered dead.

Statistical analysis

Node injury scores recorded from plants dug from each plot followed a continuous distribution within the restricted interval of [0,3]. Continuous proportion data that do not extend to +/- infinity like in a Normal distribution being restricted by a specific interval fits a Beta-binomial distribution with continuous values in the restricted interval of [0,1] (Ferrari and Cribari-Neto 2004, Stroup 2015). Thus, rating values obtained were divided by three and analyzed with this distribution. To estimate soil treatment effects on adult WCR emergence in 2016, the total number of beetles emerged from each plot was analyzed with a Negative-binomial distribution. Emergence counting data are discrete integer values that show overdispersion (variance greater than the mean) following the aforementioned distribution premises (Bliss and Fisher 1953, Tripathi 2006, Stroup 2015). Root ratings and adult emergence data were evaluated using their correspondent distribution logit functions with a generalized mixed model in SAS 9.4 software (SAS Institute, Cary, NC). A randomized complete block experiment design (RCBD) with factorial treatment design was used. Field location and insecticide treatments were adopted as factors in the statistical model. Multiple comparison of treatment means was performed using Fisher's least significant difference procedure at significance level α=0.05.

To evaluate the susceptibility of WCR larvae to insecticide active ingredients in the laboratory, the LC_{50}s of different populations were estimated by probit analysis. Mortality data for each insecticide concentration tested was submitted to POLOPlus-PC software algorithm (LeOra Software LLC) that corrects for natural control mortality using Abbot's formula (Abbott 1925) and analyzes data with a probit function and Normal distribution (Finney 1971, Russell and Robertson 1979, LeOra 1987, Robertson et al. 2007). The probit procedure also performed a Pearson goodness-of-fit test between observed data and expected regression lines, and estimated resistance ratios (RR_{50}) with correspondent 95% confidence intervals between LC_{50}s of field and lab populations. When RR_{50} confidence intervals between pyrethroid-susceptible (Saunders) and pyrethroid-resistant (Keith1 and Keith2) field populations overlapped, a test of equality of slopes and intercepts of regression lines was performed in the same software, and the statistical significance estimated at α=0.05 (Robertson et al. 2007).

Results

Field performance of formulated soil insecticides

Root injury results indicate that in both years insecticide treatments performed significantly differently depending on field location (Figure 1). Overall, significantly lower mean root injury was observed in both years for all soil insecticides tested at Saunders and Clay compared to untreated control plots. An average of 70-86% root injury reduction was observed for all insecticide treatments tested at Saunders. Conversely, mean root injury of treated plots at Keith1 and Keith2 was not significantly different from mean injury in respective untreated control plots for any of the soil insecticide treatments tested. In fact, root rating means of all treatments tested at Keith1 and Keith2 were consistently within the 0.8-1.7 range. At the Clay location, root injury in plots treated with bifenthrin soil insecticide was significantly greater than injury in cyfluthrin + OP treated plots each year (i.e. 43 and 26% in 2016 and 2017, respectively). Furthermore, mean root injury in the bifenthrin treatment was significantly greater than mean injury in the tefluthrin treatment during 2017 but not 2016 at Clay. At the same location, mean injury in the tefluthrin treatment was significantly greater than mean injury in the cyfluthrin + OP treatment in 2016 but not in 2017. The analysis of mean WCR adult counts collected in 2016 single-plant cages indicated no treatment by field interaction significantly affecting beetle emergence ($F_{6,27}$=0.83; p=0.5601) and no overall insecticide treatment effect ($F_{3,33}$=1.87; p=0.1540). However, the Saunders site had significantly higher mean WCR adult emergence per plot than Clay and Keith1 (Figure 2).

Larval laboratory bioassays with insecticide active ingredients

Probit analysis of concentration-mortality regressions effectively estimated susceptibility levels of WCR larvae to soil insecticide active ingredients (Table 1). Populations from Keith1 and Keith2 consistently showed reduced susceptibility to all three pyrethroid insecticides tested. In fact, resistance ratios (RRs) of Keith populations for bifenthrin, tefluthrin, and cyfluthrin were all near 5-fold. Although RR confidence intervals of Saunders overlapped with those of Keith populations for bifenthrin, they were found to be significantly different in the test of equality of slopes and intercepts (Keith1: $\chi^2_{(d.f)} = 30.71_{(2)}$, $p < 0.0001$; Keith2: $\chi^2_{(d.f)} = 37.41_{(2)}$, $p < 0.0001$). RRs of Keith populations estimated for tebupirimphos were all <2-fold and their confidence intervals did not overlap with those estimated for Saunders and Lab populations.

Discussion

This study confirms that a relatively low level of WCR pyrethroid resistance detected in laboratory bioassays (Pereira et al. 2015, Souza 2019) is enough to significantly reduce the performance of formulated soil-applied pyrethroid products in the field. A study that analyzed over a decade of research at multiple US maize-producing sites indicated that nearly 86% less root injury occurred in conventional maize when a soil insecticide was applied in addition to a standard seed treatment (Tinsley et al. 2015). Similar results were observed in this study, as treatments tested on the Saunders WCR pyrethroid-susceptible population provided 70-86% less root injury than untreated control plots. In contrast, the performance of commercial pyrethroids bifenthrin and tefluthrin was significantly reduced at Clay and Keith County sites, which were previously confirmed (Pereira et al. 2015, Souza 2019) to contain pyrethroid-resistant WCR populations. Particularly at Keith1 and Keith2, the 0.8-1.7 root injury ratings consistently observed for all treatments tested, were at levels that may cause significant yield loss (Sutter et al. 1989, Gray and Steffey 1998, Urías-López and Meinke 2001, Oleson et al. 2005, Dun et al. 2010, Tinsley et al. 2013).

Although the driving force behind WCR field-evolved resistance to pyrethroids is uncertain, a previous diagnostic assay survey indicated that WCR populations east of Nebraska were in general susceptible to pyrethroids whereas populations from the west exhibited resistance to bifenthrin and tefluthrin (Pereira et al. 2015). Either bifenthrin or tefluthrin were commonly used as soil insecticides in all locations surveyed, but western areas had an additional history of multiple bifenthrin aerial applications suggesting that bifenthrin foliar spraying may have been a major contributor to the WCR pyrethroid resistance observed in both adult and larval stages (Pereira et al. 2015). Results presented here not only confirm the ~5-fold pyrethroid cross-resistance between bifenthrin and tefluthrin previously detected in WCR larvae (Pereira et al. 2015, 2017) but also reports a similar level of WCR resistance to cyfluthrin, which is structurally classified as a Type II pyrethroid by the presence of a α-cyano group (Verschoyle and Aldridge 1980, Soderlund 2011). Cross-resistance between Type I and Type II pyrethroids does not always happen (Hu et al. 2011). When it does, it is commonly associated with target site mutations in the sodium-channels (*kdr* mutations) (Du et al. 2009, 2013, Burton et al. 2011, Rinkevich et al. 2012), which was already suggested to be part of the WCR pyrethroid resistance mechanism (Pereira et al. 2017).

The control failure of cyfluthrin + tebupirimphos soil insecticide formulation consistently observed in different Keith fields in two years of study was unexpected and reasons for that failure are unclear. Cyfluthrin cross-resistance observed in larval bioassays for pyrethroid-resistant Keith populations could be a factor contributing to the observed field efficacy reduction. Nevertheless, questions remain on the performance of tebupirimphos in mixture with cyfluthrin on pyrethroid-resistant WCR populations. Cross-resistance and synergism studies suggested enhanced metabolism as part of the WCR pyrethroid resistance mechanism (Pereira et al. 2017), which could mutually affect the performance of structurally related insecticides such as pyrethroids and organophosphates. In fact, a laboratory investigation of both Keith populations revealed a decreased susceptibility of pyrethroid-resistant WCR adults to the organophosphate dimethoate (Souza 2019). Examination of the activity of the main detoxification enzymes in pyrethroid-resistant WCR may clarify the magnitude of enhanced metabolism possibly contributing to the resistance trait observed.

Although there was no significant effect of soil insecticides on adult WCR emergence, the highest emergence averaged over all treatments was observed at Saunders where all insecticide treatments significantly reduced root injury. The adult emergence data collected supports previous studies (Gray et al. 1992, Boetel et al. 2003) that showed an inconsistent effect of soil insecticides on adult emergence. In-furrow or banded placement of soil insecticides were designed to protect the main maize root mass from larval injury and prevent lodging; but, because of the built-in untreated refuge between rows, a considerable number of larvae may complete development to the adult stage (Boetel et al. 2003). Hibbard et al. (2010) reported that adult emergence is reduced only when a high larval population is reached, and density dependent mortality occurs. The resistance levels present at Clay and both Keith sites may have led to greater larval survival and more density-dependent larval mortality than present at the Saunders site leading to greater adult emergence at Saunders (Branson and Sutter 1985, Elliott and Hein 1991, Onstad et al. 2006, Hibbard et al. 2010). Therefore, although excellent root protection was provided at Saunders, soil insecticide treatments did not manage the local western corn rootworm population.

In conclusion, this study revealed that relatively low levels of WCR pyrethroid resistance estimated in the lab may be sufficient to cause control failure of commonly used pyrethroid soil insecticides in the field. The reduced field performance of soil applied bifenthrin, tefluthrin and possibly cyfluthrin in southwestern Nebraska significantly restricts the insecticide options left there to protect maize roots from pyrethroid-resistant WCR (Pereira et al. 2015). Rotation of crops, plant-incorporated insecticide traits and insecticide modes of action remains as the top IPM and insecticide resistance management recommendation to manage pyrethroid-resistant WCR populations. Since evidence collected to date supports the hypothesis that adult WCR selection is impacting resistance levels expressed in the larval stage (Pereira et al. 2015, Souza 2019), aerial applications of insecticides on maize should be used wisely (Sparks and Nauen 2015, Souza 2019) to prolong the efficacy of soil insecticide compounds available and to delay the evolution of WCR insecticide resistance.

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Tables and Figures

Table 1. WCR larval susceptibility of pyrethroid-susceptible (Lab; Saunders) and pyrethroid-resistant (Keith1; Keith2) populations estimated in 2017 for the active ingredients of main commercial soil insecticides.

Insecticide	Population	N[a]	Slope±SE	LC_{50} (95%CI)[b]	χ^2 (d.f)	RR_{50} (95%CI)[c]
Bifenthrin	**Lab**	241	3.98±0.58	0.88 (0.76-0.98)	0.32 (2)	*
	Saunders	303	3.84±0.51	2.78 (2.32-3.21)	1.72 (3)	3.13 (2.54-3.86)
	Keith1	366	1.95±0.19	4.12 (3.29-5.04)	1.44 (4)	4.64 (3.60-5.97)
	Keith2	634	1.57±0.17	3.82 (2.87-4.89)	1.52 (4)	4.30 (3.20-5.79)
Tefluthrin	**Lab**	302	9.74±1.24	0.54 (0.50-0.57)	2.92 (3)	*
	Saunders	240	6.86±0.76	1.18 (1.10-1.27)	1.93 (2)	2.18 (1.98-2.41)
	Keith1	420	10.42±1.96	2.92 (2.10-3.25)	7.46 (5)	5.41 (4.81-6.09)
	Keith2	421	5.04±0.59	2.21 (1.86-2.49)	6.20 (5)	4.10 (3.65-4.61)
Cyfluthrin	**Lab**	300	2.35±0.29	3.31 (2.65-4.06)	2.34 (3)	*
	Saunders	298	1.21±0.19	2.29 (1.52-3.11)	1.10 (3)	0.68 (0.45-1.03)
	Keith1	301	1.28±0.15	19.42 (13.43-26.79)	0.66 (3)	5.78 (3.85-8.68)
	Keith2	243	1.13±0.20	14.11 (7.42-21.0)	1.13 (2)	4.20 (2.47-7.14)
Tebupirimphos	**Lab**	423	11.32±1.11	0.44 (0.42-0.46)	4.14 (5)	*
	Saunders	429	9.38±0.80	0.38 (0.36-0.40)	4.22 (5)	0.86 (0.81-0.92)
	Keith1	241	17.50±2.16	0.52 (0.50-0.53)	1.47 (5)	1.17 (1.11-1.23)
	Keith2	240	7.66±1.01	0.66 (0.60-0.72)	1.38 (5)	1.51 (1.36-1.67)

[a] number of insects tested; [b] ng/cm^2; [c] resistance ratios relative to pyrethroid-susceptible laboratory population (Lab)

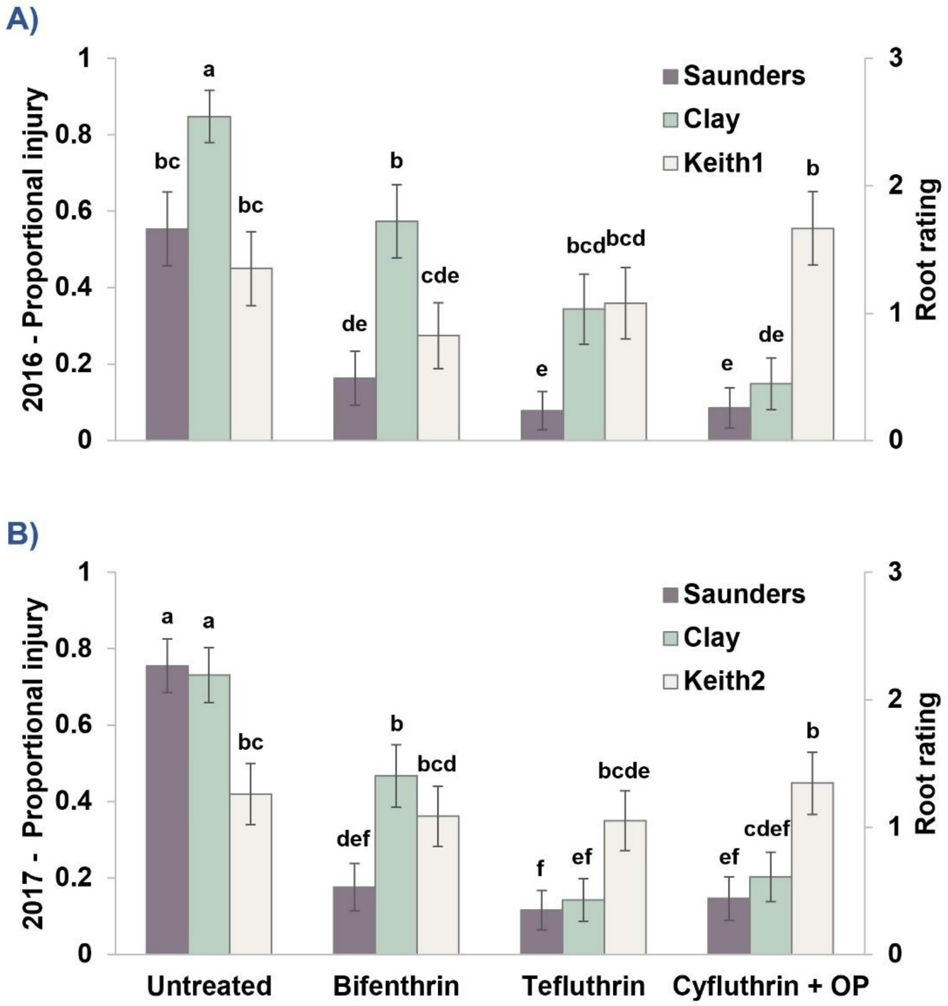

Figure 1. Field performance of commercial soil insecticides on WCR larvae populations. Graph presents inverted link of proportional root injury means ±SE and correspondent root rating evaluated at three different Nebraska-US field locations in **A)** 2016 ($F_{6,27}$=4.60; p=0.0024) and **B)** 2017 ($F_{6,27}$=5.33; p=0.0010). Saunders represented a pyrethroid-susceptible field, whereas Clay and Keith Co. populations represented moderate and high pyrethroid-resistant fields respectively. Treatment combination means followed by the same letter were not statistically different (p >0.05).

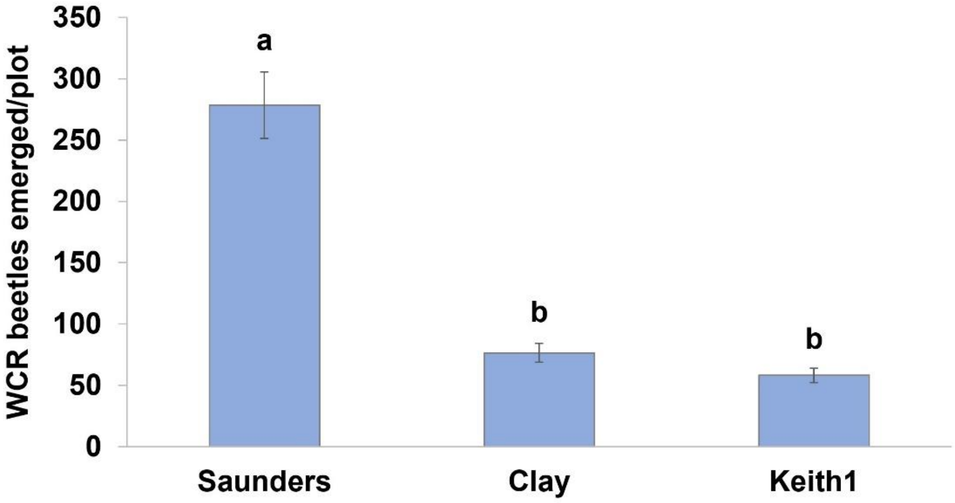

Figure 2. 2016 WCR adult emergence at the three different Nebraska-US field locations testing performance of commercial soil insecticides. Graph presents inverted link means of beetles emerged from each experimental plot ±SE (three single-plant emergence cages per plot). Saunders had a significantly higher mean adult emergence than the other two sites ($F_{2,9}$=71.61; p<0.0001). Means followed by the same letter were not statistically different (p >0.05).

CHAPTER 4. ACTIVITY OF DETOXIFICATION ENZYMES IN PYRETHROID-RESISTANT POPULATIONS OF THE WESTERN CORN ROOTWORM *DIABROTICA VIRGIFERA VIRGIFERA* LECONTE

Introduction

Field-evolved resistance to pyrethroids has been confirmed among populations of the western corn rootworm (WCR), *Diabrotica virgifera virgifera* LeConte (Coleoptera: Chrysomelidae), in the western Corn Belt of the United States (US) (Pereira et al. 2015, 2017). Laboratory bioassays revealed WCR cross-resistance to bifenthrin and tefluthrin during both adult and larval stages (Pereira et al. 2017). A reduced performance of formulated pyrethroids that are aerially sprayed and soil-applied for WCR adult and larval control was also confirmed (Souza 2019a, 2019b). Treating field-collected pyrethroid-resistant WCR adults with insecticide synergists S,S,S-tributyl phosphorotrithioate (DEF) and piperonyl butoxide (PBO) prior to insecticide exposure partially reduced resistance to pyrethroids suggesting that both target site insensitivity and enhanced metabolism could be components of the resistance mechanism (Pereira et al. 2017).

Reduced adult susceptibility to the organophosphate dimethoate and increased susceptibility to the oxadiazine indoxacarb were also detected by active ingredient dose-response bioassays conducted on pyrethroid-resistant WCR populations (Souza 2019b). Cross-resistance between structurally related insecticides such as pyrethroids and organophosphates is often associated with increased activity of detoxification enzymes such as P450 monooxygenases, esterases and glutathione S-transferases

(Hemingway et al. 1993, Cahill et al. 1995, Carvalho et al. 2013, Chigure et al. 2018). Activity of esterase/amidases could be particularly important in hydrolyzing amide-containing insecticides such as dimethoate, and also in bioactivating the pro-insecticide indoxacarb (Yu and Nguyen 1998, Wing et al. 2000).

Non-synonymous nucleotide substitutions in the voltage-gated sodium channel gene can also provide resistance to insecticides that act as sodium channel modulators such as pyrethroids and DDT (Soderlund and Knipple 2003). More than 50 sodium channel mutation combinations were reported to provide resistance to pyrethroids in various arthropod pests (Dong et al. 2014). Mutations in the *para*-homologous sodium channel loci L1014 and T929 are the most common in conferring knock-down resistance (*kdr*) to pyrethroids in different insect species and also in providing variable levels of cross-resistance between not only Type I and Type II pyrethroids, but also between pyrethroids and DDT (Usherwood et al. 2007, Burton et al. 2011, Dong et al. 2014). In another chrysomelid beetle, the Colorado potato beetle *Leptinotarsa decemlineata* (Say), mutations at both loci L1014 and T929 were identified as a major mechanism of pyrethroid resistance (Rinkevich et al. 2012). The *para*-homologous sodium channel gene locus M918 has also been shown to confer high levels of *kdr* resistance in a number of different insect species (Williamson et al. 1993, 1996, Dong et al. 2014). The cross-resistance between the two classes of pyrethroids and DDT previously observed in pyrethroid-resistant WCR populations suggests that *kdr* mutations may also be involved in the resistance mechanism (Pereira et al. 2017, Souza 2019a).

Despite laboratory and field studies that have clarified the implications of the WCR pyrethroid resistance trait, the mechanisms of resistance remained unknown. Artificial selection has been widely used to investigate insecticide resistance mechanisms and to understand the evolution of resistance traits (Roush and McKenzie 1987). Therefore, laboratory selection of a pyrethroid-resistant WCR population was initiated by exposing several generations to high selection pressure. The selection process can increase the frequency of resistance-associated genes over time and provide a more homogeneous genetic background for study (Georghiou 1972, Georghiou and Taylor 1977). Furthermore, the realized heritability of resistance (h^2) is often estimated during the process of selection (Falconer 1989, Tabashnik 1992), which incorporates the estimation of the resistance development rate that is critically important to resistance evolution modelling and insect resistance management (IRM) planning (Georghiou and Taylor 1977, Tabashnik 1992, Oswald et al. 2011).

The characterization of WCR pyrethroid resistance is important to IRM and Integrated Pest Management (IPM) throughout US maize producing areas. Biochemical and genetic studies would greatly contribute to the understanding of the resistance mechanisms involved in the WCR pyrethroid resistance, complement the laboratory and field data collected thus far (Pereira et al. 2015, 2017, Souza 2019b, 2019a) and potentially improve resistance detection methods. Therefore, the objectives of this study were: (1) to select a pyrethroid-resistant WCR population in the laboratory and obtain a preliminary estimate of the realized heritability of the resistance trait; (2) screen pyrethroid-resistant WCR populations for voltage-gated sodium channel loci that commonly harbor *kdr* mutations in other insect species; and (3) evaluate the enzyme activity of pyrethroid-resistant WCR populations.

Methods

Chemicals

Analytical standards of bifenthrin, DEF and PBO were purchased from Chem Service Inc. (West Chester, PA, Cat. No. N-11203-100MG, N-13194-250MG, and N-13061-100MG respectively). DNAzol® reagent was obtained from Invitrogen (Carlsbad, CA, Cat No. 10503027). PolyAcryl Carrier was provided by Molecular Research Center Inc. (Cincinnati, OH, Cat No. PC152) and RNase A by MACHEREY-NAGEL GmbH & Co. KG (Düren, Germany, Cat No. 740505). Proteinase K and QIAquick PCR Purification Kit were purchased from Qiagen Inc. (Germantown, MD, Cat No. 19131 and 28104 respectively). GoTaq® Flexi DNA polymerase kit was obtained from Promega (Madison, WI, Cat No. M8291). Triton™ X-100 and Pierce™ bicinchoninic acid (BCA) assay kit were provided by Thermo Scientific (Rockford, IL, Cat No. 85112 and 23227 respectively). The Native Sample Buffer (161-0738) and 10×Tris Glycine/SDS buffer (161-0732) was purchased from Bio-Rad Laboratories (Hercules, CA). Sigma-Aldrich Corp. (St. Louis, MO) provided all PCR primers and remaining chemicals used including: dimethoate (45449-100MG); reduced L-Glutathione (G4251-5G); 1-Chloro-2,4-dinitrobenzene (237329-10G); p-nitroanisole (103543-5G); p-nitrophenyl acetate (N8130-5G); α-naphthyl acetate (N8505); β-naphthyl acetate (N6875); D-Glucose 6-phosphate sodium salt (G7879-1G); NADP disodium salt (10128031001); glucose-6-phosphate dehydrogenase (G6378-500UN); and fast Blue RR salt (F0500).

Screening for WCR kdr mutations

Three pyrethroid-resistant WCR adult populations were screened for *para*-homologous *kdr* mutations in the voltage-gated sodium channel gene. Two were collected from corn fields ~14 Km apart from each other in Keith County, NE (R-Field1 and R-Field3) in 2015 and 2016, respectively. The third population was the fourth generation of R-Lab maintained in the lab under bifenthrin selection. Glass vials were coated with a pre-established bifenthrin diagnostic concentration (LC_{99}) (Pereira et al. 2015) and infested with mixed-age WCR beetles from pyrethroid-resistant populations. At 24h after infestation, survivors were flash frozen in liquid nitrogen and kept in -80 °C freezer. WCR beetles purchased from Crop Characteristics (S-Lab1) were used as pyrethroid-susceptible controls. Genomic DNA was extracted from six WCR beetles (1:1 sex ratio) from each population using DNAzol ® reagent according to the manufacturer's instructions with the following modifications for homogenization and lysis steps. WCR abdomens were removed with micro scissors and remaining body parts were placed in 1.5 mL tubes. Each sample was homogenized with disposable microtube pestles in 980 μL of DNAzol and 10 μL of PolyAcryl carrier. Homogenates were treated with 10μL of RNase A and placed in a thermomixer (Thermomixer 5350 Mixer, Eppendorf AG, Hamburg, Germany) at 37 °C. After 1 hour, each sample received 8 μL of proteinase K and was incubated at 55 °C for one hour in the thermomixer. Tubes with the resulting mixture were then left on the laboratory bench for 3 h at room temperature and processed as recommended for DNA isolation.

Polymerase chain reactions (PCR) were performed in a 50 μL final reaction volume containing 2.0 μL of template DNA, 1u of GoTaq® Flexi DNA polymerase, 1× Colorless

GoTaq® Flexi buffer, 0.2 mM dNTP, 1.5 mM $MgCl_2$ and 0.2 μM of each primer. The PCR temperature profile for each fragment included an initial heating step at 95 °C for 2 min, followed by 35 cycles of 94 °C for 30 s, annealing temperature for 90 s and 72 °C for 1 min, and a final extension of 60 °C for 30 min. The forward (5'-GGTTTTCAGATAATGTAGATAG-3') and reverse (5'-TTCCCAACCACCACATTTTT-3') primers were used with an annealing temperature of 54 °C to amplify a ~350 bp region around the *kdr* locus L1014. Also, forward (5'-ATGGAGGCATGTTGTCGAGA-3') and reverse (5'-GCCACGAAAGACCGAAAGAA-3') primers were used with an annealing temperature of 65 °C to amplify a ~530 bp region containing both M918 and T929 *kdr* loci. Primers were designed in Primer3web version 4.0.0 (Koressaar and Remm 2007, Untergasser et al. 2012). A WCR genome under development and not yet publicly available was used as the template for primer design. To locate the *kdr* polymorphic sites, sequences extracted from a WCR sodium channel contig were aligned to the sodium channel sequence of housefly *Musca domestica* L. (*Vssc1*) deposited in GenBank (Acession No: AAB47604). DNA concentration and quality before and after PCR were determined by spectrophotometry using the Nanodrop 2000 (Thermo Scientific™, Waltham, MA). PCR products were analyzed by 1.3% agarose gel electrophoresis, purified with QIAquick PCR Purification Kit and sequenced with the Applied Biosystems (ABI) 3730 DNA Analysis Instrument (Life Technologies, Grand Island, NY). Reads were quality trimmed with pregap4 v1.6-r and assembled by gap4 v4.11.2-r using PuTTY for secure remote shell access and Xming X11 display server for Microsoft Windows operating system. The consensus sequences were aligned and mapped to a scaffold of the WCR sodium channel gene using Geneious Basic 5.6.7 (Kearse et al. 2012), and screened for targeted *kdr* polymorphisms.

Enzyme activity of pyrethroid-resistant WCR populations

Enzyme preparation

In 2017, the activity of P450s, esterases and glutathione S-transferase were compared in five WCR adult populations. Three populations were pyrethroid-resistant collected from Keith Co., NE 8-14 Km apart from each other (R-Field1, R-Field2 and R-Field3). One was the ninth generation of R-Lab selected for bifenthrin resistance. A population collected from Saunders Co., NE (S-Field) was included as pyrethroid-susceptible control. All field populations were collected in 2016 and reared in the lab for one generation prior to testing. Two experiments were performed with three biological replicates of ten WCR adults (48h-old and 1:1 sex ratio) from each population. Whole body preparations were used in the first experiment whereas only WCR abdomens were used in the second. Each replicate was homogenized on ice with a Polytron homogenizer (Brinkmann Instruments, Westbury, NY) in a Teflon glass Potter-Elvehjem-type tube with 1.3 mL of ice-cold 0.1M Tris-HCl homogenization buffer (pH 7.8) containing 10 mM $MgCl_2$, 100 mM $NaCl_2$, 0.1 mM dithiothreitol, 1mM phenylthiourea and 10% v/v glycerol. The homogenates were transferred into 1.5 mL tubes and centrifuged for 20 min at 4 °C and 10 000 *g*. The supernatants were transferred into new 1.5 ml tubes. An aliquot of 40 μL from each enzyme preparation was diluted 5-fold in 0.1 M Tris-HCl homogenization buffer for both enzyme activity measurement and protein determination. Protein concentration for all preparations was determined with Pierce™ BCA assay kit following manufacturer's instructions and using bovine serum albumin standards.

Microplate assays

Activities of P450-dependent demethylation, esterase and glutathione S-transferase were measured (30s intervals) using a microplate spectrophotometer (PowerWave™ HT, BioTek® Instruments, Inc., Winooski, VT) and model substrates in 96-well sterile plates (Corning® Costar®, Corning, NY, Cat No. CLS3595). Protocols were adapted from methods developed previously (Rose et al. 1995, Yang et al. 2004). The P450 substrate solution was prepared using the homogenization buffer to a final concentration of 2 mM p-nitroanisole and 0.05M Tris-HCl. Reaction mixtures contained 90 μL of non-diluted enzyme preparation and 100 μL of substrate solution per well. The reaction was initiated by the addition of 10 μL of a NADPH regenerating system (0.25 mM $NADP^+$, 2.5 mM D-Glucose 6-phosphate, 1 u of glucose-6-phosphate dehydrogenase) after a 3 min incubation period at 30 °C. The absorbance of product p-nitrophenol was read at 405 nm and 30 °C for 15 min. For the esterase assays, 10 μL of the 5-fold diluted enzyme and 190 μL of substrate solution (5.26 mM p-nitrophenyl acetate, 0.05M Tris-HCl) were added to each well and p-nitrophenol absorbance read at 405 nm and 30 ºC for 4 min. Both P450 *O*-demethylation and esterase activities were determined using the extinction coefficient of 18 mM^{-1} cm^{-1}. Glutathione S-transferase substrate solution was prepared with the homogenization buffer adjusted for a pH 7.4 and to a final concentration of 1.3 mM 1-Chloro-2,4-dinitrobenzene, 6 mM L-Glutathione reduced, and 0.05 M Tris-HCl. Plates received 10 μL of diluted enzyme and 190 μL of substrate solution. The absorbance of S-(2,4-dinitrophenyl) glutathione was measured at 340 nm, 30 °C for 15 min, and the activity of glutathione S-transferase calculated using the extinction coefficient of 9.6 mM^{-1} cm^{-1}. Three technical replicates were used in all microplate assays. Enzyme activities were subjected to analysis of variance in completely randomized experimental design followed by Fisher's least significant difference procedure for comparison of treatment means at significance level $\alpha = 0.1$.

In-gel esterase activity

The 5-fold diluted homogenates freshly prepared from WCR whole bodies was also used for in-gel esterase activity assays adapted from Wright et al. (2000) and Thangthaeng et al. (2011). Sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS-PAGE) was performed in a vertical electrophoresis chamber (Bio-Rad Protean II, Richmond, CA) using 4-15% Mini-PROTEAN TGX Precast Gel (Bio-Rad Laboratories, Hercules, CA, Cat No. 4561086) and 1× Tris Glycine/SDS buffer (25 mM Tris, 192 mM glycine, 0.1% SDS). Individual wells were loaded with 20 μL solution containing 10 μg of total protein, 6% v/v sucrose and 3 μL of Bio-Rad native sample buffer. Gels were run at 4 ºC, 90 V for 15 min and then at 110 V for 1 h. Following SDS-PAGE, gels were incubated at room temperature for 30 min in 3% Triton™ X-100 solution, rinsed with ultrapure water and then incubated at 40 ºC for 20 min in 100ml staining solution of 50 mM Tris-HCl (pH 7.4) containing 50 mg α- or β-naphthyl acetate dissolved in 1 mL ethanol, and 50 mg of solid Fast blue RR salt. Upon development of visible bands, gels were briefly rinsed with ultrapure water and the reaction stopped by fixing the gel in a solution of 50% v/v methanol and 10% v/v acetic acid.

Insecticide synergism

Synergism bioassays were performed comparing the ninth adult generation of the bifenthrin selected WCR lab population (R-Lab) and a pyrethroid-susceptible WCR population purchased from French Agricultural Research, Lamberton, MN (S-Lab2). After a 30 s anesthetization in CO_2, mixed-age WCR beetles were topically treated on the ventral abdomen with 1 μL acetone solution containing either 2 μg of PBO or 0.2 μg of DEF known to be inhibitors of P450's and esterases, respectively. A solution of acetone-only was used on control groups. After 1.5 h, treated beetles were transferred to glass vials pre-coated with increasing concentrations of either bifenthrin or dimethoate active ingredients. Triplicates of six to eight insecticide concentrations were used and each vial received ten WCR adults in an even sex ratio. All treatments were maintained at a temperature of 23 ± 1 °C and 13 ± 1 h photophase. WCR mortality was recorded at 48h after infestation and data analyzed with a probit link function in POLOPlus-PC software. Resistance ratios (RR_{50}) and correspondent 95% confidence intervals (95%CI) were estimated in POLOPlus-PC dividing the estimated LC_{50}s of R-lab by the estimated LC_{50} of S-Lab2 within each synergist and insecticide combination (Robertson et al. 2007). The relative percent synergism ($R\%S_{50}$) was calculated according to methods described previously (Brindley and Selim 1984), which uses the logarithm of LC_{50}s estimated by probit analysis and scale the synergistic effect that occurred in each population relative to the maximum synergistic effect expected.

Realized heritability of WCR bifenthrin resistance

In the summer of 2014, 500 WCR adult males collected in Perkins County, NE and confirmed to be pyrethroid-resistant were crossed with 500 non-diapausing WCR virgin females purchased from Crop Characteristics, Inc., Farmington, MN. The cross was performed to obtain a non-diapausing WCR offspring (R-Lab) that would carry alleles conferring pyrethroid resistance and serve as a base population for laboratory selection. Non-diapausing females were chosen for the cross because it has been reported that the diapause characteristic arises mainly from a maternal contribution (Branson 1976, Krysan et al. 1977, Krysan 1978).

The resulting population (R-Lab) was maintained under continuous rearing conditions (Wangila et al. 2015) in the Department of Entomology of the University of Nebraska-Lincoln. The second, fourth, sixth and seventh adult generations were selected for pyrethroid resistance by exposure to glass scintillation vials (Wheaton™, Thermo Fisher Scientific Inc., Waltham, MA, Cat. No. 03-340-25N) treated with a pre-established bifenthrin diagnostic concentration (LC_{99}) (Pereira et al. 2015). Vials were also treated with increasing bifenthrin concentrations to perform concentration-response bioassays and estimate the susceptibility of the fourth and eighth R-Lab adult generations. An analytical standard of bifenthrin diluted in acetone was used in all treatments and controls consisted of acetone-only treated vials.

Ten unsexed WCR adults were individually transferred to treated vials at 48h post-emergence and before mating. All treatments were maintained at a temperature of 23 ± 1 °C and 13 ± 1h light period and mortality was recorded after 24h of exposure. Insects that did not respond to prodding or were unable to walk consistently when placed ventral side down were considered dead. WCR adults surviving the LC_{99} of bifenthrin were maintained under the same lab rearing procedure. Mortality data collected from the fourth and eight generation of R-Lab concentration-response bioassays were analyzed by Probit analysis in POLOPlus-PC LeOra Software LLC (Finney 1971, Russell and Robertson 1979, LeOra 1987). Slopes and LC_{50} values were used to calculate the realized heritability of bifenthrin resistance (h^2) and the number of generations required for a 10-fold increase in LC_{50} (G) following methods previously described (Tabashnik 1992).

Results

Screening for WCR kdr mutations

WCR populations were screened for L1014, T929, and M918 *kdr* para-homologous mutations in the voltage-gated sodium channel gene (Figure 1). However, relative to the pyrethroid-susceptible population S-Lab1, no mutations were found for the targeted loci in any of the pyrethroid-resistant WCR populations tested (R-Lab, R-Field1, and R-Field3).

Enzyme activity of pyrethroid-resistant WCR populations

Significant enzyme activity differences were observed in WCR populations (Fig 2). All pyrethroid-resistant WCR populations tested (R-Field1, R-Field2, R-Field3, and R-Lab) showed a significantly higher activity of P450-dependent *O*-demethylation than the pyrethroid-susceptible population S-Field (Fig 2A). In addition, the *O*-demethylation level was higher in field-derived populations R-Field2, R-Field3 than in the lab-derived resistant population R-Lab (Fig 2A).

Relative to pyrethroid-susceptible S-Field, whole-body esterase activity using p-nitrophenyl acetate was also significantly higher in pyrethroid-resistant WCR field populations R-Field1, R-Field2 and R-Field3, whereas R-Lab was not statistically different (Fig 2C). The whole-body esterase activity pattern observed for the WCR populations tested (Fig 2C) was consistently similar to that observed in WCR abdomen only (Fig 2D). Activity of glutathione S-transferase in whole-body homogenates towards 1-Chloro 2,4-dinitrobenzene was not significantly different among WCR populations (Fig 2B).

The in-gel esterase activity against α-/β-naphthyl acetate substrates (Fig 3) did not differ among WCR populations as clearly as the microplate assays using p-nitrophenyl acetate (Fig 2). α-naphthyl acetate provided a better esterase activity visualization than the β-isomer and captured a faint uppermost esterase band that was only present in the pyrethroid-resistant WCR populations (Fig 3). Also, this uppermost esterase band seemed to be more active in R-Lab than in the pyrethroid-resistant field WCR populations R-Field1, R-Field2, and R-Field3 (Fig 3).

Insecticide synergism

Both WCR populations tested (R-Lab and S-Lab2) presented increased susceptibility to bifenthrin and dimethoate when the insecticide synergists PBO and DEF were used (Table 2). PBO reduced bifenthrin LC_{50} by ~4-fold for R-Lab and ~15-fold for S-Lab2 providing a higher relative percent synergism ($R\%S_{50}$) for the later

(59.52%) than for the first (29.03%). The lower bifenthrin R%S$_{50}$ observed for R-Lab under PBO treatment reflected in a calculated bifenthrin RR$_{50}$ that significantly changed from 6.36- to 26.16-fold. The synergist DEF reduced bifenthrin LC$_{50}$ ~3-fold for both populations tested with estimated R%S$_{50}$s of 39.95% for R-Lab and 31.52% for S-Lab2. Bifenthrin RR$_{50}$s estimated for either untreated or DEF-treated R-Lab were not significantly different from each other. In dimethoate bioassays, either PBO or DEF provided a LC$_{50}$ reduction of ~2-fold for both WCR populations tested. Confidence intervals of dimethoate RR$_{50}$s estimated for R-Lab under either PBO or DEF treatments were not significantly different than the correspondent untreated R-Lab control. However, PBO and DEF R%S$_{50}$s were higher for R-Lab (41.73 and 26.79%, respectively) than for S-Lab2 (26.34 and 19.07%, respectively).

Realized heritability of WCR bifenthrin resistance

The laboratory selection experiment of WCR bifenthrin resistance provided all necessary parameters for realized heritability (h^2) estimation (Table 1). For a 0.61 selection intensity (i) with a phenotypic standard deviation ($\boldsymbol{\sigma_p}$) of 0.41, the mean percentage surviving selection (p) was 57.92 and mean selection differential per generation (S) was 0.25. Based on three generations of laboratory selection and a 0.14 response to selection (R), the estimated h^2 of R-Lab bifenthrin resistance was 0.58. The number of generations required for a 10-fold increase in bifenthrin LC$_{50}$ (G) was estimated to be 6.7.

Discussion

Field evolved WCR pyrethroid-resistance has been under investigation since 2014, but the mechanisms of the resistance trait are still unclear (Pereira et al. 2015, 2017, Souza 2019b, 2019a). Although it was suggested that target-site insensitivity was possibly part of the WCR pyrethroid-resistance mechanism, no point mutation was found in the present study at previously identified locations associated with *kdr* resistance in Colorado potato beetle and other insect species (Rinkevich et al. 2012, Dong et al. 2014). DNA-seq results collected here suggest that if there is any *kdr* mutation present in pyrethroid-resistant WCR, it would represent a novel mutation not previously identified within Chrysomelidae. A thorough screen of the voltage-gated sodium channel gene in pyrethroid-resistant WCR could potentially identify other *kdr* mutations associated with the resistance trait.

Previous research also suggested that enhanced metabolism could be contributing to WCR pyrethroid resistance (Pereira et al. 2017, Souza 2019b), and this study confirmed higher P450 and esterase activity in pyrethroid-resistant WCR populations. The fact that P450-dependent demethylation and esterase activity observed in the laboratory selected WCR population R-Lab were not as high as in pyrethroid-resistant field populations may indicate that some P450 and esterase genes could have been lost during introgression into a non-diapause background and selection process changing the pool of genes selected. Examining differences between lab-selected and field-derived DDT-resistant *Drosophila* populations over-transcribing *Cyp6g1*, researchers found that continuous laboratory selection can co-select other P450 genes (Brandt et al. 2002, Seong et al. 2017). Furthermore, if the original gene is removed from the population by population cross and backcross before selection, different P450 genes can be selected (Le Goff et al. 2003). Differences in expression of P450 genes were also observed in other insect species when comparing lab-selected and field-derived pyrethroid-resistant populations (Yang et al. 2006), including up- and down-regulation of P450 genes (Yang and Liu 2011).

It is also possible that isoenzymes with less specificity for the substrates used in the microplate assays could have been selected in the R-Lab populations. For example, conflicting results when using p-nitrophenyl acetate and α-/β-naphthyl acetate substrates to measure esterase activity were reported previously (Montella et al. 2007). In fact, the in-gel enzyme activity assay performed in this study with α-naphthyl acetate might suggest that not only an esterase isozyme is active only in pyrethroid-resistant WCR populations, but also that it is more active in the laboratory selected population R-Lab than in field populations. Multi-gene enzyme systems such as P450s and esterases exist in living organisms with differing specificities for endogenous substrates. These enzymes might not be discriminated in assays using traditional substrates and may require newer substrates that more closely mimic endogenous substrates of these enzymes as well as a complementary molecular investigation (ffrench-Constant et al. 2004, Montella et al. 2012, Stitt and Gibon 2014). Application of antibody techniques (e.g. ELISA) and more complex enzyme kinetic analyses providing functional information about proteins (e.g. k_{cat}, K_m and V_{max} values) could be further used to determine if differences in enzyme activity were due to properties of the enzyme itself or due to differing amounts of enzyme produced by WCR populations (Schilder et al. 2011, Stitt and Gibon 2014). Previous insecticide lab bioassays indicated that the level of pyrethroid-resistance (RR_{50}s) among all resistant WCR populations tested here was similar (Souza 2019b), which not only reinforces the possible involvement of multiple enzyme systems, but also that *kdr* mutation(s) could still be an important contributor to WCR pyrethroid resistance.

The compounds DEF and PBO are widely used as insecticide synergists due to their ability to inhibit esterase and P450 detoxification systems, respectively (Metcalf 1967). Both bifenthrin and dimethoate LC_{50}s were reduced in the lab selected WCR population (R-Lab) after pre-treatment with PBO and DEF suggesting that correspondent enzymes inhibited may be contributing to both bifenthrin and dimethoate reduced toxicity observed previously in the same population (Souza 2019b). Nevertheless, it is important to remember that synergists used are not completely specific to a single enzyme class and can provide both inhibition and induction depending on the dose administered and target species population (Scott et al. 1998, Snoeck et al. 2017). For example, DEF was shown to not inhibit carboxylamidase in *Spodoptera frugiperda* (Smith) larvae (Yu and Nguyen 1998) and to act as an inhibitor of P450s in *Blatella germanica* (L.) (Sanchez-Arroyo et al. 2001). Furthermore, PBO was shown to act as an inhibitor of esterases (Young et al. 2005, 2006, López-Soler et al. 2011) and to induce expression of several P450s, including those from the CYP6 family usually implicated in conferring resistance in insect pests (Daborn et al. 2002, Amichot et al. 2004, Willoughby et al. 2007, Chiu et al. 2008, Müller et al. 2008, Puinean et al. 2010, Zhu et al. 2010, Chan et al. 2014, Zimmer et al. 2017).

Higher PBO synergism provided in the susceptible population during bifenthrin bioassays suggests a more pronounced enzyme inhibition in that population, which was previously observed in synergism bioassays performed with other insect species (Huang et al. 2010, Malek Mohamadi et al. 2010). However, it is possible that while some enzymes were inhibited in both populations tested, other enzymes could have been somewhat induced in the lab selected population following PBO treatment as a compensation strategy to minimize the effect of reduced enzyme activity (Chan et al. 2014, Snoeck et al. 2017). For example, Zimmer et al., (2017) showed that exposing a pyrethroid-resistant population of whitefly *Bemisia tabaci* (Gennadius) to PBO+cypermethrin mixture increased its susceptibility to cypermethrin (lower the LC_{50} values), but also upregulated the expression of the P450 gene *Cyp6cm1*. RNA-seq analysis following treatment with synergists could possibly clarify their effect on WCR genome-wide transcription.

The laboratory selection of a non-diapausing pyrethroid-resistant WCR population and realized heritability (h^2) estimation performed in this study was a pilot investigation that suggests that bifenthrin resistance phenotypic variance is due to genetic factors, and that a substantial increase in WCR resistance could be expected after ~7 generations of insecticide exposure. The value of h^2 is not constant as it tends to decline once homozygotes are accumulated after selection and variation becomes fixed (Johnson 1979). Also, the h^2 estimate does not necessarily apply to other WCR populations since heritability is a population parameter that depends on population specific factors such as allele frequencies under defined insecticide selection intensities (Falconer 1989, Shi et al. 2015). The cross between a non-diapause susceptible and a field-derived resistant WCR population may have changed the initial frequency of resistant alleles in the selected population thereby impacting the heritability estimate. A more rigorous study involving simultaneous selection of multiple WCR populations could provide the estimation of errors and confidence intervals associated with the heritability parameter. However, the h^2 estimated can be used to generate predictions about WCR response to bifenthrin resistance selection and provides evidence of the potential WCR pyrethroid resistance evolution.

We conclude that increased P450s and esterase activity in pyrethroid-resistant WCR are likely part of the resistance mechanism along with *kdr* sodium-channel mutation(s) not previously observed in Chrysomelidae. Additional work is needed to investigate other potential *kdr* sites in the sodium channel gene of pyrethroid-resistant WCR and to also identify the P450's and esterase isozymes expressed differently in pyrethroid-resistant WCR populations. High-Throughput RNA-Sequencing in progress will significantly contribute to the molecular characterization of WCR pyrethroid resistance (see Chapter 5). Our pilot analysis of WCR selection for resistance suggests that WCR has substantial potential for achieving increasing pyrethroid resistance levels in the field within a relatively short period of time. This reinforces the importance of considering WCR resistance management strategies within IPM programs, especially in areas of the US western Corn Belt where WCR pyrethroid resistance was confirmed.

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Tables and Figures

Table 1. Estimation of realized heritability (h^2) for bifenthrin resistance in a laboratory selected WCR population.

No. of generations selected (n)	Mean selection response per generation			Mean selection differential per generation						h^2
	Initial log LC_{50}	Final log LC_{50}	R	p	i	Initial slope	Final slope	(σ_p)	S	
3	0.01	0.44	0.14	57.92	0.61	3.33	1.58	0.41	0.25	0.58

i = selection intensity; σ_p = phenotypic standard deviation; p = mean percentage surviving selection; S = mean selection differential per generation; R = response to selection

Table 2. Susceptibility of pyrethroid-resistant (R-Lab) and pyrethroid-susceptible (S-Lab2) WCR adult populations to bifenthrin and dimethoate active ingredients following or not topical treatment with insecticide synergists PBO and DEF.

Insecticide	Population	Synergist	N[a]	Slope±SE	LC_{50} (95% CI) [b]	χ^2 (d.f)	$R\%S_{50}$[c]	RR_{50} (95% CI)[c]
Bifenthrin	**S-Lab2**	**None**	149	3.24±0.43	0.61 (0.50-0.73)	2.30 (3)	-	-
		PBO	240	2.04±0.27	0.04 (0.03-0.05)	2.07 (5)	59.52	
		DEF	180	3.22±0.48	0.26 (0.20-0.32)	1.76 (4)	31.52	
	R-Lab	**None**	152	2.13±0.27	3.89 (2.89-5.14)	1.38 (3)	-	6.36 (4.54-8.90)
		PBO	210	2.60±0.44	1.03 (0.68-1.38)	2.83 (5)	29.03	26.16 (16.92-40.30)
		DEF	212	3.11±0.44	1.32 (1.04-1.63)	1.16 (5)	39.95	5.16 (3.76-7.07)
Dimethoate	**S-Lab2**	**None**	150	4.42±0.65	0.35 (0.30-0.41)	1.26 (3)	-	-
		PBO	181	3.66±0.49	0.21 (0.17-0.25)	0.37 (3)	26.34	
		DEF	180	5.17±0.80	0.25 (0.20-0.32)	3.06 (4)	19.07	
	R-Lab	**None**	359	3.72±0.54	1.46 (1.18-1.72)	0.21 (4)	-	4.17 (3.26-5.33)
		PBO	360	2.81±0.36	0.65 (0.46-0.89)	1.08 (4)	41.73	3.16 (2.40-4.16)
		DEF	360	2.47±0.29	0.91 (0.73-1.12)	1.12 (4)	26.79	3.60 (2.62-4.94)

[a] number of insects tested; [b] μg a.i/vial; [c] relative percent synergism;

Sodium-channel *kdr* polymorphic sites [a]

	L1014	T929	M918
	5′		3′
Amino acid	**L V V L N G I**	**L V F T L N G**	**T R G M I S I**
mRNA	**UGAAUGGUGUUCUAAUGGUUA**	**GUCGUGUUUACAAUCCAAUGG**	**UCAAGAUGGGUAAUAACUCUA**
S-Lab1_1	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
S-Lab1_2	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
S-Lab1_3	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
S-Lab1_4	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
S-Lab1_5	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
S-Lab1_6	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
R-Lab_1	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
R-Lab_2	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
R-Lab_3	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
R-Lab_4	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
R-Lab_5	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
R-Lab_6	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
R-Field1_1	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
R-Field1_2	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
R-Field1_3	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
R-Field1_4	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
R-Field1_5	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
R-Field1_6	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
R-Field3_1	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
R-Field3_2	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
R-Field3_3	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
R-Field3_4	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
R-Field3_5	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT
R-Field3_6	ACTTACCAC**AAG**ATTACCAAT	CAGCACAAA**TGT**TAGGTTACC	AGTTCTACC**CAT**TATTGAGAT

[a] *kdr* sites are numbered according to the amino acid sequence of Vssc1 deposited in GenBank (Accession No: AAB47604)

Figure 1. Screening of pyrethroid-resistant (R-) and pyrethroid-susceptible (S-) WCR populations for *kdr* mutations. Data shows partial DNA-seq alignment of PCR product sequences amplifying three *kdr* loci (L1014, T929, and M918).

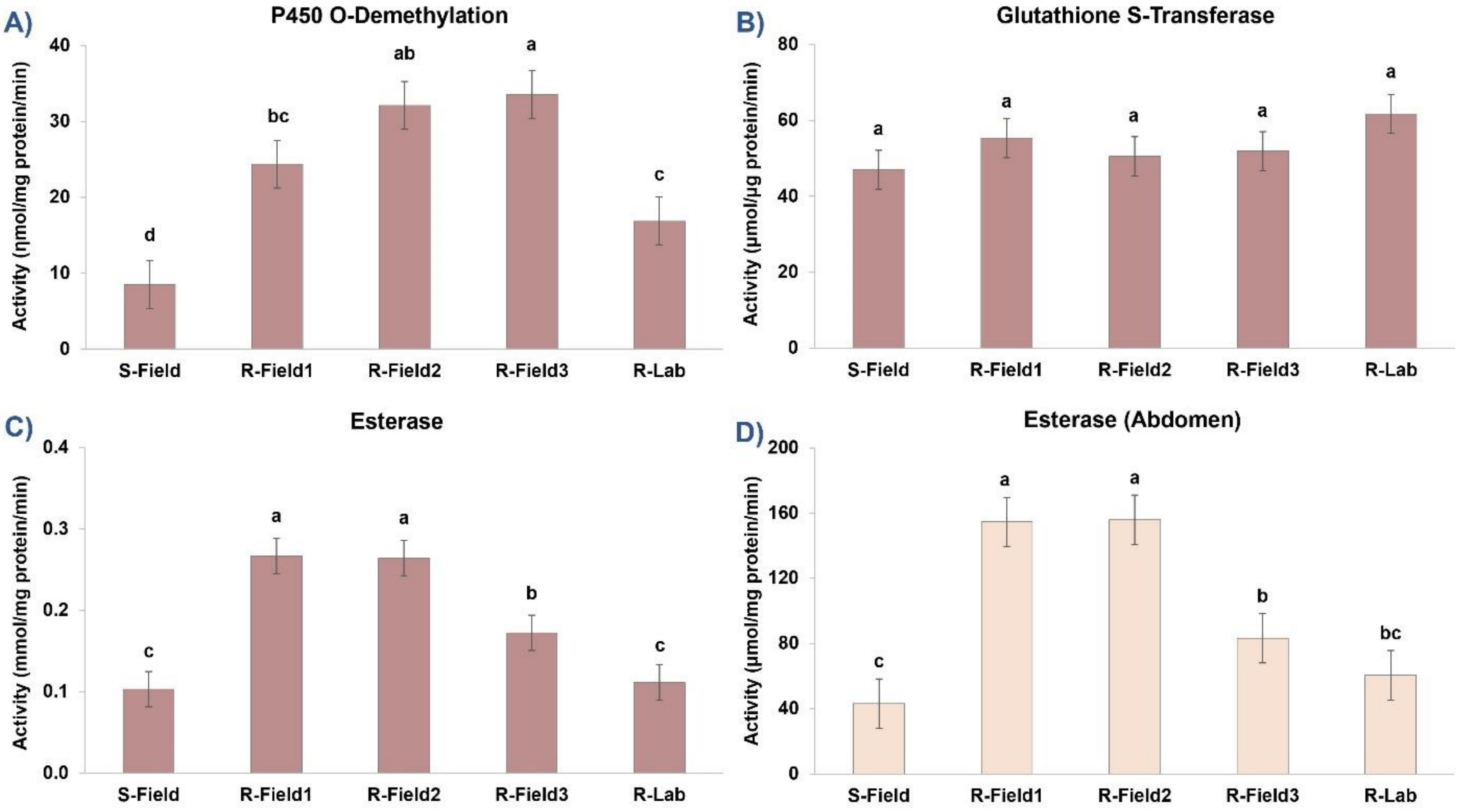

Figure 2. Enzyme-specific activity of WCR populations. (A) *O*-Demethylation by cytochrome P450 monooxygenases $F_{4,10}$=11.08, p=0.0011; (B) Glutathione S-transferase $F_{4,10}$=1.17, p=0.3799; (C) Esterase $F_{4,10}$=13.44, p=0.0005; (D) Esterase (abdomen) $F_{4,10}$=12.27, p=0.0007. Means followed by the same letter were not statistically different at the significance level α=0.1.

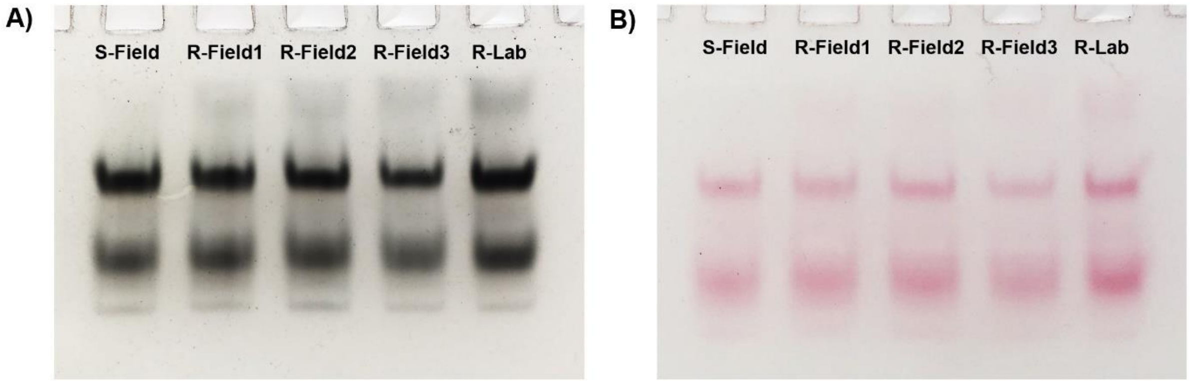

Figure 3. In-gel (SDS-PAGE) whole body esterase activity of WCR populations for (A) α-naphtyl acetate and (B) β–naphtyl acetate.

CHAPTER 5. MOLECULAR CHARACTERIZATION OF WESTERN CORN ROOTWORM PYRETHROID RESISTANCE

Introduction

Estimates of more than 1 billion dollars a year have been associated with yield losses and management costs of the western corn rootworm (WCR), *Diabrotica virgifera virgifera* LeConte (Coleoptera: Chrysomelidae), in the United States (US) (Sappington et al. 2006, Dun et al. 2010, Wechsler and Smith 2018). Without proper adoption of resistance management and integrated pest management (IPM) practices, populations of this major pest of maize (*Zea mays* L.) have been continuously adapting to control tactics used thus far (Gray et al. 2009). Particularly in the US western Corn Belt, limited rotation of WCR management strategies and increased reliance on pyrethroid aerial applications have been imposing high selection pressure on WCR populations (Wangila et al. 2015, Archibald et al. 2018). As a result, several WCR populations in southwestern Kansas and Nebraska have developed resistance to pyrethroids significantly impacting the performance of major insecticide formulations used for WCR control (Pereira et al. 2015, Souza 2019a, 2019b).

The toxicity of pyrethroids depends mainly on the level of exposure and their ability to bind and disrupt voltage-gated sodium channels of animal nerves, although information has been published on secondary target sites like voltage-gated calcium and chloride channels (Ray et al. 1996, Hildebrand et al. 2004, Symington and Clark 2005, Breckenridge et al. 2009, Soderlund 2011). Mutations in the insect voltage-gated sodium channels can lead to reduced sensitivity of the nervous system to pyrethroid insecticides, and consequently to so called knockdown resistance (*kdr*) (Soderlund and

Knipple 2003, Soderlund 2011). A variety of nonsynonymous amino acid substitutions in the sodium channel gene have been identified as *kdr* mutations conferring pyrethroid resistance to insects (Dong et al. 2014). Since pyrethroids and DDT (dichloro-diphenyl-trichloroethane) share the same target site, *kdr* mutations may also provide cross-resistance between these two insecticides (Williamson et al. 1993, Chandre et al. 1998, Schuler et al. 1998, Brengues et al. 2003, Enayati et al. 2003, Rodríguez et al. 2005).

The amount of insecticide that directly interacts with sodium channels is significantly lower than the total insect exposure due to insects' elaborate system of enzymes such as cytochrome P450 microsomal monooxygenases (P450s), esterases and glutathione S-transferases that metabolize and detoxify xenobiotic compounds (Yu 2014). A number of instances of pyrethroid resistance in arthropods are related to enhanced metabolism involving esterases (Dowd et al. 1987, Sogorb and Vilanova 2002, Young et al. 2005, 2006, Kamita et al. 2016), P450s (Lee and Scott 1989, Pittendrigh et al. 1997, Kasai and Scott 2000, Nikou et al. 2003, Zhu and Snodgrass 2003, Yang et al. 2006, Djouaka et al. 2008, Bariami et al. 2012, Stevenson et al. 2012) and glutathione S-transferase (Fragoso et al. 2003, 2007, Lumjuan et al. 2011, Chigure et al. 2018).

It was previously reported that WCR resistance to pyrethroids was not only partially suppressed by inhibitors of esterases and P450s but also provided WCR cross-resistance to DDT (Pereira et al. 2017). Furthermore, the activity of cytochrome P450 monooxygenases and esterases measured in microplate enzyme kinetic assays was found to be higher in pyrethroid-resistant WCR populations (Souza 2019c). Collectively, these investigations suggest that both enhanced metabolism and target site insensitivity to pyrethroids (*kdr* mutations) may be mechanisms of WCR pyrethroid resistance (Pereira et al. 2017, Souza 2019c). The current study was conducted to test this hypothesis and to characterize the differential gene expression of pyrethroid-resistant WCR individuals.

Methods

WCR populations

Four WCR adult populations were tested throughout this study. In 2016, WCR beetles were collected from Saunders County, NE (S-Field) and Keith County, NE (R-Field) representing pyrethroid-susceptible and pyrethroid-resistant field populations, respectively. A pyrethroid-resistant lab population (R-Lab) that was originally collected from Perkins County in 2014 and then reared in a non-diapause background for nine generations under adult bifenthrin selection (Souza 2019c) was also included and compared to a non-diapausing control population purchased from Crop Characteristics, Inc., Farmington, MN (S-Lab). Both field collected and lab populations were reared simultaneously for one generation prior to testing using standard lab rearing procedures (Wangila et al. 2015). All populations were maintained under laboratory conditions of 23 ± 1 °C and 13 ± 1 h photophase in the Department of Entomology, University of Nebraska, Lincoln, NE. In 2017, WCR beetles (48h-old) were collected from rearing cages, transferred to individual Eppendorf tubes, flash-frozen in liquid nitrogen and stored in a -80ºC freezer until use for RNA and DNA extractions.

RNA extraction and library preparation

Total RNA was individually extracted from ten whole adults of each WCR population tested (1:1 sex ratio) using a Qiagen RNeasy mini kit (Germantown, MD, Cat No. 74104) according manufacturer's instructions. RNA concentration and quality were determined by spectrophotometry using a Nanodrop 2000 (Thermo Scientific™, Waltham, MA) and fluorimetry using Qubit (Thermo Scientific™, Waltham, MA). Also, an Agilent 2100 Bioanalyzer (Santa Clara, CA) was used for assessment of the relative RNA Integrity Number (RINe) quality metric. Barcoded mRNA-seq libraries were prepared by polyA selection and sequenced in three lanes of Illumina HiSeq 4000 to an expected sequencing depth of ~26 million reads per sample.

Gene expression analysis

A suite of free tools provided by the national cyberinfrastructure CyVerse in the Discovery Environment (Goff et al. 2011, Merchant et al. 2016) was used for the RNA-seq analyses. Data analysis of laboratory and field populations followed the same workflow in separate pairwise comparisons. Low quality bases and Illumina adapter sequences were trimmed from paired reads using the Trimmomatic 0.36 program (Bolger et al. 2014), with the following parameters: ILLUMINACLIP:contaminants:2:30:10, LEADING:3, TRAILING:3, HEADCROP:7, CROP:138, SLIDINGWINDOW:5:20, MINLEN:50. FastQC 0.11.5 (Andrews 2016) was used to evaluate the qualities of raw and trimmed sequencing data. Trimmed reads were aligned to a WCR genome under development not yet publicly available (WCR_genome.fa) using HISAT2 2.1 (Kim et al. 2015) and transcripts assembled with

StringTie 1.3.3 (Pertea et al. 2015). A single transcript sequence was obtained using StringTie 1.3.3-merge (Pertea et al. 2016) and used to build an index file in Kallisto 0.42.3-index (Bray et al. 2016). An alignment-free transcript quantification approach was then performed for each paired-reads using Kallisto 0.42.3-quant (Bray et al. 2016) with 100 bootstrap iterations to provide a measure of the accuracy of the quantification by random resampling with replacement. Pairwise comparisons of Kallisto quantification outputs were made between pyrethroid-resistant and pyrethroid-susceptible populations using sleuth 0.29.0 package (Pimentel et al. 2017) in R 3.5.0 software (R Foundation for Statistical Computing, Vienna, Austria). A likelihood ratio test (LRT) was performed to verify goodness of fit of transcripts to the full statistical model that considers the pyrethroid resistance status as a factor. Considering a correction of p-values for type I error of false positives, i.e. false discovery rate (FDR) correction, expression levels with q-value ≤ 0.05 were determined significant. Significantly diferentially-expressed transcripts were translated into amino acid sequences using EMBOSS Transeq (https://www.ebi.ac.uk/Tools/st/emboss_transeq/) (Rice et al. 2000). Sequence similarity searches were performed for longest open reading frames (ORFs) of significant transcript sequences on BLASTp (Altschul et al. 1997) and InterPro Scan (Jones et al. 2014). Also, local protein sequence alignment between some significant transcripts were performed in EMBOSS Water (https://www.ebi.ac.uk/Tools/psa/emboss_water/) (Rice et al. 2000) with default settings (matrix:BLOSUM62; gap penalty:10; and extension penalty:0.5) to verify similarity between them.

WCR voltage-gated sodium channel gene screening

Voltage-gated sodium channel amino acid sequences from Colorado potato beetle (CPB) *Leptinotarsa decemlineata* (Say) and Asian longhorned beetle (ALB) *Anoplophora glabripennis* (Motschulsky) were used to localize homologous sequences in the WCR transcriptome. Similarity searches were performed with local tBLASTn where the CPB and ALB protein sequences available in the NCBI (Accessions: XP_023023069.1 and XP_018568941.1, respectively) were used as queries and the WCR_genome.fa was used as database. Contigs identified in tBLASTn were filtered from HISAT2 alignment *bam* files and then merged using Samtools 1.7 (Li et al. 2009) available in the Discovery Environment of CyVerse (Goff et al. 2011, Merchant et al. 2016). The resulting merged file was screened for non-synonymous nucleotide substitutions in Tablet 1.17.08.17. (Milne et al. 2013) using the visual application for tag variants. Furthermore, the sequences from CPB and ALB used earlier in tBLASTn were aligned to sequences extracted from WCR sodium channel contig and to the sodium channel sequence of housefly *Musca domestica* L. (*Vssc1*) deposited in GenBank (Acession No: AAB47604) using T-Coffee (https://www.ebi.ac.uk/Tools/msa/tcoffee/) (Notredame et al. 2000). The predictions of WCR sodium channel domain structures and transmembrane segments were performed with SMART (http://smart.embl-heidelberg.de/) (Letunic and Bork 2017), HMMER 3.2.1(https://www.ebi.ac.uk/Tools/hmmer/) (Finn et al. 2011, Potter et al. 2018) and TMHMM v.2.0 (http://www.cbs.dtu.dk/services/TMHMM/) (Krogh et al. 2001).

DNA Sanger sequencing *kdr* investigation

The location of non-synonymous substitutions found in the voltage-gated sodium channel screening, numbered L1422 and I1558 in *Vssc1*, were investigated in WCR populations in greater detail by DNA Sanger sequencing. Genomic DNA was extracted individually from ten adults (1:1 sex ratio) of each WCR population using a Qiagen DNeasy kit (Germantown, MD, Cat No. 69504) according to the manufacturer's instructions. Polymerase chain reactions (PCR) were performed in a 50 µL final reaction volume containing 2.0 µL of template DNA, 1u of GoTaq® Flexi DNA polymerase, 1× Colorless GoTaq® Flexi buffer (Promega, Madison, WI, Cat No. M8291), 0.2 mM dNTP, 1.5 mM $MgCl_2$ and 0.2 µM of each primer. The PCR temperature profile for each fragment included an initial heating step at 95 °C for 2 min, followed by 35 cycles of 94 °C for 30 s, annealing temperatures for 90 s, 72 °C for 1 min, and a final extension of 60 °C for 30 min. The forward (5'- CCTTAAACCGTCACTGGCAG-3') and reverse (5'-ACAAGCATTCACATCAGGGA-3') primers were used with an annealing temperature of 59 °C to amplify a ~493 bp region surrounding the site L1422. Also, forward (5'-TGAGCAGATGGGACGTGAAT-3') and reverse (5'-TTCGCACCACCCTAATGACT -3') primers were used with an annealing temperature of 56 °C to amplify a ~360 bp region surrounding the I1558 location. Primers were designed in Primer3web version 4.0.0 (Koressaar and Remm 2007, Untergasser et al. 2012). DNA concentration and quality before and after PCR were determined by Nanodrop 2000 (Thermo Scientific™, Waltham, MA). PCR products were analyzed by 1.3% agarose gel electrophoresis, purified with QIAquick PCR Purification Kit and sequenced by Genewiz, South Plainfield, NJ with the Applied Biosystems (ABI) 3730 DNA Analysis Instrument (Life

Technologies, Grand Island, NY). Sequences were aligned and mapped to the WCR sodium channel gene contig using Geneious Basic 5.6.7 (Kearse et al. 2012), and screened for targeted *kdr* polymorphisms

Results

RNA extraction and library preparation

All RNA samples used for library preparation were of high integrity with an average A260/A280=2.12 and RINe = 10. The Illumina HiSeq platform produced a total of 1.29 billion paired-reads of 150bp in length yielding 389,876 Mbases of a mean quality score 37.96 (91% Bases≥ Q30). An average of 32.3±0.5 (SE) million reads were produced per library. Illumina sequencing data from this study have been submitted to the NCBI BioProject (https://www.ncbi.nlm.nih.gov/bioproject) under accession number PRJNA430262. These data are also available from the NCBI Sequence Read Archive (SRA; https://www.ncbi.nlm.nih.gov/sra) under accession numbers that go from SRX3594800 to SRX3594839.

Gene expression analysis

Out of 53,929 transcripts from WCR field populations, seven were differentially expressed and expressed at a higher level in R-field compared to S-Field population (q-value ≤ 0.05) (Supplementary Table 1 and 3). Similarity searches of translated amino acid sequences predicted that three were cytochrome P450 monooxygenases (P450$_{(1\text{-}3\text{Field})}$, two were transcription factors, and one was a junctophilin (Figure 1). The transcript mean abundance of P450$_{(1\text{Field})}$, P450$_{(2\text{Field})}$ and P450$_{(3\text{Field})}$ were 9.2-, 11.8-

and 26.2-times greater in R-Field than in S-Field, respectively (Figure 1). The two transcription factor candidates were 8.5- and 23.9-times more abundant in R-Field. The mean abundance of predicted junctophilin (100% identity and query cover to either ALB or CPB in BLASTp) was 10.7-times greater in R-Field than in S-Field. No sequence similarity was found for one of the significant transcripts overexpressed in R-Field.

For pairwise comparison between laboratory populations S-Lab and R-Lab, 47,255 transcripts were analyzed and 99 exhibited significantly different expression (q-value ≤ 0.05). A total of 64 transcripts were expressed at a higher level in pyrethroid-resistant R-Lab whereas 35 were expressed at a lower level in the same population (Supplementary Table 2 and 3). Protein similarity searches suggest that ten transcripts differentially expressed in lab-derived populations were P450s ($\text{P450}_{(1\text{-}10\text{Lab})}$) (Figure 2) and for eight of them ($\text{P450}_{(1\text{-}8\text{Lab})}$), the mean abundance in R-Lab was 2.7 to 39.8 times greater than in S-Lab (Table 1). In general, functions predicted for transcripts overexpressed in R-Lab were: oxidation; hydrolysis; proteolysis; transport; DNA transcription; nervous system activity; immune response; membrane barrier; catalysis; and cell division (Table 2). Two P450s ($\text{P450}_{(9\text{-}10)\text{Lab}}$) and three enzymes also involved in oxidative metabolic processes appear to be underexpressed in R-Lab along with 13 other predicted proteins (Table 2). The mean abundance of $\text{P450}_{(9)\text{Lab}}$ and $\text{P450}_{(10)\text{Lab}}$ was 22.6 and 9.5 times lesser in R-Lab than in S-Lab, respectively (Figure 2 and Table 1). No sequence similarity was found in protein search databases for 23 significant transcripts (17 underexpressed and 6 overexpressed in R-Lab), and thus remain with unknown identity and function.

The longest and most complete P450 transcript sequences (~500 aa) differentially expressed in WCR populations were P450$_{\text{(3)Lab}}$ (499 aa), P450$_{\text{(6)Lab}}$ (499 aa) and P450$_{\text{(8)Lab}}$ (442 aa). All remaining P450 transcripts were translated into shorter amino acid sequences (<300 aa). P450$_{\text{(3)Lab}}$ presented 100% identity to P450$_{\text{(2)Lab}}$, 88.4-99.3% identity to P450$_{\text{(1-3)Field}}$ and P450$_{\text{(4-5)Lab}}$, and 36.5-51.9% identity to remaining P450 transcripts (Table 3). P450$_{\text{(6Lab)}}$ showed 98.5% identity to P450$_{\text{(10Lab)}}$ and 29.2-51.7% identity to all other P450s differentially expressed in WCR populations (Table 3). The identity between P450$_{\text{(8)Lab}}$ and all other P450 transcripts varied from 25.8 to 53.1% (Table 3). Protein search databases revealed that all P450s differentially expressed in either field-derived or lab-derived WCR populations presented >40% sequence identity to CYP6-like hits (Supplementary Table 1 and 2).

WCR voltage-gated sodium channel gene screening

Two potential non-synonymous substitutions were found in the voltage-gated sodium channel gene of some R-Lab and R-Field individuals when screening the RNA-seq reads against the WCR genome. Locations of substitutions were L1422P and I1558A in *Vssc1* (Supplementary Fig. 1), which could be *kdr* mutations not reported previously in pyrethroid-resistant insects. However, the sequencing coverage at those regions was too low to enable confirmation. Sodium channel domain structures and transmembrane segments were predicted (Supplementary Fig. 1) along a 2042 amino acid sequence for WCR (Supplementary Fig. 2).

DNA Sanger sequencing *kdr* investigation

Relative to the pyrethroid-susceptible individuals from populations S-Lab and S-Field, no mutations were found for the L1422P and I1558A loci in pyrethroid-resistant WCR. However, the 360bp PCR product covering the I1558 locus did not amplify in all WCR samples (Figure 3) and therefore fewer sequences (14 out of 40) were compared at this locus.

Discussion

This study supports the idea that constitutive enhanced metabolism is a mechanism of WCR pyrethroid resistance and suggests that P450s may play a major role in the resistance trait relative to other detoxification enzymes. Although several hydrolytic enzymes were differentially expressed in lab-derived WCR populations, P450s were the only metabolism-related proteins differentially expressed in field-derived WCR populations. In fact, nearly 50% of transcripts differentially expressed in the field-derived pyrethroid-resistant WCR population were overexpressed P450s as well as ~13% of transcripts overexpressed in the lab selected pyrethroid-resistant WCR population. Enhanced oxidative metabolism resulting from the overproduction of P450 enzymes has been commonly observed in pyrethroid-resistant arthropods (Pittendrigh et al. 1997, Kasai and Scott 2000, Zhu and Snodgrass 2003, Yang et al. 2006, Djouaka et al. 2008, Adelman et al. 2011, Bariami et al. 2012) since it accelerates the production of metabolites that are less toxic, less stable and that cannot reach the target site of action (Yu 2014).

The overexpression of P450s observed in resistant insects may be derived from gene amplification or upregulation of expression often promoted by substitutions, insertions and deletions in promoter sequences and/or regulatory loci (Li et al. 2007, Puinean et al. 2010, Bass et al. 2013). Further investigation is necessary to identify not only the mechanism behind P450s overexpression in pyrethroid-resistant WCR but also specific P450 genes involved. Most P450 proteins are ~500 amino acids long (Feyereisen 1999) and the fact that the majority of P450 transcripts differentially expressed in WCR populations were translated in ~200 amino acid sequences may indicate that they were fragments of longer sequences. Although incomplete sequences can prevent the identification of the encoding P450 genes, all P450s differentially expressed shared >40% similarity to CYP6 hits in protein search databases. Results from multiple alignments and the variable expression observed between them suggest that multiple P450 genes may be involved. Also, differences in percent identity of amino acid sequences may suggest that P450s overexpressed in the field-derived pyrethroid-resistant population are related but not necessarily the same P450 genes overexpressed in the WCR population selected for pyrethroid resistance in the laboratory. This supports previous research results that showed differences of P450-mediated *O*-demethylation comparing lab-selected and field-derived pyrethroid-resistant WCR populations in enzyme activity microplate assays (Souza 2019c).

Differences in expression of P450 genes were observed in *Helicoverpa armigera* (Hübner) when comparing lab-selected and field-derived pyrethroid-resistant populations (Yang et al. 2006), including up- and down-regulation of P450 genes (Yang and Liu 2011). Examining differences between lab-selected and field-derived DDT-resistant *Drosophila* populations over-transcribing *Cyp6g1*, researchers found that continuous laboratory selection can co-select other P450 genes (Brandt et al. 2002, Seong et al. 2017), and if the original region encompassing *Cyp6g1* is removed by population cross and backcross before selection, different P450 genes can be selected (Le Goff et al. 2003). It is possible that some P450 alleles upregulated in the pyrethroid-resistant WCR populations could have been lost in the lab-selected WCR population during introgression into a non-diapause background. Further investigations would be necessary to test this hypothesis.

Pyrethroids bind to voltage-gated sodium channels causing a delay in channel closing, and prolonged sodium inactivation (Yu 2014). Repetitive action potentials are generated across neurons finally disrupting the normal flow of information to the central nervous system. Some proteins with functions in the nervous system were also differentially expressed in the pyrethroid-resistant WCR populations tested, which could play a role in insecticide resistance trait. Junctophilin, overexpressed in the field-derived pyrethroid-resistant WCR population, is a protein commonly found in human excitable cells such as neurons where it is involved in coupling membrane neurotransmitter receptors and intracellular channels (Landstrom et al. 2014). A study showed that a junctophilin gene from fruit fly *Drosophila melanogaster* Meigen is functionally equivalent to mammal homologues and that flies with altered junctophilin expression also have marked neuronal alterations (Calpena et al. 2018). The predicted E3 ubiquitin-protein ligase and neprilysin, overexpressed in the lab-selected pyrethroid-resistant WCR populations, also play a role in the nervous system of insects. Overexpression of E3 ubiquitin-protein ligase gene in *Drosophila* glial cells was found to cause synaptic impairments and down regulation of Na+/K+ pumps (Hope et al. 2017) whereas neprilysin modulates neuronal activity, viability and survival (Bland et al. 2008, Meyer et al. 2009, Klein et al. 2013).

The number of targets differentially expressed in the R-Lab population was higher when comparing laboratory WCR populations, which may support the theory that artificial insecticide selection favors a polygenic response (Georghiou 1972, Roush and McKenzie 1987). Several hydrolytic enzymes and ABC transporters commonly associated with insecticide resistance (Devonshire and Moores 1982, Sogorb and Vilanova 2002, Zhou et al. 2004, Bariami et al. 2012, Carvalho et al. 2013) were overexpressed in the lab-selected WCR population whereas their expression does not appear to be significantly different in the field resistant population. Results found in the present study indicate that although laboratory selection of pyrethroid-resistant WCR populations is useful for predictions and investigations of resistance mechanisms, the heterogeneity and population dynamics present in the field are more likely to provide conditions for selection of rare variants corresponding to resistance (Meinke et al. 2009, ffrench-Constant 2013).

This study did not detect *kdr* mutations in pyrethroid-resistant WCR populations. However, the RNA sequencing coverage of the WCR sodium channel was too low to enable a thorough screen. Previous research found DDT cross-resistance in pyrethroid-resistant WCR (Pereira et al. 2017) and in most cases this is an indication of *kdr* mutations in the target site (Williamson et al. 1993, Pittendrigh, Reenan, et al. 1997, Martinez-Torres et al. 1999, Brooke 2008). However, overexpression of some P450s, such as *Cyp6g1* have also beenassociated with DDT cross-resistance (Daborn et al.

2001, 2002, Brandt et al. 2002, Le Goff et al. 2003). It is possible that one or more P450s overexpressed in pyrethroid-resistant WCR populations could be contributing to the DDT cross-resistance observed.

Understanding the molecular basis of WCR pyrethroid resistance is critical to implement efficient resistance management strategies and to develop protocols for resistance detection. This study revealed that P450-mediated detoxification is probably a major mechanism positively selected in pyrethroid-resistant WCR populations, which could have an important impact on the efficacy of other insecticides sharing similar metabolic pathways. WCR resistance monitoring is recommended and the P450 genes differentially expressed in this study could be further characterized and used for that purpose. A single tactic approach to manage WCR is unlikely to be sustainable and the integration of insecticides with biotechnological and cultural approaches, such as rootworm-resistant transgenic maize and crop rotation, is necessary to prolong the durability of technologies available.

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Tables and Figures

Table 1. Differential expression of P450 transcripts in pairwise comparison of lab-derived WCR populations known to be susceptible (S-Lab) or resistant (R-Lab) to pyrethroids.

P450 candidate	**Transcript ID**	**Abundance ratio** $\left. \text{R-Lab}_{(\text{TPM})} \middle/ \text{S-Lab}_{(\text{TPM})} \right.$ [a]
P450$_{(1)\text{Lab}}$	MSTRG.19112.1	39.06
P450$_{(2)\text{Lab}}$	MSTRG.63174.1	28.14
P450$_{(3)\text{Lab}}$	MSTRG.22143.1	22.32
P450$_{(4)\text{Lab}}$	MSTRG.71693.1	47.18
P450$_{(5)\text{Lab}}$	MSTRG.59366.1	39.84
P450$_{(6)\text{Lab}}$	MSTRG.36287.1	2.70
P450$_{(7)\text{Lab}}$	MSTRG.3101.1	8.71
P450$_{(8)\text{Lab}}$	MSTRG.24813.1	7.28
P450$_{(9)\text{Lab}}$	MSTRG.56151.1	0.04
P450$_{(10)\text{Lab}}$	MSTRG.66987.1	0.12

[a] TPM = mean abundance in transcripts per million (TPM) units

Table 2. Predicted identity and function of transcripts differentially expressed (q-value ≤ 0.05) in the pyrethroid-resistant laboratory population R-Lab.

Predicted function	Proteins predicted (No. of targets)	
	Overexpressed	**Underexpressed**
Oxidation	P450s (8)	P450s (2), Lysyl oxidase (1), Glyoxylate/hydroxypyruvate reductase (1), Sorbitol dehydrogenase (1)
Hydrolysis	Carboxypeptidase (1), maltase (1), beta-hexosaminidase (1), chitinase (1), aldose-epimerase (1), myrosinase (1), glycoside hydrolase (1)	Myrosinase (1), beta ureidopropionase (1)
Conjugation		Glutathione S-transferase (1)
Proteolysis	Cysteine proteinases (2)	
Transporter	ABC transporters (4), sugar transporters (2), peptide transporters (4)	
Transcription factors	Zinc finger type proteins (4), Nuclear factor NF-kappa-B p110 subunit-like (1), Transcription activator MBF2 family (1)	Zinc finger type proteins (2)
Nervous system	E3 ubiquitin-protein ligase MYCBP2 (1), neprilysin (1)	
Immune response	Coleoptericin (1), Leucine-rich repeat protein SHOC-2-like (1)	
Membrane barrier	Tetraspanin-2A (1)	
Catalysis	Uridine phosphorylase (1), Glutamine-fructose-6-phosphate aminotransferase 2 (1)	
Cell division	Protein skeletor, isoform B/C (1)	Dynactin subunit 2 (1)
Other	Reverse transcriptase (3), Laminin subunit gamma-1-like (1), Galectin (1), mucin (1)	Reverse transcriptase (2), heat shock protein beta-1 (1), elongation factor Tu (1), retrovirus-related Pol polyprotein LINE-1 (1), Alpha-tocopherol transfer protein-like (1), Asialoglycoprotein receptor 2/C-type lectin precursor (1)

Table 3. Percent identity matrix of local alignments performed for P450s differentially expressed in WCR populations.

P450 Transcripts	**Longest transcripts (>400 aa)**		
	P450$_{(3)Lab}$	**P450$_{(6)Lab}$**	**P450$_{(8)Lab}$**
P450$_{(1)Field}$	99.3	51.7	50.3
P450$_{(2)Field}$	93.7	47	45.6
P450$_{(3)Field}$	88.9	48.5	50.3
P450$_{(1)Lab}$	88.4	48.2	50.3
P450$_{(2)Lab}$	100	29.2	25.8
P450$_{(3)Lab}$	*	41.9	39.6
P450$_{(4)Lab}$	98.7	47.7	46.2
P450$_{(5)Lab}$	93.7	47	45.6
P450$_{(6)Lab}$	41.9	*	51.7
P450$_{(7)Lab}$	38.1	41.2	42.7
P450$_{(8)Lab}$	39.6	51.7	*
P450$_{(9)Lab}$	36.5	35.6	34.1
P450$_{(10)Lab}$	51.9	98.5	53.1

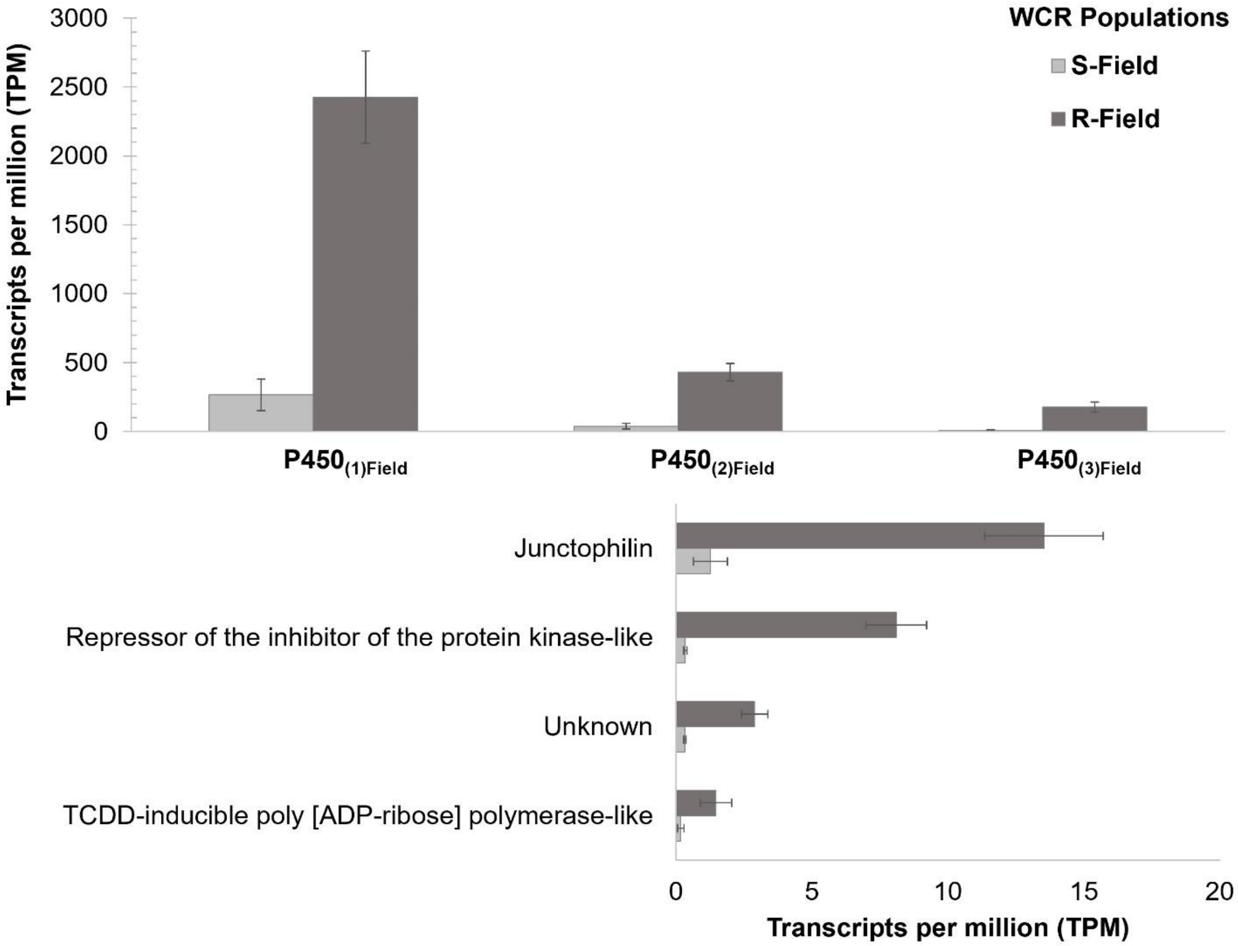

Figure 1. Differential expression of transcripts in pairwise comparison of field-derived WCR populations known to be susceptible (S-Field) and resistant (R-Field) to pyrethroids. Data shows the transcript mean abundance in transcripts per million (TPM) units ±SE and their identity predicted by protein similarity search databases.

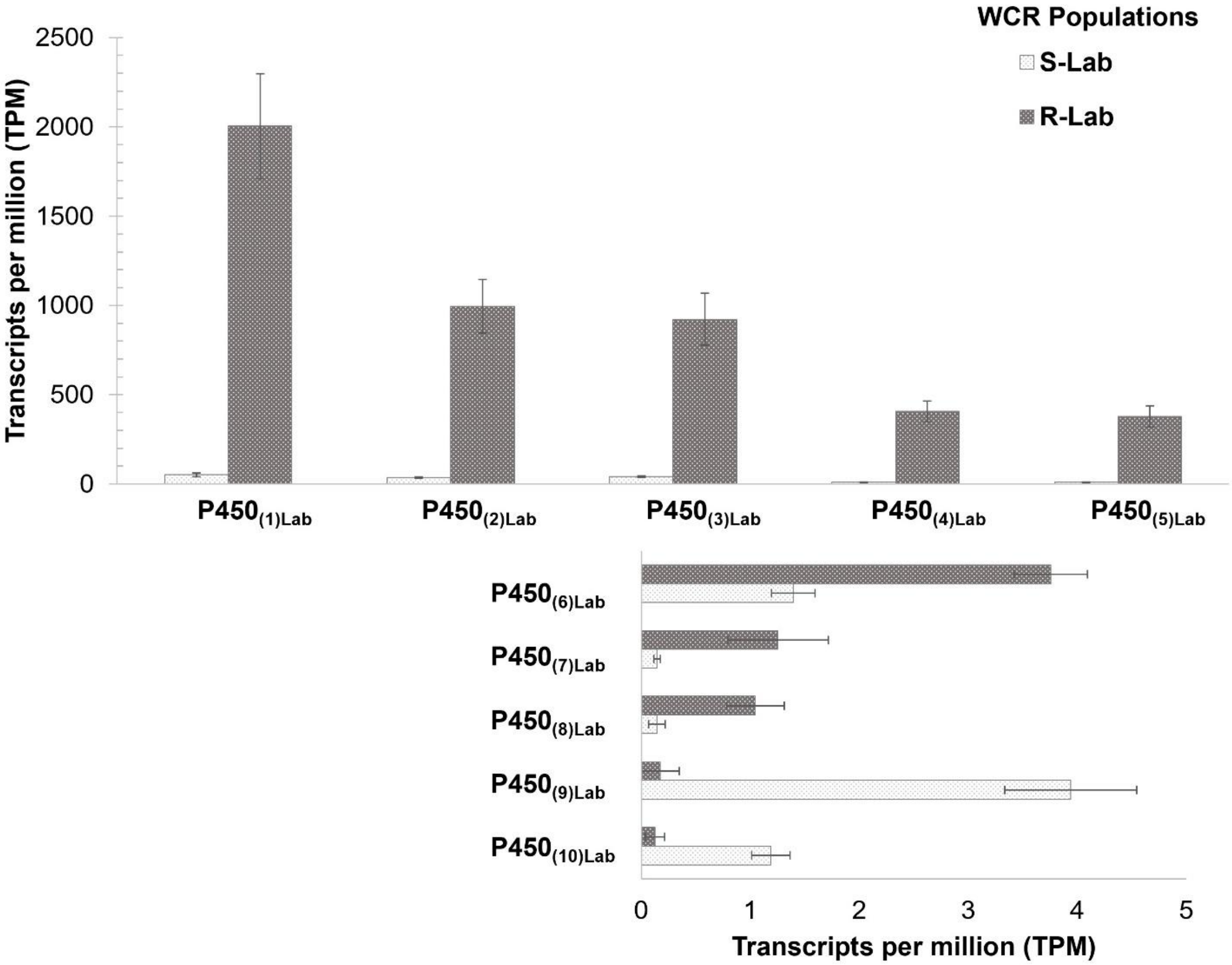

Figure 2. Differential expression of P450 transcripts in pairwise comparison of lab-derived WCR populations known to be susceptible (S-Lab) and resistant (R-Lab) to pyrethroids. Data shows the transcript mean abundance in transcripts per million (TPM) units ±SE.

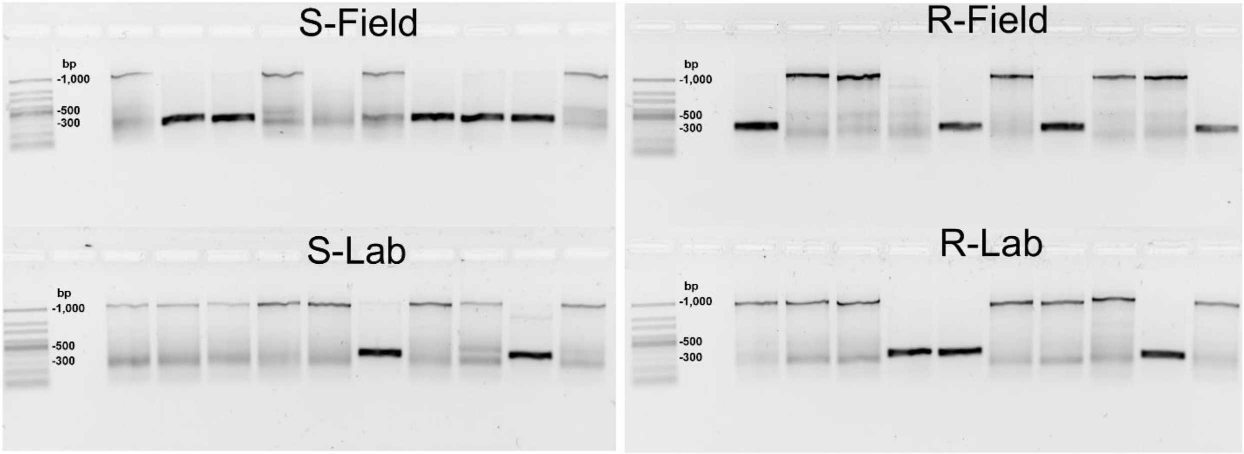

Figure 3. PCR products obtained from targeting a 360bp region containing the I1558 loci. Figure shows individual samples from WCR populations known to be susceptible (S-Lab; S-Field) and resistant (R-Lab; R-Field) to pyrethroids.

APPENDIX 1 Chapter 5 Supplementary Material

Table 1. Transcripts significantly differentially expressed (q-val<0.05) in field-derived pyrethroid-resistant WCR population R-Field.

Transcript ID	Blastp hit (Query cover;Identity)	Expression relative to S-Field	InterPro Scan	Query: Open reading frame peptide sequences (length)	Transcript nucleotide sequence (length)
MSTRG.84401.1	(1) 52 kDa repressor of the inhibitor of the protein kinase-like [Melanaphis sacchari](91%;41%)/PREDICTED: 52 kDa repressor of the inhibitor of the protein kinase-like [Tribolium castaneum](87%;40%) (2) 52 kDa repressor of the inhibitor of the protein kinase-like [Melanaphis sacchari](79%;57%)	Higher	(1) No hit (2) No hit	(1)630-352 MFSGLELNKSSNGSFKNDIGYSINQNVDNFTKCQLLERPWQPQNRINSHILFTQRKKRKKRYLDHQHLEQISWWVLSHSQKGLFYKYCVLFF* **(93)** (2)326-81 MTAQSLVPKPLTSFAKLMGKDGAIQTHEKTSYHNEYVQLGLNFLQSYRNPQKSVINQIDSQRSKQIQEKKKDYDTSRVQCS* **(82)**	CTCATTGCTAGGTCCAGCATCTTCGTCCAGAAGCAGAAGGCCATCATCACGGTGGCCTCTCAGAGGAATATTTTGTCGATCTAAGAACACTGGACTCTACTAGTGTCGTAGTCTTTCTTTTTTTCTTGTATCTGTTTAGACCTTTGAGAGTCTATCTGGTTAATAACTGACTTTTGCGGGTTGCGATAACTTTGTAGAAAATTCAGCCCAAGTTGAACGTACTCGTTGTGGTATGATGTTTTTTCGTGGGTTTGTATGGCTCCGTCTTTGCCCATTAGTTTGGCGAAAGATGTTAAAGGTTTCGGGACAAGGCTTTGGGCTGTCATCCCTTTATTGTGACCATATTTTTCATTAGAAAAATAAAACGCAATACTTGTAAAACAATCCCTTTTGACTGTGTGAAAGTACCCACCAACTTATTTGTTCTAAATGCTGGTGATCCAAGTAACGCTTTTTTCTTTTTTTTTCTTTGTGTGAACAGAATATGGGAATTGATACGATTTTGAGGCTGCCAAGGTCGTTCTAACAATTGGCACTTTGTAAAATTATCGACATTTTGATTTATAGAATATCCTATGTCATTCTTAAAGCTACCGTTACTGCTTTTGTTCAATTCTAGTCCAGAAAACATATTTATCTCCTGTTTTGTATATATATAAATATGTGTTTGAAACTAAAAACATTTAAACAGCAAATATTTAAATTTATATTTTTTACATTCTCGGGAGGGGCCATGGCCCCCATGGCCCCCTCCCTGGATCCGCCCTTG **(768)**
MSTRG.96000.1	(1) No hit	Higher	(1) No hit	(1)653-519	TTAACCCTTTCGCTGCGGAGCGGCTGAGACGATTTGCATCCCGTCGCTGCGGCGCTAATAGACGTCTCCCGCAGTGATGCAA

				FNPLTAGTAYLRNFSSARDVRQTHLCDRANRFAAVSDYLGIDKI* **(45)**	ATATTTTTGGCTTTTAGGTTACAGTTGACTTAATTGTTGGAATTATATCATTTGTTTTACTTTATTATTTTATTTCAACTATTTATTGCCAATTCTAGAACTATTATAATATATTATTATATTATAATAAATAATGTAGTAAAACAAATGATAGGGTTCATTTGTTCTTATGGTTCTTACAATTCCGCCATCGAATAATATTTACCCCTTTTTGGTGGCAGCGGCATGATGTAATACTTATTACCAGTATTTTTGAGTCCAAACAAAACGTAATAATTAGCGACAAATTCACTTTACGGTACTAACGCATTCGCAAAACTTAACACCTTCTCAGTTACCCCTCCTACTCATCCCGGTCGAGGCACTTTAGGTGGGCGGTTCACGCCCATTCATTAAGAAAACATCTGATAACATTATATTTTATATTTTGTTTACGTTATATTTTGTCTATACCCAAATAATCGCTAACCGCAGCGAAGCGGTTAGCCCTGTCGCATAAATGCGTTTGCCGCACATCTCGTGCACTACTGAAATTACGCAAATATGCGGTTCCCGCAGTCAAAGGGTTAAA **(653)**
MSTRG.24907.1	(1) P450 6k1-like [Leptinotarsa decemlineata](87%;71%)/P450 6k1-like [Anoplophora glabripennis](90%;67%)	Higher	(1) Cytochrome P450 superfamily (IPR036396)/ Cytochrome P450 family (IPR001128)/ Cytochrome P450, E-class, group I Family (IPR002401) GO:0055114 oxidation-reduction process GO:0005506 iron ion binding	(1)500-3 MQFFAAGFETTSSTTSFTLYELCLNKTIQNKLRSEILANIRENKGITYEGVMSMKYLDQCIKETLRKYPVLPFLDRRCINNYTIPGTDLVIEKGSSVYIPMFGLHYDETYFPEPMKYMPERFENANYNTNGLVYFPFGEGPRICIGGLEVGEVSKIFFGRILFDVE **(167)**	TGTTCTACGTCAAAAAGTATTCGACCAAAAAAAATTTTAGACACTTCTCCCACCTCTAACCCCCCTATGCATATTCTAGGACCTTCTCCAAATGGAAAATAGACCAAACCATTAGTATTGTAATTTGCGTTTTCAAATCTTTCAGGCATGTATTTCATTGGTTCAGGGAAATATGTCTCGTCATAATGTAGACCAAACATAGGAATATAAACGCTAGAGCCTTTTTCAATCACAAGGTCCGTTCCAGGTATTGTATAATTGTTTATACATCTTCTATCCAAAAACGGCAAAACTGGGTATTTTCGTAGTGTTTCTTTAATGCACTGATCTAAATACTTCATTGACATAACGCCTTCGTACGTTATTCCCTTATTCTCTCTTATATTGGCCAGAATTTCGCTTCTTAATTTATTTTGTATTGTTTTGTTCAGGCACAGTTCGTAAAGTGTGAACGAAGTGGTCGAACTTGTAGTCTCAAAACCGGCAGCGAAGAATTGCATACTTGATCCCTGAATTGACCCGATATCTGTAACAATACG

			GO:0016705 oxireductase activity, acting on paired donors with incorporation or reduction of molecular oxygen GO:0020037 heme binding		TTAATTTTGTTTTTATTGTATATTTACAAACATGTTAAAAACATT **(584)**
MSTRG.24908.1	(1) P450 6K1-like [Leptinotarsa decemlineata](98%;70%)/P450 6k1-like [Anoplophora glabripennis](98%;70%)	Higher	(1) Cytochrome P450 superfamily (IPR036396)/ Cytochrome P450 family (IPR001128)/ Cytochrome P450, E-class, group I Family (IPR002401) GO:0055114 oxidation-reduction process GO:0005506 iron ion binding GO:0016705 oxireductase activity, acting on paired donors with incorporation or reduction of molecular oxygen	(1)74-514 MQFFAAGFETTSSTTSFTLYELCLNKTIQNKLRSEILANIRENKGITYEGVMSMKYLDQCIKETLRKYPVLPFLDRRCINNYTIPGTDLVIEKGSSVYIPMFGLHYDETYFPEPMKYMPERFENANYNTNGLVYFPFGEGPRICIV* **(147)**	CATGTTTGTAAATATACAATAAAAACAAAATTAACGTATTGTTACAGATATCGGGTCAATTCAGGGATCAAGTATGCAATTCTTCGCTGCCGGTTTTGAGACTACAAGTTCGACCACTTCGTTCACACTTTACGAACTGTGCCTGAACAAAACAATACAAAATAAATTAAGAAGCGAAATTCTGGCCAATATAAGAGAGAATAAGGGAATAACGTACGAAGGCGTTATGTCAATGAAGTATTTAGATCAGTGCATTAAAGAAACACTACGAAAATACCCAGTTTTGCCGTTTTTGGATAGAAGATGTATAAACAATTATACAATACCTGGAACGGACCTTGTGATTGAAAAAGGCTCTAGCGTTTATATTCCTATGTTTGGTCTACATTATGACGAGACATATTTCCCTGAACCAATGAAATACATGCCTGAAAGATTTGAAAACGCAAATTACAATACTAATGGTTTGGTCTATTTTCCATTTGGAGAAGGTCCTAGAATATGCATAGTTTGAATGTTAAATATGTTTGTATTGTATGGTTGTACGTTTGCTGCGAACGACGAGCGTAAAATCAAACTT **(580)**

			GO:0020037 heme binding		
MSTRG.75321.1	(1) Junctophilin-2-like [Anoplophora glabripennis](100%;100%)/ Junctophilin-1-like [Leptinotarsa decemlineata](100%;100%)	Higher	(1) MORN motif repeat (IPR003409)	(1)217-2 SGSCFEGQWQNGKRHGLGVETRGRWIYRGEWTQGFKGRYGVRQSNTSTAKYEGTWANGLQDGYGSETYADDG **(73)**	TACCGTCATCGGCATAAGTCTCTGACCCATATCCATCCTGTAATCCATTCGCCCAAGTGCCTTCATACTTGGCAGTCGACGTGTTTGATTGTCTAACTCCGTATCTGCCCTTGAAACCTTGCGTCCACTCTCCCCTATATATCCATCGACCCCTCGTCTCCACACCCAGGCCATGCCTCTTTCCATTTTGCCACTGACCCTCGAAACAACTTCCACTAG **(219)**
MSTRG.75696.1	(1) P450 6k1-like [Anoplophora glabripennis] (100%;58%)/P450 6k1-like [Leptinotarsa decemlineata] (100%;53%)	Higher	(1) Cytochrome P450 superfamily (IPR036396)/Cytochrome P450 family (IPR001128) GO:0055114 oxidation-reduction process GO:0005506 iron ion binding GO:0016705 oxireductase activity, acting on paired donors with incorporation or reduction of molecular oxygen GO:0020037 heme binding	(1)476-3 MLLTSSWIVDVLAFSLTFSTLLYVYFTRHFSYWKKRNVFYQKPAPFFGNFKDVVTMKTTIGEWLRDEYNKAAKQPYFGIFVFDEPKLVIKSPEIIKNIMIKDFNNFCDRTFASPEYNEVESNFLFMMHNPKWKKHRSQLSPAFTSGKLKGMLPIIHEV **(159)**	CCAACTTCATGTATAATGGGAAGCATTCCTTTCAGTTTTCCTGAGGTGAAAGCTGGAGAAAGCTGAGACCTATGTTTCTTCCATTTAGGATTATGCATCATAAATAAGAAGTTCGACTCTACTTCATTGTATTCTGGACTTGCGAATGTTCTGTCACAGAAATTGTTAAAATCTTTTATCATAATATTTTTTATTATTTCTGGAGATTTAATCACTAATTTCGGTTCGTCGAAAACAAAAATTCCAAAGTAGGGTTGTTTAGCTGCTTTGTTATATTCGTCTCGTAACCATTCTCCAATGGTTGTTTTCATGGTTACTACATCTTTAAAATTACCAAAAAATGGCGCTGGCTTTTGGTAAAAGACATTACGTTTCTTCCAATAGCTAAAATGTCTGGTGAAATATACGTACAACAGTGTTGAAAATGTTAGAGAGAAAGCAAGAACGTCTACTATCCATGATGATGTTAAGAGCATCT **(478)**
MSTRG.23988.2	(1) TCDD-inducible poly [ADP-ribose] polymerase-like [Anoplophora	Higher	(1) No hit	(1)834-1046 MIIANVLIGNSCRGNSDMAIPPINCDTSTNDNQNVFVK	TATAGGCATTCCGCTGATTTCGCACCGCAGTCATTATAGTTGCAATTTGCAATGCCAGAAAAATTACAAAAAGTGATGTTATTTGAAGTGTGGTTTGTAGGTTTTAAAAAATTG

	glabripennis](87%;53%]/PREDICTED:poly [ADP-ribose] polymerase 11 [Tribolium castaneum](73%;55%)			YDDNTFYPSFIIHFGGIDYKNKNRTSVTTRSF* **(71)**	GAAATGGATCTTATTATGGTAATAGTCATAATTATATTATTCTCCATACTACTAGTGTACTTAACTACTTCCCACTACAACTACGATACTGCCGCAATTACTCCTTCTCCAACTTTAAGGAGTACTGGTACAACAGCCAACAGTACTCCAACAGCTCTTGAACCAGTACGAAAAGATCCAGAAATCTTAACAAAACTAATGAGTAGTTTATACATTTATACATATTTTTACCCAAACTTGACCGATGATGTATTTGAAGTAGAAAGTCTGAGAGAATAAGAGTCCCCGCAATATCAACTTATCAACAGCATATTTTGTCAAACTACAAATTTTTACAAATTTAACATAAATTTGAATGATTTCCAATTAGAAAGCCTGAGAGAAGAGTCTTTGGAATATCAAATTATAAATAGGAGATTTTTGCAATCTACTAGAAACAGAAGTTTTTTTAAATTACATAGTATCGAGAAAGTACACAATCCTTATCTTCTACTACAATATGGACTAAAAAAAATGAATATGATCGCAGAAGAATCGTTTACGAAGAAACATTACTGTTCCACGGAACTAAGAAAGACAATATTGACGATATTTGCCGAAATAATTTTAACTGGAGATTAACAGGTACCGCTTTTGGTTCCAGAGTCGGACAAGGTGTAAATTTCGCATCAGAAGCTTACTTTTCAACACATTACTGTGACGATGGATATAACAAAGTGATGATAATAGCTAATGTTTTAATTGGTAACAGCTGTAGGGGAAATAGTGACATGGCTATACCACCGATTAATTGTGATACCAGCACGAACGACAATCAGAACGTATTCGTTAAATACGACGATAATACTTTCTATCCATCTTTTATTATTCATTTTGGAGGAATAGACTACAAGAACAAGAATCGAACAAGTGTCACTACTAGAAGTTTTTAATAATCTTCTATTTATATATATACACAATCTACATTCGTCCGTATACTGCGAAAACCAGGTAAATGTAGAAATACCGAAATCGAGAAAAAACGTTTTTAAAGTTTATTGCTTTATTTTGAATTAGGCGGACCAGTTGTGTTTGATATTCGATATGCTAATGAAAGATGCATATATCAGAAATAACATTCTATCATTAGTTTGAAAAAGTGAAG

					AGACCTAGCTGATTAAACCTAAATTTAAGATCAGTTATCAGCTTTTTACTGAATATGGTAGATATACAGCGGTAGAAATATATTGTTTTCCGGCAAATATATATGTGCTCTTAGTTGGTTTTACATGCAACAGAACTTTGATTTTATGGAAGTAAGTAGCGATATATTGTTTTATTTGAAAATGAAAAGTTGGTTAGGTGTAACTTATTTGTTTATTATATAAATTATCTGCTGAATGGTAAATTGTATCATTTATTGAGTTTTACCTGTATGTAGAACGTAAAAAGCTGAGAATTTTGGTATACTTAGCTCAATATTTTAAAATTTATCATTTACCTGGTTTTCGCAGTATACGGACGAATATATCAATATAATCTTACATATTTCAGCATAAACCTGATTTTGCCGAAATCCTTCATTTTCGCATATTTCATACAGCTCAATAGATAAAAACCGACTTTATTCAGTCGTGTTTCGTTTGTGGTCATCTGAGTAGATGGCACTTTTGCAACTATCCACTGTTAGTGGAAAATATCAAGACATGTTTATCTTTCTGTTTCTATCTACCCGGATCTCTGACGATGCAGGGTTATGCTAAAACATGTAAGATCCTATTGATACCAATGCATATACAAAGGGTTTAACGAATTGTGCTCTTGCGCCATATGTTTTCTTTTAATTGGATCAAAGCGTTGGCAAAGCTTTTGTCGAAATCCAATTTCACACATATTTCATACAGCTCAAAAGAAGAAGCTGACTTTATCGAGTCGTGTTTCATTTATGGCCATCAGAGTAGATGGTTCTTTTGTAGCTATCCACTGGTAGTGGGAAATATCTAGAGACATTTTTCGAACTTTCTGTTTATGAATTTGTAGGTATCTGCGCGGATCTCTGACGATGTAGGTTTATGCTGAAACGTATAAAAACCTATTGATATCAAAGATGTTTTAACGAATTTTGAGCAAGATATGTCGTTTCAATTGCATCTAAGCGATGTCAAAGCATTTGCCAAAATTTGAGTTCTCGCATATTTCATACAGCTCAAAAGTTAGGCATAGACTTTATCGAATCGTGTTTCGTTTATAGCTATCAGAGTAAATGGCCCATAGCTATCCACTGATATTGGGAAATATCTAGAGATATTCT

					TCAACCTTTCTATTTATGAATTTACATCTACCAGGATCTCTGACAATGCAGGGTTATCCTGAATATGTAAGGTCCTATTGATATCAATTCATATACAGAGTATTTCGAACTTTCTGTTTATGAATGTGTATCTGCCCGAATCTCTGACGATGCAGCGTTATGCTGAAACATGTAAGGTCCTATTGATACCAATTCATATACAGAGGGTTTAACGAATTGTGCTGTTGCGCAAGACATTTGGTTTCAATTGCATCAAAGCGTTGGCAAAGCTTTTGCCGAAATCCTTTATTCTTGTATATTTCTTATATCTCAAAAGTTAGACACCGACTTTATCGAGTCGAGTTTCGTTTATGGTCGTCAAAGCAGATGACACCTTTGTAGCTATCCACTGGTAGTGGGAAATATCTAGAGACATTATTCGAACTTTCTGTTTATGAATTTGTAGGTTACTGCGCGGATCTCTGACGATGCTGGGTTATGCTGAAACATGTAAGATCCTATTGATACCAATTCATATACAGACGGTATAACGAATGGTGTTCTTGCGCCATATGCTTTGTTTTAATTGCATCAAATCTTTGGCAAAACTTTTGCCACAATCTGATTTCTTGCATATTTCATACAGCTCAACAAATAGAAACCGACTTTATCGACTCGTGTTTCGTTTAAGGCCATCAGAGTAGACAGCCCTTTTGTAGCTATCCACTGGTAGTGGGAAATATCTAGAGACATTTTTCGAACTTTCTGTTTATGAATTTGTAGGTATCTGCGCGGATCTCTGACGATGTAGGTTTATGCTGAAACGTATAAAAACCTATTGATATCAAAGATGTTTTAACGAATTTTGCGCAAGATATGTGGTTTCAATTGCATCTAAGCGTTGGCAAAGCTTTTGCCAAAATTTGAGTTCTCGCATATTTCATACAGCTCAAAAGTTAGACACCGACTTTATCGAGTCGTGTTTCGTTTATGGCTATCAGAGTAGATGGCCCATAGCAATCCACTGGTATTGGGAAATATCTAGAGATATTCTTCAACCTTTCTATTTATGAATTTACATCTACCAGGATCTCTGACAATGCAGGGTTATCCTGAATATGTAAGATCCTATTGATATCAACTCATATACAGAATACT

					TCGAACTTTCTGTTTATGGATGTGTATCTGCCCGGATCTCTGACGATGCAGGGTTATGCTGAAACATGTAAGATTCTATTGATACCAATTCATATACAGATGGTTTAACGAAATTGCGCTCTTGCGCGGTATGTTTGGTTTTAATTGCAGTAAAGCGTTGTCACAGCTTTTGCTGAAATCCTTTATTCTCGCATGGGTATTTTACACAGCTCAAAAGATAGAAACCGACTTTATCGACTGGTGTTTCGTTTAAAGCCATCAGAGTAGATGGCTTTTTTGTAGCTATCCACTGGTAGTGGGAAATATCAAGAGACATTCTTCGAACTTTCTGTTGATGAATTTGTATCTGCCCGGATCTCTGACGATGCAGGGTTATGCTGAAAGATGTAAGATCCTACTGATACCAATTCATATACAGAGGGTTTAACCAATTGAGGTCTTGCGCCGTATGTTGGGTTTTAATTGCTTTAAAGCGATGGTAAAGCTTTTGCTGAAATCCTTCATTCTCGCATATTTCATACAGCTCAAA **(4,070)**

Table 2. Transcripts significantly differentially expressed (q-val<0.05) in lab-derived pyrethroid-resistant WCR population R-Lab.

Transcript ID	Blastp hit (Query cover;Identity)	Expression relative to S-Lab	InterPro Scan	Query: Open reading frame peptide sequences (length)	Transcript nucleotide sequence (length)
MSTRG.22143.1	(1) P450 6k1-like [Leptinotarsa decemlineata] (99%;57%)/P450 6k1-like [Anoplophora glabripennis](99%;54%)	Higher	(1) Cytochrome P450 superfamily (IPR036396)/Cytochrome P450 family (IPR001128)/Cytochrome P450, E-class, group I Family (IPR002401)	(1)176-1675 MLLTSSWIVDVLAFSVTLSTLLYIYFTRHFSYWKKRNVFYRKPTPFFGNFKDVASMKTTIGEWLRDEYNKAAKQPYFGIFVFDEPKLVIKSPEIIKNIMIKDFNNFCDRTFASPEHNEVESNFLFMMHNPKWKKHRTQLSPAFTSGKLKAMLPIIHEVGQSLQKYLSDNQTVLEAKEVMAKYSTDVIGKCFLGINPHCFDNDDALFRVLGRAMFDFSIKNALKQTAYFSTPGIVKFFKISFFE	ATTGCAAATTGATAAAATTCCTATGCAGTTTGAAAAATAGACAACTTTATTGAAGTACGTATCTGCATCCTTAGATAAAACAAAATTAAATCTAAAACTGACTATATAAATTCGTAGAAAGTAGTTGTACAATACATAATTCACAAAATAATTTTAGTGCGTTTATGTCTCAAAGATGCTGTTAACATCATCATGGATAGTAGACGTTCTTGCTTTCTCTGTAACATTATCAACACTGTTGTACATATATTTCACCAGACATTTTAGCTACTGGAAGAAACGCAATGTCTTTTACCGAAAACCAACGCCATTTTTTGGTAATTTTAAAGATGTAGCAAGCATGAAAACAACCATTGGAGAATGGTTACGAGACGAATATAACAAAGCAGCTAAACAACCCT

			GO:0055114 oxidation-reduction process GO:0005506 iron ion binding GO:0016705 oxireductase activity, acting on paired donors with incorporation or reduction of molecular oxygen GO:0020037 heme binding	QWVTDHFVDVFSKSYEAREKSKIRKNDFIDILRDMERKGVIDKDIGSIQGSSMQFFAAGFETTSSTTSFTLYELCLNKTIQNKVRSEILANIRENKGITYEGVMSMKYLDQCIKETLRKYPVLPFLDRRCINNYTIPGTDLVIEKGSSVYIPMFGLHYDETYFPEPMKYMPERFENANYNTNGLVYFPFGEGPRICIGERFGLMSSKLALIYVLTKFEVEKCESTPDPLEFEPKSLVLQSKVGVPMRFKHLVPSPA* **(500)**	ACTTTGGAATTTTTGTTTTCGACGAACCGAAATTAGTGATTAAATCTCCAGAAATAATAAAAAATATTATGATAAAAGATTTTAACAATTTCTGTGATAGAACATTCGCAAGTCCAGAACACAATGAAGTAGAGTCGAACTTCTTATTTATGATGCATAATCCTAAATGGAAGAAACATAGGACTCAGCTTTCTCCAGCTTTTACCTCAGGAAAACTGAAAGCAATGCTTCCCATTATACATGAAGTTGGCCAGTCTCTTCAAAAATATTTAAGTGACAATCAAACAGTTTTAGAAGCAAAAGAAGTTATGGCCAAATATAGCACAGATGTGATAGGAAAATGTTTTTTGGGCATTAATCCTCATTGCTTCGATAACGATGATGCATTGTTCAGAGTTTTGGGACGGGCTATGTTTGATTTTAGTATAAAAAACGCATTAAAGCAAACTGCGTATTTTTCTACACCCGGAATTGTTAAGTTCTTTAAAATTAGTTTCTTCGAGCAATGGGTCACAGATCATTTTGTTGACGTCTTTAGTAAATCCTATGAGGCACGGGAAAAATCTAAAATTAGGAAAAATGATTTCATCGATATTCTACGAGACATGGAACGTAAAGGAGTTATTGATAAGGATATCGGGTCAATTCAGGGATCAAGCATGCAATTCTTCGCTGCCGGTTTTGAGACTACAAGTTCGACCACTTCGTTCACACTTTACGAACTATGCCTGAACAAAACAATACAAAATAAAGTAAGAAGTGAAATTCTGGCCAATATAAGAGAGAATAAGGGAATAACGTACGAAGGCGTTATGTCAATGAAGTATTTAGATCAGTGCATTAAAGAAACACTACGAAAATATCCAGTTTTGCCGTTTTTGGATAGAAGATGTATAAACAATTATACAATACCTGGAACGGACCTTGTGATTGAAAAAGGCTCAAGCGTTTACATTCCTATGTTTGGTCTACATTATGACGAGACATATTTCCCTGAACCAATGAAATACATGCCTGAAAGATTTGAAAACGCAAATTACAATACTAATGGTTTGGTATATTTTCCATTTGGAGAAGGTCCTAGAATATGCATAGGTGAAAGATTTGGATTAATGTCTTCTAAGCTCGCGCTGAT

					ATATGTTTTAACGAAATTCGAAGTAGAAAAATGTGAATCTACTCCCGATCCACTGGAGTTCGAACCCAAATCTCTTGTTTTACAATCTAAAGTTGGCGTTCCTATGAGATTTAAACATTTAGTTCCATCGCCCGCATAACAGAAAAACTGAGATATAAAATCTTGTATATTTACCTTCGATTATTATAAGATGTTCCTCGTAGTTACATTTTATTGTAATTTTAAAAATACAGTGAAATGTATTTTTAATATAAATAAACTAATGCAA **(1804)**
MSTRG.63174.1	(1) P450 6k1-like [Leptinotarsa decemlineata] (99%;52%)/P450 6k1-like [Anoplophora glabripennis](97%;42%)	Higher	(1) Cytochrome P450 superfamily (IPR036396)/Cytochrome P450 family (IPR001128) GO:0055114 oxidation-reduction process GO:0005506 iron ion binding GO:0016705 oxireductase activity, acting on paired donors with incorporation or reduction of molecular oxygen GO:0020037 heme binding	(1)1-360 SGQSLQKYLSDNQTVLEAKEVMAKYSTDVIGKCFLGINPHCFDNDDALFRVLGRAMFDFSIKNALKQTAYFSTPGIVKFFKISFFEQWVTDHFVDVFSKSYEAREKSKIRKNDFIDILRD **(121)**	TCAGGCCAGTCTCTTCAAAAATATTTAAGTGACAATCAAACAGTTTTAGAAGCAAAAGAAGTTATGGCCAAATATAGCACAGATGTAATAGGAAAATGTTTTTTGGGCATTAATCCTCATTGCTTCGATAACGACGATGCATTGTTCAGAGTTTTAGGAAGGGCTATGTTTGATTTTAGTATAAAAAACGCATTAAAGCAAACTGCGTATTTTTCTACACCCGGAATTGTTAAGTTCTTTAAAATTAGTTTCTTCGAGCAATGGGTCACAGATCATTTTGTTGACGTCTTTAGTAAATCCTATGAGGCGCGGGAAAAATCTAAAATTAGGAAAAATGATTTCATCGATATTCTACGAGATAT **(362)**
MSTRG.71693.1	(1) P450 6k1-like [Leptinotarsa decemlineata] (100%;54%)/P450 6k1-like	Higher	(1) Cytochrome P450 superfamily	(1)78-551 MLLTSSWIVDVLAFSVTISTLLYVYFTRHFSYWKKRNVFYRKPTPFFGNFKDVAS	TACAGTCTTTGTTGATTTGAATTATGATTATAAAATCTAGTTTCAAAATGATTTTATTGATTTATATTATTTTTTAGATGCTGTTAACATCATCATGGATAGTAGACGTTCTTGC

	[Anoplophora glabripennis](100%;58%)		(IPR036396)/Cytochrome P450 family (IPR001128) GO:0055114 oxidation-reduction process GO:0005506 iron ion binding GO:0016705 oxireductase activity, acting on paired donors with incorporation or reduction of molecular oxygen GO:0020037 heme binding	MKTTIGEWLRDEYNKAAKQPYFGIFVFDEPKLVIKSPEIIKNIMIKDFNNFCDRTFASPEHNEVESNFLFMMHNPKWKKHRTQLSPAFTSGKLKAMLPIIHEV **(159)**	TTTCTCTGTAACAATATCAACACTGTTGTACGTATATTTCACCAGACATTTTAGCTACTGGAAGAAACGCAATGTCTTTTACCGAAAACCAACGCCATTTTTTGGTAATTTTAAAGATGTAGCAAGCATGAAAACAACCATTGGAGAATGGTTACGAGACGAATATAACAAAGCAGCTAAACAACCCTACTTTGGAATTTTTGTTTTCGACGAACCGAAATTAGTGATTAAATCTCCAGAAATAATAAAAAATATTATGATAAAAGATTTTAACAATTTCTGTGATAGAACATTCGCAAGTCCAGAACACAATGAAGTAGAGTCGAACTTCTTATTTATGATGCATAATCCTAAATGGAAGAAACATAGGACTCAGCTTTCTCCAGCTTTTACCTCAGGAAAACTGAAAGCAATGCTTCCCATTATACATGAAGTTGG **(553)**
MSTRG.94228.1	(1) Endonuclease-reverse transcriptase [Blattella germanica](95%;47%) (2) Reverse transcriptase [Bactrocera tryoni] (99%;39%)	Higher	(1) No hit (2) Reverse transcriptase domain (IPR000477)	(1)1954-1493 MRVYKTIIRPTITYESETWTLNQRETTKLLVLERKILRTIYGPCREETTGEWRIRHKDELQIIYGDANIVRYIKANRMRWAGQVLRSSDERLLNATFWERPDGRRSVGRPRKRWKDAVASDLRKMGVQQWEIAAQDRQQWREIVNAAKTHIDL* **(154)** (2)2537-2139 MVEIGVPGKLVRLAHVSTENASARIRIGSTTSEEFLIETGLRQGDPLAPLLFNFALEHAVRKAQPQLANGFAAIGSKILLAFADDVDTIAQCTRDAKEVFTLFENGAKEVG	CTCCTGTCTTCGTTTGTCGGTAGAGTTTCTGGACACCCTGTATATCAAGAAGCACGTGGGCTCTAGATGGATAACTAGAGCGCCAGACAGAGTAGACTGAAAAAGGATTGGGAAAGCCTATGTCCAAATATGGACCGAAGAAGGCTAATTAAAAAGATAGATAGACTATTTTCTTTGCTTTTTCTCCGAAATATTTTCAACACTTCTGGACTAAGTTCATCGTTTCTAAGAGCTTTCACAGAATTTTTCTTTTCTATTGCTTCCTCTAGTTCTTCTTCCTGGATAGCTTTTGTTTCTTCAGATTTTTCCTGTGATCCGCCAATTACATTGTTTGCATTTTCCTTTGTTTTTCCTTGCTTTCCGTTCAACATTGTTCGAAAGGTTCACTCCATCTTTCCATTATATACTTGTCGTTGGTTAATATTGTTTCATTTGTGGTTATCATTTGTCTTAGCATTATTTCTTTGTTGCTTTGTAGTTTTTCAGTGTTCTATAACACAATTTTACATTTTTACA

				FKVNEDKTKYMVVTEEPKTNN* **(133)**	CCGCCCACCCAGAATATGCGTCTCTTCATTATCTTGGGAGAGTTTAACAAGATTTAAAAGGCAGCATAAGCAAAAAGCTACAACTTGACATGCACTATAAGAGGTTATATGTATAGTCTTAATTCATAATACATAGTTTTCTTCTTAGTAATAGGTACTGTAGATGAAACTGTATTTTATATTTTATTTTCTTTTTATTAAATGTTAGTAAAAAAGTACAGGTAATATTAAAAACATTTAACCTAGTCAATAGTTTAAGATATAGTGTACATTTGTAATTTAGAATACAAGGGCTGCATTTTTTCTAAGACCTTAAAATTTTAAATACTCCGTTTTTACACTTTATAATATTCACTTTCAGTAAAAAATATTTAGTTGGTAGCATTTATTGGTACCTACATTATTTTACTAATAGTGGTCACGTGAATGATACGCTTCGCGTCGGTTCACTTCAATGCTCTCACAAAGTCTTTCCTGATGAGACGTAAACGTAAAAACACGTGTAGGAGAATGGTGAGATGAATTTTGAAATGAATCGAAATGCAACCATATAATATTTATTTTTTTAGATGTTTTTCTATTTCAAAGTTCTTATACATGTTCATTTGATTGTGTAAATTTAATTATTCGTTGACAGTGTGACACTTGTCTGTGTAAACTTAATTACGACTATTACTAAGGCGGCCGATAAGTACTTAGCCCTCAAAAGAAAAACGAAAGTTTTGGAAAAGTGGTGATTTATTTCTGAACTTAGTCTCCTTTTAGCTCGATATACTTGACCCTGCGATGCTCCACCTTCTTTAACCAGTCTGAAAAATACCTTTTCTCGAGGTCTGCAAAGTATGCTTCCGTGGAGGTGATGAACTCTTTATTCGACTTACATTTCTGCCAGCGAGTGACTTTTCAAGTTTGGAAACAAAAAGAAGTTGTATAGGCCCAAATCTAGAGAATACATCATCATCATCATCATTTGGCTCTACAAATCTATGTGAGTCTTGGCCGCGTTTACTATTTCTCTCCATTGTTGTCGGTCCTGAGCAGCTATTTCCCATTGCTGTACTCCCATTTTGCGTAGATCACTGGCTACTGCGTCCTTCCATCTCTTTCTTGGACGACCAACTGACCTTCTGCCATCGGGCCTT

					TCCCAAAATGTGGCGTTCAGAAGTCTTTCGTCACTCGATCTTAGCACTTGACCCGCCCATCTCATTCGGTTTGCTTTGATGTAGCGTACTATGTTTGCATCTCCATATATTATCTGAAGTTCATCTTTGTGTCTTATTCTCCATTCTCCTGTTGTCTCTTCTCTGCAAGGCCCATAGATAGTCCGCAGTATCTTTCTTTCAAGCACCAGTAATTTTGTTGTTTCCCGCTGGTTCAGAGTCCATGTCTCGCTTTCATACGTTATTGTAGGACGAATTATTGTCTTATATACTCTCATTTTTGCTGGCCTTGAGAGTATTTTTGATTTAAGTACGGTAATTAATGAGTAATATGCCCTGTTTCCTGCAATGATCCTGGCTGCCACGTACTTTTCATATTTATTTTCAGCTGTTATGATCGCTCCCAGGTACTTAAATTCTTTGACGACTTCAAAGTTGTATTCATTAATTGTTACGTTTTGTCTAATTATTGGTCTTGGGTTCTTCCGTAACCACCATGTACTTGGTCTTGTCCTCGTTTACCTTAAAACCAACTTCCTTGGCTCCGTTCTCGAATAGGGTGAAAACTTCTTTTGCATCTCTGGTGCATTGTGCAATTGTGTCCACGTCATCCGCAAAGGCCAATAGTATTTTTGATCCTATGGCGGCAAATCCGTTTGCCAGTTGTGGCTGAGCTTTCCTTACTGCATGTTCCAGTGCGAAGTTAAACAGCAGGGGGGCGAGAGGATCTCCTTGTCTAAGCCCGGTCTCAATGAGGAATTCCTCCGACGTGGTGCTGCCAATTCTGATTCGTGCGGAAGCGTTCTCCGTGCTCACATGTGCTAATCGTACCAGCTTTCCAGGCACTCCTATTTCTACCATAGTCTCCCAAATCTAGAGAATACGTTGGATAGAACAGTTTGTAGCCCAATTCGACCAATTTGGTCATGGCGATGGCGGAGGTGTGACCCGGAACATTGTCATAATGTAGACAAACAAACAAATTCGGCGCATAATCAGGCTAATAATGCGGCATAGGAAAGCCCTCTGATCGTTTTGCCCTTTTCCAGGAAGTGGATATAGATCACAACTTGTGAATCCCAAATAATGGTGGTCATCGCCTTTCCAGCCGAT

					TGGAGAGTCTTCGCTCTTCTCGGAGCACGTTTGAGGGGTGACGTCCACTGTATCGACTGTTCCTTGGACTCCGGTGTATACCAGTGGAACCATGTTTCCTCTACAGTTATGAATCAACGTAGAAACTCATTTGGATTATGTTATTATTAGCATCAGACACTGGTCTGAACGGGTTTTATGTTTGCGTTTATTGTTTGAAGTTCGAAAATGCGGCGGCCATCGCGCCGTCAATTTTTTTATGCCCAAAATTTCAGGCAGGATATAACCAACGAGATCTTTTGTGATGCCTAGTGTCTCAGCTATCTCACGCACCTTCAGTCCGCGGTCTACCAATACAAGATTGTGGATTTCTTACACGTTATCCTCAGTGGTAGGTGTTTTCGAGGCACCTGGGAGTGACTTATCAAAAACCGACGTTCCACCACGTTGAAATTCGTTAAACCATTTTTGACGGTTTCCTTCGAAGGAGGAGAGTCACCGTTTACAGCATTCAAGCGCTTTTAGATTTCGCTGCGGGATTTCCCTTCTATAAACAAGAGTCGAATCACCGACTGATATTGCTCTTTTTTCATTTTTCTAAAATCCCCAAACACGCCCGCTTATAAACGCGGTCAAAACAAAGCTACGAGTATGATTTGGCTGATATTTTGGTATAGGTCTTCTACAATAATTACACGATGATAGATTTCTCTTGCGACAGTGGCGCCATCGAGTGGAGAGGCTAAGTACTTATCAGACCACCCACGTGGTTAACAGTAAGTATAACATGGGTCGCCCACGTTTTCTCAACTGTCATCAATACGACTAACTTCACGCGTAACTTGGATACGAGAATTATAAAAAAAAATTTAAAGCACTCATGGGAGTGCCGACAGAAGTGAAAACTTCTTATAGTATATAAATTACGAGATCCATGCTTTTCCCCATCCAAAAAGAAGTGCTATAACATACCTATTTTATATACGCGTTGCGTACGTTCTATGCTATTTATGTATACATACACATAATATAATATATAAACGTACGAAACTTAGTTTGGCGAAGTGATGACGGTCACAGACTCAATACTTTTTTCCTACCTAAAAAGTGCACAACGTCCCTAAAGAAGTTTTCACTTTAAAAATTTATTT

					CGCCAAACAATGACAGTCGCTTATTTAATACTTTTTCCCCATCCAAAAAGTGCACAACGTCCCTAAAGAAGTTTTAACTTCAAAACTTTATTTCGTCGAAGCAATGACAGTCGCTAATTTAATACTTTTTGCCCATCCAAATGTGCACAACGTCCCTAAAGAAGTTTTCACTTCAAAAATTTATTTCGCCGAAGCGATGAGGGTCGCTAATTCAACACTTTTTCCCCATCTAAAAAGTGTATAACGTCCCTAAAAAAGATTTCGCTTCAAAAATGTATTTCGTCGAACCAATGACGGTCGCTAATTTAATATTTTTCCCCATCTAAAAAGTTCACAACGTCCCTACAGAACTTTTCACTTCAAAAATTGATTTCGCCGAAGCGATGACGGTCGCTAATTCAATACTTTTTCCCCATCTAAAAAGTTCACAACGTCCCTACAGAACTTTTCACTTCAAAAATTGATTTCGCCGAAGCGATGACGGTCGCTAATTCAATACTTTTTCCCCATCTAAAAGTGCACAACGTTCTTAAAGAAGTGTTCACTTCAAAAATGTATTTTGTCGAAGCAATGACGGTCGCTAATTAAGTACTTTTTCCCCATCTAAAAAGTGCACAACGTACCTAAAGAAGTTTTCACTTCAATAATATTACTATTATTATACATACATTATAATAATATACGTACAAAATTTATTTTGTCGAAGCGATGACGGTCGTGATGACGGTCGCGAAATAAATCCATTTTCCCCATCCAAAAATAAGTTTTACATTTATTTAAAATTTAAATACTTTTATACAATTTATGTATACATACACATAATATAGATACGTACAAAATTTATTTCGCCGAAGCGATGACGGTCGCGATGATGGTCGCGAAATCAATCCTTTTTCCCCATCCTAAAATAGGTTTTACATTTATTTTAAATTTAAATACCTCCGCACAATTTATATACACACATAATATAGTATAAGCGATGTGCGATGACGGTCGCAATGACGGTCGTAATGACGGTCGCGATGACGGTTGCAAATTCAATGCTTTTTCCCCTATCCAAAAATCACACAACGTCCCTAAAGAAGTTTTCACTTCAAGAAATATGCATTGAAATCCAGATCCCGTAATTTTTTGAGCGTTAT

					AAAGTGAGAACAAATACATACATATTTCTTTGCCGATAAGGTAGAGTCCTGTTGAGAAAACCTGGCGTGGCCAGTATAACATATCACTGCAATTAAGATTAAACATCAACAATAAAAGGTTAAATGACATTATTTAGAAAAAGAGTATTT **(5,211)**
MSTRG.9784.1	(1) E3 ubiquitin-protein ligase MYCBP2-like [Leptinotarsa decemlineata] (48%;42%)/zinc finger BED domain-containing protein 4-like [Onthophagus Taurus](32%;52%)	Higher	(1) No hit	(1)394-86 INGALKFLIKLLGLLWKRIEVELSNLTLINLIAGVLESKMISDDEISIPGTPPELVEAVNTASLELLPKKSREKYENAYRRFMDLCRTLTTVRKYHFLTVRK* **(103)**	TTTTCCGCAAATCGCCAGGAAATTTTGACATTCCTGTCAAAATTTCTTGAAGAAAAAGTCAGGACTTCCTTACTGTAAGGAAATGTCATTTCCTTACTGTAAGGAAATGATATTTCCGTACAGTTGTTAGTGTTCTACATAAATCCATAAAACGTCTGTATGCATTTTCGTACTTTTCTCTTGATTTCTTTGGCAATAATTCTAATGAAGCAGTATTCACTGCCTCAACCAGCTCTGGAGGAGTCCCAGGAATGGAAATTTCATCATCACTTATCATTTTACTTTCGAGAACACCAGCAATTAAATTTATAAGCGTCAAGTTTGACAATTCAACCTCAATACGTTTCCATAGTAACCCAAGTAATTTTATTAGGAATTTCAAAGCACCATTTAT **(394)**
MSTRG.19112.1	(1) P450 6k1-like [Leptinotarsa decemlineata] (80%;71%)/P450 6k1-like [Anoplophora glabripennis](82%;67%)	Higher	(1) Cytochrome P450 superfamily (IPR036396)/ Cytochrome P450 family (IPR001128)/ Cytochrome P450, E-class, group I Family (IPR002401) GO:0055114 oxidation-reduction process GO:0005506 iron ion binding	(1)81-626 MQFFAAGFETTSSTTSFTLYELCLNKTIQNKLRSEILANIRENKGITYEGVMSMKYLDQCIKETLRKYPVLPFLDRRCINNYTIPGTDLVIEKGSSVYIPMFGLHYDETYFPEPMKYMPERFENANYNTNGLVYFPFGEGPRICIGGLEVGEVSKIFFGRILFDVEQHGIFIFGISLGTLFT **(183)**	TTTTTAACATGTTTGTAAATATACAATAAAAACAAAATTAACGTATTGTTACAGATATCGGGTCAATTCAGGGATCAAGTATGCAATTCTTCGCTGCCGGTTTTGAGACTACAAGTTCGACCACTTCGTTCACACTTTACGAACTGTGCCTGAACAAAACAATACAAAATAAATTAAGAAGCGAAATTCTGGCCAATATAAGAGAGAATAAGGGAATAACGTACGAAGGCGTTATGTCAATGAAGTATTTAGATCAGTGCATTAAAGAAACACTACGAAAATACCCAGTTTTGCCGTTTTTGGATAGAAGATGTATAAACAATTATACAATACCTGGAACGGACCTTGTGATTGAAAAAGGCTCTAGCGTTTATATTCCTATGTTTGGTCTACATTATGACGAGACATATTTCCCTGAACCAATGAAATACATGCCTGAAAGATTTGAAAACGCAAATTACAATACTAATGGTTTGGTCTATTTTCCATTTGGAGAAGGTCCTAGAATATGCATAGGGGGGTTAGAGGTGGGAGAAGTGTCTAAAATTTTTTTTGGTCGAATACTT

			GO:0016705 oxireductase activity, acting on paired donors with incorporation or reduction of molecular oxygen GO:0020037 heme binding		TTTGACGTAGAACAACACGGTATTTTTATTTTTGGAATATCGCTGGGGACATTGTTCACTA **(627)**
MSTRG.24781.1	(1) No hit (2) No Hit (3) No hit	Higher	(1) No hit	(1)198-46 MFNYFFTTTCYQLILLVLLMYLAQDDTVDRCCLRVLSPDAILNLNTFPYC* **(51)** (2) 668-525 QGRIQGRFSGGAVNFFCRGVPGIWGQFLKIRVTPVSFKALFTHYWVP***(48)** (3)335-228 MNLTKSSRMLLFYIYLKSRESCSTCRSVFSSNMTE* **(36)** (4)1-75 ATVMMAFCFWTKMLDLAIRESVKV* **(25)** (5)362-412 MLLLSGLVLPLSLNFH***(17)**	GCCACCGTGATGATGGCCTTCTGCTTCTGGACGAAGATGCTGGACCTAGCAATAAGGGAAAGTGTTAAGGTTTAAAATCGCATCAGGAGATAAGACTCTTAAACAACACCTATCCACAGTATCATCCTGAGCAAGATACATCAGTAGCACTAGTAAAATCAATTGATAACATGTTGTGGTGAAAAAATAATTGAACATATAATAAATCAGGTTCAAAATGTAAATTATTACTCTGTCATATTTGACGAAAAGACCGACCTACAGGTGGAACAGCTTTCTCTAGATTTGAGATAAATATAGAATAACAACATTCGTGAAGATTTTGTCAAATTCATTGGCGCTTATGAGAACATAAAAATAATTAATGAAAATTAAGAGAGAGAGGAAGAACAAGGCCTGACAGGAGAAGCATTGGGGAAAATAGTATTAAATTTATTGAAATAACTGCACTTGGATTCGAAGAAATGTGTAGGACTAGGTACTGACTTTAATAATACTTTAATAATTATATGTTTTGAATGTATTTATGGCACCCAATAGTGTGTGAAAAGGGCCTTAAAACTCACCGGCGTAACCCTAATTTTTAAAAATTGCCCCCAAATCCCCGGTACCCCTCTGCAAAAAAAGTTCACGGCCCCTCCCGAAAATCGGCCCTGGATCCGCCCTTG **(668)**
MSTRG.58405.1	(1) Zinc finger MYM-type protein 1-like [Myzus persicae] (79%;46%)/repressor of the	Higher	(1) No hit (2) No hit	(1)188-433 MTAQSLVPKPLTSFAKLMGKDGAIQTHEKTSYHNEYVQLGLNFLQSYRNPQKSV	TGGCAGCCTCAAAATCGTATCAATTCCCATATTCTGTTCACACAAAGAAAAAAAAGAAAAAAGCGTTACTTGGATCACCAGCATTTAGAACAAATAAGTTGGTGGGTACTTTCACACAGTCAAAAGGGATTGTTTTACAAG

	inhibitor of protein kinase-like [Myzus persicae] (85%;46%) (2) Zinc finger MYM-type protein 1-like [Myzus persicae] (64%;51%)/ repressor of the inhibitor of protein kinase-like [Trachymyrmex cornetzi](92%;40%)			INQIDSQRSKQIQEKKKDYDTSRVQCS* **(82)** (2)1-162 WQPQNRINSHILFTQRKKRKKRYLDHQHLEQISWWVLSHSQKGLFYKYCVLFF* **(54)**	TATTGCGTTTTATTTTTCTAATGAAAAATATGGTCACAATAAAGGGATGACAGCCCAAAGCCTTGTCCCGAAACCTTTAACATCTTTCGCCAAACTAATGGGCAAAGACGGAGCCATACAAACCCACGAAAAAACATCATACCACAACGAGTACGTTCAACTTGGGCTGAATTTTCTACAAAGTTATCGCAACCCGCAAAAGTCAGTTATTAACCAGATAGACTCTCAAAGGTCTAAACAGATACAAGAAAAAAAGAAAGACTACGACACTAGTAGAGTCCAGTGTTCTTAGATCGACAAAATATTCCTCTGAGAGGCCACCGTGATGATGGCCTTCTGCTTCTGGACGAAGATGCTGGACCTAGCAATAAGGGAAAGTGTTAAGGTTTAAAATCGCATCAGGAGATAAGACTCTTAAACAACACCTATCCACAGTATCATCCTGAGCAAGATACATCAGTAGCACTAGTAAAATCAATTGATAACATGTTGTGGTGAAAAAATAATTGAACATATAATAAATCAGGTTCAAAATGTAAATTATTACTCTGTCATATTTGACGAAAAGACCGACCTACCCCAGGTGGAACAGCTTTCTCTAAATTTGAGATAAATACAGAATAACAACATTCGTGAAGATTTTGTCAAATTCATTGGCGCTTATGAGAACATAAAAATAATTAATGAAAATTAAGAGAGAGAGGAAGAACAAGGCCTGACAGGAGAAGCATTGAGGAAAATAGTATTAAATTTATTGAAATAACTGCACTTGGATTCGAAGAAATGTGTAGGACTAGGTACTGACTTTAATAATACTTTAATAACTATATGTTTTGAATGTATTTATGGCACCCAATAGTGTGTGAAAAGGGCCTTAAAACTCACCGGCGTAACCCTAATTTTTAAAAATTGCCCCCAAATCCCCGGTACCCCTCTGCAAAAAAAGTTCACGGCCCCTCCCGAAAATCGGCCCTGGATCCGCCCTTG **(1,128)**
MSTRG.59366.1	(1) P450 6k1-like [Leptinotarsa decemlineata] (100%;53%)/P450 6k1-like	Higher	(1) Cytochrome P450 superfamily	(1)3-476 MLLTSSWIVDVLAFSLTFSTLLYVYFTRHFSYWKKRNVFYQKPAPFFGNFKDVVT	AGATGCTCTTAACATCATCATGGATAGTAGACGTTCTTGCTTTCTCTCTAACATTTTCAACACTGTTGTACGTATATTTCACCAGACATTTTAGCTATTGGAAGAAACGTAAT

	[Anoplophora glabripennis](100%;58%)		(IPR036396)/Cytochrome P450 family (IPR001128) GO:0055114 oxidation-reduction process GO:0005506 iron ion binding GO:0016705 oxireductase activity, acting on paired donors with incorporation or reduction of molecular oxygen GO:0020037 heme binding	MKTTIGEWLRDEYNKAAKQPYFGIFVFDEPKLVIKSPEIIKNIMIKDFNNFCDRTFASPEYNEVESNFLFMMHNPKWKKHRSQLSPAFTSGKLKGMLPIIHEV **(159)**	GTCTTTTACCAAAAGCCAGCGCCATTTTTTGGTAATTTTAAAGATGTAGTAACCATGAAAACAACCATTGGAGAATGGTTACGAGACGAATATAACAAAGCAGCTAAACAACCCTACTTTGGAATTTTTGTTTTCGACGAACCGAAATTAGTGATTAAATCTCCAGAAATAATAAAAAATATTATGATAAAAGATTTTAACAATTTCTGTGACAGAACATTCGCAAGTCCAGAATACAATGAAGTAGAGTCGAACTTCTTATTTATGATGCATAATCCTAAATGGAAGAAACATAGGTCTCAGCTTTCTCCAGCTTTCACCTCAGGAAAACTGAAAGGAATGCTTCCCATTATACATGAAGTTGG **(478)**
MSTRG.13177.1	(1) Digestive cysteine proteinase 1 [Anoplophora glabripennis] (99%;61%)/ cathepsin L precursor [Tribolium castaneum](98%;63%)	Higher	(1) Papain-like cysteine peptidase superfamily (IPR038765)/Peptidase C1A family (IPR013128)/Cathepsin propeptide inhibitor domain I29 (IPR013201)/ Peptidase C1A, papain C-terminal (IPR000668)/	(1)3-1595 LAIGDPPVPEWSDTYSVEGTIHLPYAEIVEPFHAWYDGKSKNSRIDYYNGTAKTYQLGGNGNGVQLKVIPFTTEEVLNQITCFQINGTEDDPVTPQSILPDLEGFEYQGIQEYGDRELEVWFLKTVQLEKENEYTLWVVRDEHGKAIPVKYDMRGYNSLLGSHYDHYYLLYTWKSYRTHKIDPSVFEVETNSECRSFPGPGNQHVHIMNPMAEYIRPEKSEHVDSNFGDFINNHNKNYADTKEHAFRKEVFRQNVRFIESVNRQNKGYSLAINHLADKTDKEIKYLNGRLSSGGNNGGQPFPYTDADTD	ATTTAGCGATAGGCGATCCACCAGTTCCAGAATGGAGTGACACTTATAGCGTAGAAGGAACTATCCATTTGCCTTATGCAGAAATAGTAGAGCCTTTCCATGCTTGGTATGATGGAAAATCTAAAAATTCGCGCATTGATTACTACAATGGAACGGCTAAGACATACCAACTTGGAGGAAATGGAAATGGTGTCCAACTGAAAGTAATTCCATTCACTACAGAGGAGGTCCTAAACCAAATAACGTGCTTCCAGATCAATGGAACTGAAGACGATCCAGTGACTCCTCAATCGATTTTGCCAGATTTAGAAGGATTTGAATATCAAGGCATACAGGAGTATGGAGATAGAGAACTAGAGGTATGGTTTCTAAAAACTGTCCAGTTAGAAAAAGAAAACGAATACACTCTATGGGTTGTCCGAGACGAGCATGGTAAAGCTATTCCAGTTAAATATGATATGAGAGGATACAATTCGTTATTGGGAAGCCACTACGATCATTACTATTT

			cysteine active site (IPR000169)/ histidine active site (IPR025660)/ asparagine active site (IPR025661) GO:0006508 proteolysis GO:0008234 cysteine-type peptidase activity	DLPDQYDWRLFGAVSPVKDQAICGSCWSFGTVGTLEGSLFLKNGGRLVQLSQQALVDCSWGFGNNGCDGGEDWRAYQWIQKHGGIPIDSHYGGYKGEDGFCSADEVEKTAKITGWVNVTENDENALRLALVKQGPISVSIDASQKSFSFYSHGVYYEENCGNREEDLDHSVLAVGYGSIDGENYWLIKNSWSTYWGNDGYILMSSRNNNCGVMTAATYVTM* **(531)**	GCTATACACATGGAAGTCTTACAGGACTCATAAGATTGATCCCTCCGTTTTTGAAGTAGAAACTAATAGTGAATGCAGAAGTTTTCCTGGACCCGGAAATCAACATGTTCACATCATGAACCCCATGGCCGAATACATTCGTCCCGAAAAAAGTGAGCACGTGGACTCAAACTTTGGCGATTTTATAAATAACCACAACAAAAATTACGCAGACACAAAAGAACACGCATTTAGAAAAGAGGTTTTCCGTCAAAACGTCAGGTTCATCGAATCTGTCAACCGACAAAATAAAGGATATAGTCTAGCAATTAATCATCTTGCTGATAAGACTGACAAGGAAATTAAATACCTGAATGGAAGACTTTCAAGTGGAGGCAACAATGGAGGACAACCTTTCCCTTACACAGATGCTGATACCGATGATTTACCTGATCAATATGACTGGAGACTGTTTGGAGCTGTTTCACCAGTAAAAGATCAAGCCATATGCGGATCTTGCTGGTCTTTTGGAACCGTCGGCACCCTTGAAGGATCACTTTTTTTGAAAAATGGTGGTCGGTTGGTACAATTATCCCAGCAAGCTTTGGTGGATTGTTCTTGGGGCTTTGGTAACAATGGTTGTGATGGAGGGGAGGATTGGAGGGCTTACCAATGGATCCAAAAACACGGTGGAATACCAATCGATAGTCATTATGGAGGCTACAAAGGAGAGGATGGATTTTGCTCAGCTGATGAGGTGGAGAAGACAGCCAAAATTACTGGTTGGGTAAACGTAACCGAAAACGATGAAAATGCTCTTCGTTTGGCACTCGTGAAGCAAGGACCAATTAGTGTTAGCATCGACGCTAGCCAAAAATCTTTCAGTTTTTATTCACATGGAGTCTATTACGAAGAAAATTGCGGAAACAGAGAAGAAGATTTGGACCATTCGGTTTTAGCTGTTGGATACGGTTCAATCGACGGCGAAAACTATTGGTTAATCAAAAAACAGTTGGTCTACTTATTGGGGAAATGACGGCTACATCTTGATGTCTTCCAGAAACAACAACTGTGGAGTCATGACGGCGGCTACCTATGTAACTATGTAGATATTTAACATAACATCCATATTTAAATAAAAAAAT

					AAGAAATCCAATTTATTTATATTGTAAATATTTATCAAATAAATTTTCTTCATAATATTT **(1,691)**
MSTRG.36287.1	(1) P450 6k1-like [Leptinotarsa decemlineata] (98%;41%)/P450 6k1-like [Anoplophora glabripennis](98%;40%)	Higher	(1) Cytochrome P450 superfamily (IPR036396)/ Cytochrome P450 family (IPR001128)/ Cytochrome P450, E-class, group I Family (IPR002401) GO:0055114 oxidation-reduction process GO:0005506 iron ion binding GO:0016705 oxireductase activity, acting on paired donors with incorporation or reduction of molecular oxygen GO:0020037 heme binding	(1)66-1565 MLLTSSWIVDTIILTVTLSLLVYKYLTRHFDYWRKRKVTHEKPMLLFGNFYEVFTFKTTIQEHIKKIYDRIDAPYFGIHILDEPILVLKDPKLVKDVLIKDSAVFSNRRPATPTHPLMKHALFFLNYPHWKPLRAKITPVFTSAMLKNAHNQYLTDIGQSMTKFLNKNKETIDSRRIGEYFASEMIFKYFFGANANCFEDIPSVFEPYVKKMGEFSVRNAVIQNLYFIKPSWVTFLKLDFISESIMTFFERVFIEGMINRKSYDGKPQTFVDMANKAVRDTESGKEDTLDFNMSISTAIFFLIAGRDTLNTLIAFTLYEIAMHADIQDKLREAIQENVEKYGGITYEGVHDNKYLDMCIKESMRKYPPIPFLDRMPLSDYTLEGTDLVVKKDMTVIIPFFALHRDENLFPNSDGYDPERFREEIQSEGLFYLPFGAGPRACIGKRLGLLGLLVSLSYIVLNFKVEKCPETPSKIEFEPKSFPLVSKQGLPLRITPIEHK* **(500)**	TAAACTTTTAGTTAATGAATCGGTATAGCCATTGAGCACCAGCGAGTACAGTGAGTCACTTAAAGATGCTTTTGACTTCGTCATGGATCGTAGATACCATAATATTGACAGTAACACTAAGCTTGCTGGTGTACAAATATCTCACAAGGCATTTTGACTATTGGAGGAAAAGAAAGGTCACCCATGAGAAACCTATGCTACTTTTTGGAAACTTCTATGAAGTTTTCACCTTCAAAACAACTATTCAAGAGCACATAAAGAAGATTTACGATAGAATAGATGCTCCATATTTTGGAATTCATATTCTTGATGAACCAATACTAGTTTTAAAAGATCCTAAGCTGGTTAAAGACGTTCTAATCAAAGATTCTGCTGTGTTTTCCAACAGACGACCTGCCACACCTACACATCCTCTTATGAAACACGCATTATTCTTTCTGAACTATCCTCACTGGAAACCTCTTAGAGCTAAAATAACTCCAGTTTTCACTTCTGCTATGTTAAAAAATGCACACAATCAATATTTGACTGACATCGGTCAATCCATGACGAAATTTTTGAACAAAAATAAAGAAACCATAGATAGCAGACGTATTGGGGAATACTTTGCATCAGAAATGATCTTCAAATACTTTTTTGGAGCTAATGCTAACTGCTTCGAAGATATACCATCTGTATTTGAACCATACGTAAAAAAGATGGGTGAATTCAGTGTTAGAAACGCCGTTATTCAAAACCTGTACTTTATCAAACCATCGTGGGTAACGTTCTTGAAGCTGGATTTCATCTCAGAAAGTATAATGACATTTTTTGAACGTGTTTTTATAGAAGGAATGATAAACAGGAAAAGTTATGATGGCAAGCCACAAACTTTTGTCGATATGGCAAATAAAGCTGTGAGAGACACTGAAAGTGGGAAGGAGGATACCCTAGATTTCAATATGTCCATCTCGACTGCAATATTCTTCCTCATAGCTGGCAGAGACACTTTGAATACATTAATTGCTTTTACTTTGTATGAAATTGCTATGCATGCGGATATCCAAG

					ACAAACTCAGAGAAGCCATCCAAGAAAATGTAGAAAAGTACGGAGGCATTACCTATGAGGGAGTACACGACAACAAATATTTAGACATGTGTATTAAAGAGTCAATGAGAAAATATCCGCCTATACCGTTCCTGGATAGGATGCCTTTGTCTGACTACACACTAGAGGGTACTGATTTAGTGGTCAAAAAGGATATGACAGTAATAATACCATTCTTTGCACTTCACAGGGATGAAAATCTTTTCCCTAACTCTGATGGATACGATCCAGAAAGGTTCAGAGAAGAAATACAATCAGAGGGACTATTTTACCTTCCGTTTGGAGCAGGTCCCAGAGCTTGTATAGGTAAAAGACTTGGACTGTTAGGTTTATTGGTATCATTATCATATATAGTACTTAATTTTAAAGTAGAAAAATGCCCAGAAACTCCATCGAAGATTGAATTTGAACCCAAAAGTTTTCCATTGGTTTCTAAACAAGGACTGCCTCTTAGAATTACGCCTATTGAACATAAATAAAAGCAACATTGTGATGTAGATTTTTTATGTTAAAAAATTATTGTATGAATAAAATAAATATGTAGTTGTTAGTAAGTCAACCA **(1,648)**
MSTRG.39495.1	(1) No hit (2) No hit (3) No hit (4) No hit (5) No hit	Higher	(1) No hit	(1)402-283 MLCFLLIFYAFQPFLLATMNVDSCQQKSLKGIILLIRYL* **(40)** (2)697-590 MYSTKLENILCFPPKHLTDLRLIYNFHKFFFNCNI* **(36)** (3)101-202 MLYKKVLNCHQGICLSQRQFYNTSIVKNFWTGL* **(34)** (4)3-95 YFICVNNLLALKDNKININHHNIKTIIILD* **(31)** (5)383-472	TCTATTTTATTTGTGTAAATAATTTACTAGCGTTAAAAGACAACAAAATAAATATAAATCACCACAACATAAAAACTATTATTATTTTAGATTAAACATTATGTTATATAAAAAAGTTCTAAATTGCCATCAAGGAATTTGCTTGTCTCAAAGACAGTTTTATAATACGAGTATAGTTAAAAATTTCTGGACAGGATTATAATATGACAATATTACCTTTAGAAAATATATTCCGATTTTAATTGTGATTTTTTGCTTTCACCGATAAATGTACAGTGTGATTCACAAATACCTAATTAATAGTATTATACCTTTTAAGGATTTTTGTTGACAGCTGTCAACATTCATTGTAGCTAATAAAAATGGCTGAAATGCGTAGAAAATGAGTAGAAAACAAAGCATGAAGCAAGCAGATGATGAACAAATAAGGGAGAGCAGAAAAAAGTGTCGTTCCGATATTTCAGTAGGTTAACGCATTCAATAATGCTTACTAGCAGACGTTGGGATGCTAAAAAGC

				MSRKQSMKQADDEQIRESRKKCRSDISVG* **(30)** (6)557-640 MQTKDFCKKIRLYVTIKKKLMEIVNKS* **(28)** (7)484-567 MLTSRRWDAKKLECSSKEIILGIPDAD* **(28)** (8)672-743 MFSNLVEYMERKVRNKAVWIQRM* **(24)** (9)269-331 MYSVIHKYLINSIIPFKDFC* **(21)** (10)808-761 DFFLLLRTTVTYKTL* **(16)**	TTGAGTGTAGTAGTAAAGAAATAATTCTAGGTATACCAGATGCAGACTAAAGATTTTTGTAAAAAAATCCGCTTATATGTTACAATTAAAAAAAAACTTATGGAAATTGTAAATAAGTCTTAAGTCTGTTAAGTGTTTAGGAGGGAAACACAAGATGTTCTCTAATTTGGTGGAATACATGGAGAGAAAAGTGAGAAACAAGGCAGTTTGGATACAGAGGATGTAGTGGATATAGTATGTGTGTTAGAGTGTTTTGTAGGTCACTGTAGTTCTAAGGAGGAGAAAAAAATCAT **(810)**
MSTRG.56151.1	(1) P450 6k1-like [Leptinotarsa decemlineata] (96%;39%)/P450 6k1-like [Anoplophora glabripennis](98%;40%)	Lower	(1) Cytochrome P450 superfamily (IPR036396)/Cytochrome P450 family (IPR001128) GO:0055114 oxidation-reduction process GO:0005506 iron ion binding	(1)876-1 MLLTSTWNLSILLIFIALYVLYKYFTRNFNYWEKRGIFYIKPLPFFGNFFDTFTFKSTIAHGLKAIYDQSKGDFVGAFVFDTPVLILRSPKLIEHVLIKDFSFFKDRSLASPKHNPIVANWLLFQGYSDWKKTRPKITSIFSSGKIKGMFYTAKPIIDDMYAFITNKDVVIEVKDLSRRYSTEVVSRCYFGMGGRCFEKGNSEIQNIATRLFEFSARNAIIQGLHVFKPQWVELFKLDFMKRSDQDYMLDAFMDVVNERKKVKA	TGTCTTACCAATTTTATTATCATTGTTAGTAGATTCTTGCGTCTCCAAAATAATATCAATATAATCAAAAGCTTTTCCATCCTGTGCTTTAACTTTTTTTCTTTCATTAACCACGTCCATAAATGCATCCAACATGTAATCTTGATCACTCCGTTTCATAAAGTCAAGTTTAAATAACTCCACCCACTGTGGCTTAAATACGTGTAGCCCTTGAATTATTGCATTTCTTGCAGAAAACTCAAACAATCTTGTTGCAATGTTTTGGATCTCGGAATTACCCTTTTCGAAACACCTACCACCCATACCAAAGTAGCATCTGGAAACCACCTCTGTTGAGTATCTCCTACTAAGATCTTTAACTTCAATAACGACATCTTTATTTGTTATAAATGCGTACATGTCGTCAATTATAGGTTTGGCAGTATAAAACATTCCTTTAATTTTCCCACTGCTGAAGATTG

			GO:0016705 oxireductase activity, acting on paired donors with incorporation or reduction of molecular oxygen GO:0020037 heme binding	QDGKAFDYIDIILETQESTNNDNKIGKT **(293)**	AAGTGATCTTGGGTCTGGTCTTCTTCCAGTCCGAATACCCCTGGAACAACAACCAATTGGCCACAATAGGGTTATGTTTTGGAGATGCAAGGCTTCTGTCCTTGAAAAAGCTGAAATCTTTTATCAAAACATGTTCTATCAATTTTGGAGATCTTAGAATTAAAACTGGAGTATCAAATACAAAAGCTCCCACAAAATCTCCTTTTGATTGGTCATAAATAGCTTTTAATCCATGTGCTATGGTACTTTTAAAAGTAAATGTATCAAAGAAGTTTCCAAAGAAAGGTAAAGGTTTTATGTAGAATATTCCTCGTTTTTCCCAGTAATTAAAATTTCTTGTAAAGTATTTATATAGTACATACAGAGCTATAAATATCAATAGGATACTCAGGTTCCAGGTAGATGTCAGCAACATCT **(878)**
MSTRG.90902.1	(1) PREDICTED:Zinc finger MYM-type protein 1-like [Acyrthosiphon pisum](27%;54%) (2) Zinc finger MYM-type protein 1-like [Myzus persicae] (79%;46%)/ repressor of the inhibitor of the protein kinase-like [Myzus persicae] (85%;46%)	Higher	(1) No hit (2) No hit	(1)1696-2004 MFSGLELNKSSNGSFKNDIGYSINQNVDNFTKCQLLERPWQPQNRINSHILFTQRIKKKKALLGSPAFRTNKLVGTFTQSKGIVLQVLRFIFLMKNMVTIKG* **(103)** (2)2001-2246 MTAQSLVPKPLTSFAKLMGKDGAIQTHEKTSYHNEYVQLGLNFLQSYRNPQKSVINQIDSQRSKQIQEKKKDYDTSRVQCS* **(82)**	TGGAATCATCATAATCAATTAGCCCTGATTTTCCATTCTTGAACATAAGACTTCTACAGATATTTCTATTTTTTTCTGTTCTGCGCTTCTGCTATCCAATTGGTCTCAATTCCTTTGAGGTCGTCGGCCCATCGCGTTGAAGGTCTTCCTCGGCTCGCTTGTCTGCCCCTGGTTTCCACTCAAGCATTTTTTGTCCATCTGTCATCTTCCATTCTTGCCACATGTCCCGCCCATCTCCATTTTTGGCTTGTAATACGTTCGATGATATCGTCCACTACGAACGTCCTCGTTTCTTACTCTATTCCGTACGCTTCTTTTATTAGGATATCTTACATTAAATAAAAATGAACAGTGCGCGCACTATTGCTTCTATAAAACATCTTTATTATTGCTACTTTTTCCTCAACTGAGTACATTTCATCAACTTTATTGTTTTTTTTAACAATAAATCATAAAATCAAAATATTGACAATTCAAATATTGTTAATATGGTTTTTTTTAATACAACTTTAAGGTTACCTCATTCAAGTTTTATGACATCAGAACCTCACAGTGTTACCGAAACATCATAATAGTGATGAAATGGGGTCCCGGTGAATTCGTAACTCTTTTAATCCCCTATCATAATTACAAGCCAATTGGCAACTTTGGCCCTCAGATCATTTTTAGGAAACCAATCAACTACCGGTGAATTCGTAACTAAATACAGGTATAATTT

					TTAGACTTGAAATAAACATATGGAAAATCTCTTTGCTTTTAATTTATCAGATGGATTTAAATAATTTAACATTGCTAAACATCTAAATATTAAATTTACAATTACTTGATAAAAACCAAGCTCGTGTAGAGCTACTTGATGAAAATAATATTTATAACGCGTGTTAATGAAACACTATAATATTGTTTCAATTATTTTATTAAGATATTACAATTTTTGCTATTTTTTATAGGTACATATAATACAAATATATGATGTTTTTAAGCAAACCAAGAAACATTCGGTTTAGATTTAAGGTATTAGATTTAATCAATGGTTTCGAATTCACCAGAAGAAAGTTTCGAGTTGGCAGGTCAGGTTATAGAAAAGTTACGAATTGGCCGGTGTACATTTTGATTTGAAAATTTTTGTCACTAAAAGTTACGAGTTGGCGCGTGTCCATGAAATGTGAGGAATTTTCAAAATGTCAATTATTTAAGAATAGACTAATAAATTGTATTTTTAAAATGAAGAAAATAATCGAAGTTTCAAAATTTCTTTCGCACTTTTCACTAACGTGGAAACGAGACACGTTTTATTCATAATATTATGAAAACAGAAAAATGTATAACTTTAAATTTTAAAACTCCAATAGTGAGACACTGTAATTAAAAGTAATAAATAAACAAAATTAAAATAAAATTAAATTAAATTAAATTAAAATAAAATAAAATTAAATAAAACTAAATATTATTAAATAAAATAAACTTAAATTAAATAAATAACAATAAATTAAATTAAATTAAAAATCATCGCGTAGATAATAAGAAAGCTATACTTCCCCTTCTAGGTCACTCTCTCGCAAGGGCGGATCCAGGGAGGGGGCCATGGGGGCCATGGCCCCTCCCGAGAATGTAAAAAATATAAATTTAAATATTTGCTGTTTAAATGTTTTTAGTTTCAAACACATATTTATATATATACAAAACAAGAGATAAATATGTTTTCTGGACTAGAATTGAACAAAAGCAGTAACGGTAGCTTTAAGAATGACATAGGATATTCTATAAATCAAAATGTCGATAATTTTACAAAGTGCCAATTGTTAGAACGACCTTGGCAGCCTCAAAATCGTATCAATTCCCATATTCTGTTCACGCAAAGAATAAA

					AAAGAAAAAAGCGTTACTTGGATCACCAGCATTTAGAACAAATAAGTTGGTGGGTACTTTCACACAGTCAAAAGGGATTGTTTTACAAGTATTGCGTTTTATTTTTCTAATGAAAAATATGGTCACAATAAAGGGATGACAGCCCAAAGCCTTGTCCCGAAACCTTTAACATCTTTCGCCAAACTAATGGGCAAAGACGGAGCCATACAAACCCACGAAAAAACATCATACCACAACGAGTACGTTCAACTTGGGCTGAATTTTCTACAAAGTTATCGCAACCCGCAAAAGTCAGTTATTAACCAGATAGACTCTCAAAGGTCTAAACAGATACAAGAAAAAAAGAAAGACTACGACACTAGTAGAGTCCAGTGTTCTTAGATCGACAAAATATTCCTCTGAGAGGCCACCGTGATGATGGCCTTCTGCTTCTGGACGAAGATGCTGGACCTAGCAATAAGGGAAA **(2,331)**
MSTRG.22917.1	(1) No hit (2) No hit (3) No hit	Higher	(1) No hit (2) No hit (3) No hit	(1)1451-1215 XRNNVIFSYRVFARTPRYMVDSPNLRHNCLHSNHNKDALEINKHEEYSQIMIQECPSNIQHVLVCLFVYSAFLLWFVV* **(79)** (2)1-234 KRTYLFVSWSNIFWTNIFWTRYNIFSCLYRIQATKMRTFKRVKGIENLIKKTKTKRVLNILLVPKQNETIQLYNQKE* **(78)** (3)614-787 MNLHNIFTCALCQNAINLRHFIQKGKTCPTALSQLNKIKYFLLIVPSANSLNNFHNY* **(58)**	AAAAGAACATACCTGTTTGTTTCCTGGTCCAATATATTTTGGACCAATATATTTTGGACCAGGTACAATATTTTTTCTTGTCTCTATAGAATCCAAGCTACCAAAATGAGAACTTTCAAAAGAGTGAAAGGCATTGAAAACTTAATAAAGAAAACAAAGACAAAACGAGTACTGAATATTTTACTTGTTCCAAAACAAAATGAGACCATACAATTATACAATCAGAAAGAATAATGTCACTAAACAATCAAATAATAAATTACACTAATGAACTTGTTTCCATTGTGACTAATTTCAAAAGAAGAAAAATAACTATGTTTAGGTAAATGTACTGCCTGATTAGTTGACACTCTAAGCTCAATTCAAATAATAAATTGCTCCTCTACTGATTTGGACTTATTGCATTCAGCTATGAGCCTATGAGGTACTATCAGCTTCCAGAGTAAAGTGTTAAACAATAAAGGGTGTGGGTTAAAATGTTTCAAACTAAATGCTGATAGTGGCAGTGATTGCCTCCGAAGTAATATATTTCTGCATTCTGATTTTATTTGTAAGTTGTATAAATTGCCTCAAATACTTGCAAAACTTATGAATATTGTTGGAAACTGCTAAAATGAATTTACATAACATCTTTACATGTGCTTTATGTCAAAACGCTA

					TCAACTTAAGACATTTCATTCAAAAAGGCAAAACTTGTCCCACAGCACTTTCCCAATTAAACAAAATCAAATATTTTTTACTTATTGTACCCTCAGCAAACTCTTTGAATAATTTCCATAATTATTAAGCACATCTTAATAGCTGATTTGCATTCAAAGTTGAGACTGTCAGTACCTTACTGTCAAGGATTTTCAGAGTGTGACATTACACTGATAAAATAGCAGAATCCTTAATAAATTTAAACCTTACAATAGGACTTTTCAATGCTTCTCATTTGTTTCGAGCCTCTGTCATATGTTGTATACATATTAATATTATACAAGGATTATATTACATATAACAGAGGTTAGAAACAAATGAGAAGCGTTGAAAAGTCCTATTACTGTGTTCTTCATTCTATAAACAAAGATTTCTTTTACTAAAATCTCAATAAAGATGCACTAGAAATAAACAAAGACACGTTGAATGTTACTAGGAGCACTCCCGATGATTTATTGTAAAACATAATTTGGGATTTACAATATAGTCGATTCACTAATCTGAGACACAACTGTCTACACTACAAACCACAATAAAAATGCACTATATACAAATAAACAAACCAAGACATGTTGAATGTTCGAGGGGCACTCCTGAATCATGATTTGGGAGTACTCCTCATGCTTGTTTATTTCTAGTGCATCTTTATTGTGATTGGAGTGTAGACAGTTGTGTCTCAGATTAGGCGAATCGACCATATATCGAGGGGTTCGAGCGAAAACCCGATAACTAAAAATAACATTGTTTCGANNN **(1,452)**
MSTRG.25260.1	(1) Probable multidrug resistance associated protein lethal(2)03659 [Leptinotarsa decemlineata](100%;49%)/ ABC transporter ATP-binding protein [Oryctes borbonicus] (100%;34%)	Higher	(1) P-loop containing nucleoside triphosphate hydrolase superfamily (IPR027417)/ABC transporter type 1, transmembrane domain	(1)325-3045 MYTWEDYFLGKVDTARKLEIKKMLSLLYMRIAVETSGLLVSKLGFYLLVMTYIWVNDEAEATTVFFIMSNYGTISYTLGILIPDGITTTYEFLSTTTRLNSVLQAKELPIPKIKDKTSRPTIHIKDASISLGKENILNNITLKVTPGLTLVTGQVGSGKSSLLKLMLQSYPLNTGDVSVEGRISYASQDPWLFPSSVKQNILFGEDLDPK	TGTGGGATCGGTCCTCACCGGAGAGACCGCAGGCATTCGGATACAATTAGCGTCTCTTTGTAAAGACAATGAAGTCGACTTTAGTAACAAGACATTTACTCAACATATACACACTACACATTACACTATATGATTGCAAAATCAACTGCATCATGTCGGTAGCCATTAGTGGTCGAGGCATTTAAGCTAAATTAAAAAAATACTCTAAATGTTTTAGTGTACTTGGGAAACATATTGAAAAAATTCAGAATACAAACGAACAGATATACTGACCAACGTTTGCAAATCTTTCAAGAAGCACTCTCTGTTATAAAAATTATCAAAATGTATACATGGGAAGA

			superfamily (IPR036640)/ABC transporter-like domain (IPR003439)/AAA+ ATPase domain (IPR003593)/ABC transporter type 1, transmembrane domain/ABC transporter, conserved site (IPR017871) GO:0055085 transmembrane transport GO:0005524 ATP binding GO:0016887 ATPase activity GO:0016021 integral component of membrane	RYAEVLRICALEFDLKLLEKGDETILIDKGSNLSKGQQARINLARAVYRISDIYLLDDCLTALDNEVQDYIFKECIQTFLKGKICVLVTQTERHMKQSDIVVIMKNGEIFKTTRPTNQSLKEIKDINTLQNDDVKEKEMVENDNRENKKLLEAEQTVEQRKKVYEETIQKGSVSYKNYKKYFGFGGFALMVIYCIVCGGFQFATSYSDKLLTKWVDDQQHVINFKAKLMQFNISSLDPYQNESFTLLTNGKALKDEIKDFNFTNNNNFTKINKSKNVNTHNNNLTKENIIQGFDKAQEKAKNTFKWYYIMLFSGAVMDIIKTGIIYDICRRASINLHYTLVKNILNAVMHFFDTHFIGNILNRLSQDLVMMDERLGYILNESFGVIYMMCGTAILIVSVNKLFIFYTVFIITCLMALGRIYLPFNRNMKRLEASTRSPMIGHLNATLEGITTVRAYKAENILTDEFDRHHDLFTSTYYTRTVFHRAYGFCATFLSTTLVTMLILTFIFIDTGASAGNVGLALQQAFLLGSFIASAVNVYTDLETMMTSVERVFEYTDIETEKQDGTLVTGWPKEGSISYEYVSLTYNKTDHILKNVSFEVKSNEKIGIIGRTGAGKSSLISTIFRLYGIHGKILIDKIDIKTLPLKILRKNIAIIPQDPVLFSGTIRSNLDPFNKFNDEELWSAIDKANLKSFILDL **(908)**	CTACTTTTTAGGAAAAGTTGACACTGCTCGCAAGTTAGAAATTAAAAAAATGCTCAGTCTGCTCTACATGAGAATCGCAGTGGAAACTAGTGGACTGTTGGTATCAAAACTGGGATTCTATTTATTAGTAATGACATATATTTGGGTGAATGATGAAGCAGAAGCCACCACTGTCTTTTTTATAATGTCTAACTACGGAACGATTAGTTACACATTGGGGATTTTAATACCAGATGGTATTACGACTACTTATGAATTTTTATCAACAACAACCAGGTTAAACTCAGTTCTACAAGCAAAGGAGTTGCCTATACCCAAAATAAAGGACAAAACTTCTAGGCCTACCATACATATAAAAGATGCTTCAATTTCGTTAGGCAAAGAAAATATCTTGAACAACATTACCCTCAAAGTTACACCAGGACTTACATTGGTGACTGGGCAAGTAGGATCAGGTAAAAGTTCGTTACTAAAACTGATGTTGCAAAGTTATCCATTAAATACTGGTGACGTAAGTGTAGAAGGTAGAATATCATATGCTTCACAAGATCCTTGGCTGTTTCCATCTTCTGTGAAGCAAAATATTTTGTTTGGAGAAGATCTAGATCCGAAAAGATATGCCGAAGTGTTGCGAATATGTGCACTAGAATTCGATTTAAAACTGTTAGAAAAAGGTGACGAAACAATTCTAATCGACAAAGGATCAAATTTAAGTAAAGGCCAACAAGCCAGAATTAATTTGGCAAGAGCTGTATACAGAATCAGTGATATATACCTACTAGATGATTGCCTCACTGCCTTAGATAATGAAGTCCAGGATTATATTTTTAAAGAGTGTATACAGACATTTTTAAAAGGAAAAATATGCGTCCTCGTAACCCAAACAGAACGGCACATGAAACAGAGCGATATTGTTGTAATTATGAAGAATGGAGAAATATTTAAAACGACAAGGCCAACTAATCAAAGCCTAAAAGAAATTAAGGACATAAATACTCTTCAAAATGACGATGTAAAAGAAAAAGAAATGGTTGAAAATGATAACAGGGAAAATAAGAAACTGTTGGAGGCCGAGCAAACTGTTGAACAACGAAAGAAGGTTTATGAAGAAACGATTCAAAAAGGGAG

					TGTTAGTTACAAAAACTATAAAAAATATTTTGGATTTGGTGGATTTGCCTTAATGGTTATATACTGCATCGTATGTGGAGGTTTCCAGTTTGCCACAAGCTATTCCGATAAACTGCTGACAAAGTGGGTCGATGATCAACAACACGTCATAAATTTCAAAGCCAAGTTAATGCAGTTTAATATATCATCACTGGACCCATACCAAAACGAATCATTTACGTTATTAACGAATGGGAAAGCATTAAAAGATGAAATTAAAGATTTCAACTTTACAAATAACAACAATTTTACTAAAATAAATAAATCTAAAAATGTAAATACTCATAACAATAATCTTACGAAGGAGAATATTATTCAAGGATTCGATAAAGCTCAAGAAAAAGCCAAAAATACGTTTAAATGGTACTACATAATGCTATTCTCTGGAGCAGTGATGGATATTATCAAAACTGGTATCATATATGACATATGTAGAAGAGCATCGATAAACCTACATTATACTTTAGTAAAAAATATTCTGAATGCTGTAATGCATTTCTTTGACACTCATTTTATTGGCAATATTCTGAATAGGCTATCACAAGACTTGGTCATGATGGATGAGAGACTTGGATACATTCTCAATGAATCTTTTGGGGTAATCTACATGATGTGTGGAACAGCAATACTGATCGTATCGGTGAATAAATTATTTATATTTTATACAGTTTTTATAATAACATGTCTTATGGCATTGGGACGAATATATTTGCCTTTCAACAGAAATATGAAAAGGCTAGAAGCTTCCACTCGTAGCCCAATGATTGGTCACCTAAACGCAACCTTGGAAGGTATAACAACAGTAAGAGCATACAAAGCTGAAAATATCCTAACAGATGAATTTGATAGACACCACGACCTATTCACTTCCACTTACTATACTAGAACTGTATTTCATCGCGCATATGGATTCTGCGCAACCTTTCTTAGTACAACTTTAGTAACTATGCTCATTTTGACGTTCATTTTTATAGATACAGGTGCCAGTGCAGGAAACGTTGGCCTAGCCCTACAGCAAGCATTCCTGCTTGGAAGCTTCATCGCCTCGGCAGTGAACGTATACACAGACCTGGAAACAATGATGACATCAGTCGAA

					AGAGTCTTTGAATATACAGACATTGAAACTGAAAAACAAGACGGAACCTTAGTAACTGGTTGGCCAAAAGAAGGAAGCATATCATACGAATACGTGTCTTTAACTTATAACAAGACCGACCATATATTAAAAAACGTTAGTTTTGAAGTTAAAAGCAACGAAAAAATTGGAATAATTGGACGAACAGGAGCGGGAAAATCATCTCTTATTTCAACAATATTTAGACTGTATGGAATACATGGCAAGATACTGATAGATAAAATTGATATCAAAACGCTACCACTAAAAATCCTCAGGAAAAACATTGCTATAATTCCTCAAGATCCAGTACTTTTTTCTGGCACTATCCGATCAAACTTGGACCCCTTTAATAAATTTAACGATGAAGAGCTTTGGAGCGCCATCGATAAAGCAAATTTGAAAAGTTTCATTTTAGATTTGGA **(3,047)**
MSTRG.41828.1	(1) EAL domain-containing protein [gamma proteobacterium symbiont of Ctena orbiculata] (18%;41%) (2) Serine beta-lactamase-like protein LACTB, mitochondrial [Rattus norvegicus] (54%;31%)	Higher	(1) No hit (2) No hit	(1)3-857 HPDEYNGELERKYEKPGRLTRITGEDQIRMSELEIQYEGRWVRKYLEEQFPHFTRDQIRRTRAEPQYQELLERLREDRERTPPGSPVPGTSNTESFVNHSSGTESSPERRSVEGISEHRSNPERTASQGGDVSASLTLNVLDADAEEFVPMGNRAALATYLDEYFRTHDTWSDPEREIYRNSQLDNAEERREGVRLLLDEYITTDILSVSTGKRRSKNANSKAKTAPVINNRDHERALNYRLAQHRYRTDRSSLAQAIIDGKPLWGVDASPNIKAVEKEYRAIFS **(286)** (2)418-630 MCWTPMPRNSFRWETVRRWPLISTSILERMIHGAIRKERSIETLNWITLRNVERVSDCCWTNTSPLIYYQ* **(71)**	CACATCCTGACGAGTACAACGGGGAGCTCGAGCGGAAATACGAGAAACCTGGAAGGCTGACAAGGATCACTGGTGAGGACCAGATCCGTATGAGTGAATTGGAGATCCAATATGAGGGTAGATGGGTCCGTAAGTATCTGGAGGAGCAATTCCCCCATTTCACACGGGACCAGATTCGGCGGACGCGCGCCGAACCTCAATACCAGGAACTCCTCGAAAGACTCAGGGAGGACAGGGAACGGACCCCACCTGGGAGTCCGGTTCCCGGAACTTCTAACACCGAGTCATTCGTAAATCACTCATCGGGGACGGAATCTTCTCCTGAGAGACGGTCAGTCGAGGGCATATCGGAACACCGATCGAACCCCGAACGTACTGCTAGTCAGGGCGGTGATGTGTCAGCTTCACTGACTTTGAATGTGTTGGACGCCGATGCCGAGGAATTCGTTCCGATGGGAAACCGTGCGGCGTTGGCCACTTATCTCGACGAGTATTTTAGAACGCATGATACATGGAGCGATCCGGAAAGAGAGATCTATCGAAACTCTCAACTGGATAACGCTGAGGAACGTCGAGAGGGTGTCAGACTGTTGTTGGACGAATACATCACCACTGATATACTATCAGTGAGCACAGGGAAGCGAAGATCGAAAAATGCA

					AATTCAAAGGCGAAAACCGCCCCTGTGATCAACAACAGAGACCACGAAAGAGCGCTGAACTACCGTTTAGCGCAACATCGATATCGAACGGACAGATCTTCTCTGGCTCAGGCAATCATAGACGGCAAACCCCTATGGGGGGTCGATGCGAGCCCTAATATAAAGGCTGTTGAAAAAGAATATAGAGCGATATTCTCAT **(858)**
MSTRG.79626.1	(1) No hit (2) No hit (3) No hit (4) No hit	Higher	(1) No hit (2) No hit (3) No hit (4) No hit	(1)1467-1796 MQLCRLPMSLHSSFFIPCNFYKGGNRYKRESVSELRNPKILLFLNIYLFENGLFWVSTFCKPLYFDETESFQVRKICRNANKKKKPKTITPNSKTLKPKPKSRRKPNGN* **(110)** (2)986-798 MNSTNIKADRFILNINIRYSIFKPSNLTRTFYFQLFTSYMYHIVTLYIFFCKLYGFRENCNK* **(63)** (3)1335-1150 MDHFELFCSHQESNCNDAQSMSISKEVYFLVGVCLEWSMVRRFRKSNGFLLSDVNLWVTFH* **(62)** (4)1694-1843 MQKRQQKKKTKNHNTKLQNSKTKTKIQTKTKRKLNPETIEYCLGFRKIK* **(50)**	GAAAAGAGGGCTCTGCGCAAGAGAATTGAAGTTTGAGCTAAGAGATAGGTTGCCTAGGTACTACGTTTTCTCGACTTTTTTTTCATGAAATGAAAGCTTGGAACTTGGATGCGACATTAATGAAAAAAGTGGAGGCATTTAAGTTGTGGGTGTACAGAAGAATCCTGAAAATATCATGGACAGAACACGACACAAGCTAAAAGGTTCTGAGAAAAATTAATAAATAATTAAAATCTCATTCACTATTTAATCAAGAAAATTAGAATATTTAGGCCATACTACACGTGAACAGAGATCCAACCTGCTCAAACTGATTATGCAGTAAAAAATTCAAGTAAGGATGCAACGCTAAACTCGGCTTTTGAAAAAAAAAGATGGTCGAAATTAGCACGCAATTTGAAATAAAGTGAAGAAAGTATAAAATAGAGAAGAAGGAAGGAAGAAGAATAGAATAGAGCACCGGCTAAGTAGCTTGAGAAACAAGAGACTAAAAAGAAGGTCGGATTCGAGGGCCAGAAAAAGGAATAAAATTAAAACAGATTTCTTTCTGAAATAATTTGAGCGTGAAAGAAGGAGAGCTGGAAGAGTAAAACAGAAATTAGATAAATAAAACCAGACAGAGATCCTGAACAAACTAAAATGGAGGGCGCCAGTCTTACTCTATAGCAAATTAACAAATATATAGATAACTAAACTTTCCTGATATAAAATTTCAGTTGTTTCATCCTAAACCAACTACCCGTTGAATTGAAACTGGAAAGAGATAATATGTAATAAGCAAAAACGAATTTACTAAATTATTTATTACAATTTTCACGAAAACCGTACAATTTACAAAAGAAAATATACAATGTTACAATGTGATACATATAGCTGGTAAAAAGTTGAAAATAAAAAGTCCTAGTAA

					GATTTGATGGTTTAAAAATAGAATATCTAATATTAATATTTAAAATAAACCTATCAGCTTTTATGTTTGTACTGTTCATTGAAATTTAAATAAACTTAAAAAATAAAATACCGGAATATTTGAGATATATATTTTACCGCTTTTTGACCAGTAGCGATAGAAAATCCTGGATAAAGTCTCCCTGAAGACTTTAGTTGGCTGGTATTCACATCAGCGATCACCACACCGTGGTAGAGAGAAGTTCAATGGAACGTGACCCATAAATTCACGTCCGATAGAAGAAAACCATTCGATTTTCGGAAGCGTCTAACCATAGACCATTCCAGACAGACTCCAACCAGAAAGTAAACCTCTTTAGATATAGACATGCTCTGAGCATCATTACAGTTGCTTTCCTGATGAGAACAAAAGAGTTCGAAATGGTCCATAGAAAGATGGTAATGATCTCTGAATCGAAATTAAATATAATGCCTTTTATCTACCTACGGTTTTACTCACGTATCGAGTACTAGGAAGCAGATTTGTTGATCTTTACCTCAGTGAATTGATATGTTGTGGAATGCAACTATGTAGACTCCCCATGTCTCTACATTCATCATTCTTTATTCCTTGCAATTTTTATAAGGGTGGGAATAGGTATAAGAGAGAATCTGTTTCCGAATTAAGAAATCCAAAGATTTTATTATTTTTGAACATTTATTTGTTTGAAAATGGCCTCTTTTGGGTTTCGACATTTTGTAAACCTCTTTACTTTGACGAAACGGAAAGTTTCCAGGTACGGAAAATATGCAGAAACGCCAACAAAAAAAAAAAACCAAAAACCATAACACCAAACTCCAAAACTCTAAAACCAAAACCAAAATCCAGACGAAAACCAAACGGAAACTAAACCCTGAAACAATAGAATATTGTTTAGGATTTAGAAAAATAAAGTGACAATTTTTTTGCCGGGATAGAAAAAGAAATTCAAATAATTATTACCTTGTATAATGGATCTTCACACAAACCACTGCTTGCCACAACAGTAAAATGAAGACAATCAGATATTAGTGGTGTTTCAAAAACGAACTTTACAAAACGACGCATAGAGGTGGGAACGGATATATTTTTGGTAGGGGCTTTGTAACTGTAACAAGGA

					GAAGCACAGGGAGACGTAGAATATCAAAAGTGAGAGAATGGTACGAATGTACCATCAAATGAACTTTTCAGAGCAGATCCGTCTCTAAACAGATAGCGCTTAAATAATAAGTAATAATAAAAGAGGATCATACTTGCTGTAAGTACCTATAACGATTTTATTAGGTTTTTCCTGATATTTTATCTTCTCAATTTATTTGTATTGTAAAAACGCCCTATGGTGCTACTTGTATCATTTTGTAAAACGCAAATTCTTTTAACTGTAACTTATAGAAATTAGGCAGATTTTGTTTGGTAGCAGGAATAGGTAGTTATTAACACATGCAGGAATGTGTTCATCATTCATTCTATCTTGGCCACTACTGAACGTAGACCTCCCATAGTTCACCCCACAAATCCCTGCACTGAGCCGCTTGCATCCAATTTTGACATATCCGCTTCAGGTCATCTGTCCATCTTGTTGGTGGTCACTCTCTACTTCGAAAAACGTCCTCTCTGGATGCTTTATCCATCTGCCGTCGTTCGTTTTC **(2,574)**
MSTRG.25915.1	(1) Lysyl oxidase homolog 2-like [Leptinotarsa decemlineata](97%;77%)/Lysyl oxidase homolog 3-like [Anoplophora glabripennis] (95%;77%)	Lower	(1) SRCR-like domain superfamily (IPR036772)/ Lysyl oxidase family (IPR001695)/ SRCR-like domain (IPR017448)/SRCR domain (IPR001190)/ Lysyl oxidase conserved site (IPR019828) GO:0055114 oxidation-reduction process	(1)86-1558 MQLSGVGVCLVVISIFGFSVLCETPEEIKLQRALLVRKHLKRLKKVDGGIKLVGGRGEFEGNVEILHDGSWGAICDDEWDVTEAKIICKQLGYTGANALPTVNSYFGPARRRYWMDNIYCNGGETEISNCRFDGWGQHDCASTEAAGVICEKPEAVLKRQIPRHAREMSRLPKDTKIRLANGRVRTEGRVEIQIGNGDWEVICGDGWSLLEALVICRTLNMGYASDAMQTDFFGNLTKHSIGGVKCIGNEISISQCMHDKFATGRCESADVAAVSCTNILADLSIDHYELMRTAHLEDRQMFYLQCAMEENCVASTAYEIQKENPAWHLDSRRLLKFTAKIFNAGNADFRPAIPKHLWEWH	ATCTAGTTCATGACATATATTACAGCTCCGAACTCTGTTGCTTAATAGTTATCTAAACGCTATTACGGATGTATAGCATGAAAAAATGCAGTTAAGCGGAGTGGGAGTTTGTTTAGTTGTAATTTCGATTTTTGGATTTTCAGTTTTATGTGAAACTCCTGAGGAAATCAAGCTTCAGAGAGCGTTGCTTGTCAGAAAGCATTTAAAGCGGTTAAAAAAAGTAGACGGCGGTATTAAATTGGTTGGCGGTAGAGGAGAATTTGAAGGAAATGTGGAAATCCTCCATGACGGCTCCTGGGGAGCGATATGTGACGACGAATGGGATGTTACCGAAGCGAAAATTATATGCAAACAACTCGGCTACACAGGTGCAAATGCTTTACCAACAGTAAATTCATATTTTGGACCAGCAAGGAGAAGATATTGGATGGATAATATTTATTGCAATGGCGGTGAAACTGAAATATCAAACTGTAGATTTGACGGTTGGGGACAACATGACTGTGCTTCAACTGAAGCAGCGGGTGTAATATGTGAAAAACCAGAAGCAGTTTTGAAAAGGCAAATTCCAAGACATGCACGTGAGATG

			GO:0005044 scavenger receptor activity GO:0005507 copper ion binding GO:0016020 membrane	MCHLHYHSMEVFATFDIYDSKGQRVAEGHKASFCLEDNQCLPGIKQKYACANYGDQGISVNCSDIYKYTVDCQWVDISDLKPGLYKMKVAVNPEFKVAEMTFENNAAVCDFYYSEYYGSVTNCKVQRP* **(491)**	TCACGTCTTCCAAAAGATACAAAGATAAGATTAGCAAATGGAAGAGTTAGAACGGAAGGCAGGGTTGAAATTCAAATAGGAAATGGAGATTGGGAAGTAATTTGTGGAGACGGATGGTCCTTATTGGAGGCTTTGGTCATCTGTAGAACATTAAATATGGGATATGCAAGTGATGCCATGCAAACTGATTTCTTTGGAGGAAACCTGACAAAACATAGTATTGGCGGTGTTAAATGTATTGGAAATGAAATTTCAATTTCACAGTGTATGCATGATAAATTCGCAACAGGGCGATGCGAAAGTGCTGATGTGGCCGCTGTTTCTTGTACAAATATTCTAGCTGATCTTTCAATTGACCACTACGAGCTTATGAGAACAGCTCACCTCGAAGACCGACAAATGTTTTACTTACAGTGTGCTATGGAGGAAAACTGTGTAGCGTCCACAGCTTATGAAATTCAAAAAGAAAATCCTGCATGGCATCTGGATTCAAGAAGATTATTAAAATTTACCGCAAAAATTTTTAATGCTGGTAATGCAGATTTTAGGCCTGCAATTCCAAAACACTTATGGGAATGGCATATGTGTCATTTGCATTATCACAGTATGGAAGTTTTCGCCACATTCGATATCTACGACAGTAAAGGCCAACGAGTAGCAGAAGGTCACAAAGCATCATTTTGTTTGGAAGATAATCAATGCTTACCAGGGATAAAACAGAAATATGCATGTGCCAACTATGGAGATCAGGGCATATCGGTAAATTGTTCTGATATTTACAAGTACACAGTGGACTGTCAATGGGTAGACATTTCTGACTTGAAACCAGGACTATACAAAATGAAAGTTGCTGTTAATCCAGAGTTTAAAGTAGCAGAGATGACTTTCGAAAACAATGCTGCTGTTTGCGATTTTTATTATTCTGAGTATTATGGAAGTGTAACTAACTGTAAAGTTCAGAGACCTTAGGATCCTGTAGTAAATAGTAACCTTCTACGAAGGTTATATTTAAAAATAGTAAACTGTTTAATACACAATACTATTACTAAATATTGTAGCTATTGTAAATTATTTATTATTATACGATACATATTTAACTACGAATTTTTATAAAATATCTAATACAACGA

					CCGGAAACACACTATACATATAGTCTGGGCACATTATCGGGGAATAGGCCATTTTTGGGAAAAGTTATTTACCAGTAACTGTATTGCTGGAATCGAATCTTATGATTGTATATATTAATAATATAGGTATGCAAAGTTCGCAGATAGTGTGCTACTTTTTTTATAAACAAAATGGCGCCCGAAAATCGTATTTTTTTTTTCAATTTTTG **(1,928)**
MSTRG.65512.1	(1) Neprilysin-4-like [Leptinotarsa decemlineata] (95%;42%)/neprilysin-1 [Anoplophora glabripennis] (75%;46%)	Higher	(1) No hit	(1)2-265 ISKVDSLTAAQIRHNHGTSYENIIEEGFVTTGGSDRKSSQSLKPFDIFLRQMSLKLRNATESFLTDTEVFTNLDDVVQFTRAVFSVAV **(89)**	GATATCTAAGGTAGATAGTTTGACCGCTGCACAAATTCGACACAACCATGGTACGTCATACGAAAATATAATTGAAGAAGGTTTTGTAACAACAGGTGGATCTGATAGAAAAAGTTCACAGAGTTTAAAACCATTTGACATTTTCCTGAGGCAAATGTCTTTAAAATTGAGGAATGCCACTGAAAGTTTCCTAACTGATACCGAGGTTTTTACTAACTTGGACGATGTCGTCCAGTTTACAAGAGCTGTGTTTAGCGTCGCTGTA **(265)**
MSTRG.66987.1	(1) P450 6k1-like [Leptinotarsa decemlineata] (93%;48%)/P450 6k1-like [Anoplophora glabripennis](94%;55%)	Lower	(1) Cytochrome P450 superfamily (IPR036396)/ Cytochrome P450 family (IPR001128)/ Cytochrome P450, E-class, group I Family (IPR002401) GO:0055114 oxidation-reduction process GO:0005506 iron ion binding GO:0016705 oxireductase activity, acting	(1)2-421 ESMRKYPPIPFLDRMPLSDYTLDGTDLVVKKDMTVIIPFFALHRDENLFPNSDGYDPERFREEIQSEGLFYLPFGAGPRACIGKRLGLLGLLVSLSYIVLNFKVEKCPETPSKIEFEPKSFPLVSKQGLPLRITPIENK* **(140)**	AGAGTCAATGAGAAAATATCCTCCTATACCGTTCCTGGATAGGATGCCTTTGTCTGACTACACACTAGACGGTACTGATTTAGTGGTCAAAAAGGATATGACAGTAATAATACCATTCTTTGCACTTCACAGGGATGAAAACCTTTTCCCTAACTCTGATGGATACGATCCAGAAAGGTTCAGAGAAGAAATACAATCAGAGGGACTATTTTACCTTCCGTTTGGAGCAGGTCCCAGAGCTTGTATAGGTAAAAGACTTGGACTGTTAGGTTTATTGGTATCATTATCATATATAGTACTTAATTTTAAAGTAGAAAAATGCCCAGAAACTCCATCGAAGATTGAATTTGAACCCAAAAGTTTTCCATTGGTTTCTAAACAAGGACTGCCTCTTCGAATTACGCCTATTGAAAATAAATAAAAGCAACATTGTAATGAAGATTTTTTATGTTAAAAAATTATTATATCAATAAAATAATTATGTAGTTGTTAGTAAGTTAA **(501)**

			on paired donors with incorporation or reduction of molecular oxygen GO:0020037 heme binding		
MSTRG.87517.1	(1) Glutathione S-transferase delta class member 3 [Leptinotarsa decemlineata] (99%;68%)/Glutathione S-transferase delta [Lasioderma serricorne] (99%;69%)	Lower	(1) Thioredoxin-like superfamily (IPR036249)/ Glutahione S-transferase, C-terminal domain superfamily (IPR036282)/Glutathione S-transferase, N-terminal domain (IPR004045)/Glutathione S-transferase, C-terminal-like domain (IPR010987)/Glutathione S-transferase, C-terminal domain (IPR004046) GO:0005515 protein binding	(1)492-1142 MPIDCYYVPGGAPSRNVLLAAKACGVELNLKYMDLMSGEQMSPEFLKLNPLHTVPTINDNGFVLFESRAIMTYLADQYGKDDNLYPKDPKKRAIVDQRLYFDMSTMYGRLADYYYPVIFGGASYDPEKLEKIKEAFSFLDQLIDNNDFAAGSNLTLADLALASSVSTYELLGFDFSSYKNVVRWFEKAKATIPGYEEANAEPLQQFKALMEKLAKK* **(217)**	TTATTTCTTCAATACTACTTAACTTAATCTTTAAGAAATATAATCTCTAAATACTTACTTCGCTTCAGTTATGCTCTTTCATTGTAATGGTAATTTATTTAATTTACCTTGTAATTGTTCATGGTTAACCTCCAATTTTGATACGCTTCTGCGATAGTTCTAGTAATGATATTGCAAGTCATCGTGATTTTCTTCTTAATCATTCGCGAATTGTGCAGATAATTGTGAAGTGTTGTAGGTACATGTAAGTGTGTGTAGTGTTGCGATTTTAGATGGTTTACATTTATGTGAAAGGAGGATAAAAAAGAAGTCGGACAACACCGCTTGGAAATGACTCAAAAGTTGCGTCGAATCCCACCGGCATAAAGAAGTCGTCCAACTTATATTTTCCATTCACATATTACCAGACCGTAGACCGCATTCCGCCGGTAGTTGTGGCTAAACCAAGAAGTGTGTAAGTTCCAGATCGACTGTCTCCTTTCACCGCCAATATGCCTATTGATTGCTACTACGTTCCTGGTGGAGCCCCATCAAGAAACGTCCTTCTAGCTGCCAAAGCATGCGGAGTTGAACTTAATCTCAAATACATGGACTTGATGAGCGGAGAGCAAATGTCCCCTGAGTTCCTTAAACTGAACCCTCTGCATACTGTCCCCACAATCAACGACAATGGTTTTGTTTTGTTCGAGAGCCGAGCAATCATGACCTACCTTGCAGATCAATATGGTAAAGATGACAACCTTTATCCAAAAGATCCTAAGAAGAGGGCTATTGTTGACCAGAGACTGTACTTTGATATGAGCACTATGTATGGAAGACTTGCTGATTATTATTATCCCGTGATCTTCGGTGGAGCCAGTTACGATCCCGAAAAGTTGGAAAAGATCAAAGAAGCCTTCAGC

					TTCCTCGACCAGCTCATTGACAACAACGACTTTGCTGCTGGCAGCAACCTCACTTTGGCCGACTTGGCCCTTGCCTCATCAGTTTCCACTTACGAGCTGCTAGGATTCGATTTCAGCTCCTACAAAAACGTTGTCAGATGGTTCGAGAAAGCAAAAGCCACGATTCCTGGATACGAAGAGGCCAACGCTGAGCCGCTCCAGCAGTTCAAAGCTTTGATGGAGAAGTTGGCAAAGAAGTAGATAGGATTGGATACAGTATTATTGTTAAGGAAGTCTTGATGCTTCAAGATTATTGATTTATGCCACTTGAAGTTGTATTTTATCTTTTTTTAATAAAACCTGTTATTTTTATACTTGCTTAATTTA **(1,268)**
MSTRG.95019.2	(1) Uncharacterized protein Dyak, GE17131, isoform B [Drosophila yakuba] (72%;44%) (2) PREDICTED:RNA-directed DNA polymerase from mobile element jockey-like [Bemisia tabaci](95%;53%)	Lower	(1) No hit (2) No hit	(1)1670-1257 INTILALARPSDSDDPLPDGQTNAPSVPTSDSPPDTVTDSSSTAPTDSPPEPATDSSSASPTDSPPEPATDSSSASPTDSPSDSTTASSSGSSTDLSSDSTGATPESTTKGSAAGLFTGTKYFMATFVIVVLNYFLM* **(138)** (2)2-220 EDQVNGANRAASCLNDTIWRNKNIGKDIKGRIYKTVIRTIMTYAAETRPDTERTKRLLKTAEMKTLRKIDGG* **(73)**	GGAAGATCAAGTTAATGGAGCAAACAGAGCCGCAAGTTGCCTGAATGACACAATATGGAGAAATAAAAATATCGGAAAAGATATAAAAGGCAGAATTTACAAAACAGTCATCAGAACAATAATGACATACGCGGCAGAAACACGACCCGACACAGAGAGGACAAAAAGATTGCTCAAAACAGCGGAGATGAAAACCCTTCGAAAAATCGATGGTGGCTAAAAGTGCAGATATACGACAGAAGACAGGGTAAGAAACAGAACAATAGAATGGAATGACCACATAAGCCGAATGACAACAGAGTAGTCAGGACAGCGAGAGACGGTTTCCCAATAGGCAGACGATCAGTGGTAAGACCACGAAAACGATGGAACAACTTACTAGAGGCGCATTGAAAAAACAGACAGTAATGTCTATACAAAAAGGAGAAGAACAATTTATGAAAATTTTTATAATAAATAAACAAAATGGCATCAATAATCCATTGCTTTTGTGCTTATTTTTATTTATACAATGAGTTAACTTGTTACAATTTTCAAATAAAATTGGTTATAACTTTGTAAAATACTCTGTATAACATAACAGTCCTTTATGCATTTGTAATGGCGAAGTTAAGAAGATTTTGAATATAAAATAAAATACAGGGTATTCCAATAAATAAAAATAAAAGACTAAGTTTTCACTCTAATGGCATATAGCATATCCCACCAAAATAAAAATAAGTTTGGTCTGCCACTAT

					GTTATCGAACATCCTCTGTAACATTCTAATTAATTTTATAAATGTGAATCTCAAAGTTAGCTACAATTTGTGCTATTTACATTTAATTGGATATGTAAATAAATTCTAATTCGGTAAGATTCTCCTAAATTGATGCAACCCAACTCCAATGATAAATCGCTGTACCGTTTAGATACGACGATAAATTAAAACAACTCGATCCTTGTGATAAGTTGATGCAATCCGATACCAACTTCAACCCAACTCCAACTTTGATAAGTCGTGCGATGCACCGTTTACACACAATGATAAGTTGCAACAATTCGATTGATATTGATAAGTTGTTTGATTTATCGCTGTGTCTAAACGCCGCTTAATATTGGTCGATTCCAACGGTTATCAGCTTAATTTATTTATGTAAAAATAAAATTTTATTTACAAAATTAATTTTACAAAAATTATAATTTAATTCGAATTGACTTTACAACTATATTCATTTACAATCGTGCATAAATACAAAAATATTTATTTTGATTTAATTTACATTAAGAAGTAATTTAAAACCACGATTACAAATGTAGCCATAAAATATTTCGTGCCTGTAAATAAACCTGCAGCTGAACCTTTCGTAGTTGACTCAGGTGTTGCACCAGTTGAGTCACTTGATAAATCTGTCGATGAACCAGATGACGAAGCAGTTGTTGAGTCAGATGGAGAATCTGTAGGTGAGGCAGATGATGAATCCGTTGCTGGCTCAGGTGGAGAATCTGTAGGTGAAGCAGATGATGAATCAGTTGCTGGCTCAGGTGGAGAATCTGTAGGTGCAGTAGATGATGAATCAGTTACTGTGTCAGGTGGAGAATCTGATGTTGGAACAGATGGTGCATTAGTTTGTCCATCTGGTAATGGATCATCCGAATCGGAAGGTCTTGCTAATGCTAGAATAGTATTAAT **(1,670)**
MSTRG.5480.2	(1) Facilitated trehalose transporter Tret1-like [Anoplophora glabripennis](98%;62%)/Facilitated trehalose transporter Tret1-2	Higher	(1) MFS transporter superfamily (IPR036259)/Major facilitator, sugar	(1)210-1721 MNKDANIRVAAQEIEPLQKVKVEAPVPEEEEEPFDLTFKNIKTQLFAAIAVSWVSLIIGYSTAYTAPAEYSLRRDFGFNDNEISWISSFMPLGALLGGLGGGTLIEFIGRKWSI	ATTCACAATTCCTGCCCAAACATTGAATTTAAAAGTTCTTTGGTGATGAGTAGAGTCCGGAATTCTAAGCATAATGCTTATGGTAAATAATACAAAATGGCAACCATCGGAGACTGCAAAATACAGAGAGCCCTTGCATTTCGACTTCAACCACCGCGACGAACTTGTCGTCCCTTGCTGATTCGAACTCCGCCATA

	homolog [Leptinotarsa decemlineata](99%;60%)		transporter-like family (IPR005828)/Sugar inositol transporter family (IPR003663)/Major facilitator superfamily domain (IPR020846)/Sugar transporter conserved site (IPR005829) GO:0055085 transmembrane transport GO:0005215 transporter activity GO:0022857 transmembrane transporter activity GO:0016020 membrane GO:0016021 integral component of membrane	MLTNVCFLVSWLLCYCASSYLYLYIGRIIIGLSVGVASLTLPVYTAESLQPEVRGSLGLLPTGLGNLGVLICFTLGAFYEWQVLALVGALVSIPFLVMIWFIPETPKFLLGKGKLDKAKSSLQWLRGKKSDIGKEFTDLQRIQQESNELNATLLDLFSKKNMKLIVVALGLMFFQQFSGINAVIFYTTTIFEYAGSSLDKKYCTIIVGVVNFGSSFIAAMLIDRLGRKVLLYISSISMIVSLNVLGIYFYLKDVAHTDISAIGWLPLVSFMVYVLGFSLGYGPIPWLMMGEIFPAKIRGPAASLATAFNWTCTFIVTKTFLLIRDGIGTHYTFWMYGIIVTLSLFFVFVFVPETRGISLADIERRLTGIRTTRRISSVANLKPLPSTIG* **(504)**	AACCAGAAAAAGATGAACAAGGACGCCAACATCCGGGTGGCGGCTCAAGAAATTGAGCCTCTCCAGAAGGTGAAAGTGGAAGCGCCAGTTCCGGAAGAGGAGGAAGAACCATTTGACCTCACTTTTAAAAATATCAAAACACAATTGTTTGCTGCAATTGCTGTATCATGGGTTTCTTTAATCATAGGATACTCCACTGCATATACAGCACCAGCTGAATATTCCCTTCGGAGAGATTTCGGTTTTAACGACAATGAGATATCTTGGATTTCAAGTTTTATGCCTCTTGGTGCTCTACTTGGAGGACTTGGCGGGGGAACTCTTATTGAATTCATTGGCCGTAAATGGAGCATCATGTTAACAAACGTTTGTTTCCTGGTGTCCTGGTTGCTCTGTTACTGCGCTTCAAGCTACCTATATCTCTACATAGGCAGGATAATAATTGGGCTCAGTGTGGGGGTAGCCTCCCTAACGCTTCCTGTGTACACCGCTGAAAGTTTACAACCCGAAGTTCGAGGATCTCTAGGACTTTTGCCAACTGGTCTGGGTAACTTAGGTGTACTTATTTGCTTTACTTTGGGAGCATTCTACGAATGGCAAGTACTTGCCTTAGTGGGGGCTCTGGTATCCATTCCGTTCCTTGTAATGATTTGGTTTATACCAGAAACTCCCAAATTTCTTCTAGGAAAGGGAAAATTAGACAAAGCAAAATCATCTTTACAATGGCTTCGTGGAAAAAAATCAGACATCGGAAAAGAGTTCACAGATCTTCAAAGAATACAGCAGGAATCTAATGAGCTTAATGCAACTCTCTTAGATCTTTTTTCGAAGAAAAATATGAAACTTATAGTTGTAGCCTTAGGTTTAATGTTCTTCCAGCAGTTCAGCGGTATAAACGCTGTTATTTTCTACACAACAACAATTTTTGAATATGCAGGATCAAGTCTAGATAAAAAATATTGTACAATAATTGTTGGTGTGGTTAACTTTGGATCAAGTTTTATTGCCGCGATGCTAATCGATAGGTTAGGTAGAAAAGTTTTGTTATATATTTCAAGTATATCCATGATAGTGTCGTTAAATGTACTTGGAATATATTTCTATTTAAAAGATGTAGCACACACTGATAT

					ATCGGCCATAGGATGGTTACCCCTTGTAAGCTTCATGGTATATGTTCTTGGTTTCTCTTTGGGTTACGGCCCCATTCCTTGGCTGATGATGGGAGAGATTTTCCCAGCTAAAATAAGAGGCCCTGCGGCATCTCTTGCTACTGCTTTCAATTGGACATGTACTTTTATAGTAACCAAGACATTTTTGCTCATCCGTGACGGTATAGGCACGCATTATACTTTCTGGATGTATGGAATTATTGTTACATTATCATTATTCTTCGTATTCGTTTTTGTGCCAGAGACCAGAGGAATCAGCTTAGCTGATATCGAAAGAAGACTGACTGGAATTAGAACTACTAGAAGGATTAGCTCTGTAGCGAATCTTAAACCATTACCAAGCACTATTGGATAACCAACTAAAGCTTCTGGTATTATACAACTTAAAAATTATTGTTTGAGTTTTATAATATGGAAAAAATCTGTGAAAAATGCCATATGACTTAGGTCTACAGTTTATGTGAAGATATTTAAAAGTAGATAATTAGGTGAGGCTTACCATCAACTGTCCGTGGTCATATCTAAGTAAGGCTGAATTACAAAATAATTCTAAGTTTTTGTTATTAAATAAGGGTCTTTTTAGCAATAGAATATAGACATGTATGTATGTATATAATAAATATATTTAGGGGTTATTTATTTTGTAATAATTATTTTTATACTAAAAATAAATATCTTATTTTATGCAG **(2,055)**
MSTRG.26270.1	(1) No hit	Lower	(1) No hit	(1)4381-4103 MFIFPLPKSFEKFEKFPKWKWKSHINLILKENCGLFSTKYCKLLIVFNYFRKILIKVCFYFYSLSNLLFRLSNCIFNHSQFFIMYEGTLTPL* **(93)**	CTATACCATCAACTAGGATTTTTGAAAAATATTAAAATTTGGAAAAATGACGTGTTGAAAATTTATTTTTAAATTAGCTAAAACATTTTCAGTTTCAAAAACCGCCAAATTGACATTTTTTATCCGATCAAAAAACCTCCAGTTGGTGGTATAGAAAATAACTTATATTTCAATAATAACTTTGAAATTTTATGTTTCAGGATCTCTATTAGTACCAATCACTGCAGCAGTGGAGCTATGTTTTTATTTTTACGCTGCCAGTAGATGGCGCATAAATCGTTTAATTTTCAATATTTTTTTATGAAAATTGTTTTACCGGTACTTCTTTTTATAATAAATGCAAATTTTCAAAACAATTGGTACAGTACTTTTTATTTTAGAAATTCCCAAAAAAGTATATGAATTT

					CGTACTTTTACACTAGGATAGCCCCTTAATATATAGAATAGTCCAGCACAACTTGTTTAGCAACAAAATGAAAAAATATACTTCAAAAACAGACTCAAAATAAAATAATGCAAGATGTGTGTCTGTGAGTGTACATCTCTGGAGGTAACTTTAATTTTTTATGCAAAATGACAAACAACTTTTGATGCCAAGAAAAAATAAATCCTACAGTAAATAACCAAAAAGGGTTAATGACAATGTGTGATCTCTATCAGGGAGTAGTTCATATTTAACGTGATGTTTGCTACAAGTCACGACGTAGCTTGCAACGATCATTAACCAACCAATTGAATTGAATCGAGCCAATGTTTTTAAAATAATTTGTACCTTTTTATGGTCAAAACACTACCTTAATACATTTTAAATTTTCAATTTATGTTTAGATCAAAAATATTTTACAAAAACAATAAAAATTAATAAAAAAGTAAGGAGTGCTTTCTAACTAAAATTAATTTAAGATAAAATATTCACCTATTATTTTAATTACATAATGAATGGAATGAACATTTCAACGGAAAAATGTAAATTAATTTTGAAAAACCAACATTGGGATAATAATTTCCCAAGCAATCCAGTCTAAATATAATATCAAAACGTACTATAGTTCTACTTCGAACAGACAAAAAAATTCAAAACTTTTTTCCAAACAAGTTTTGACGTAGCACCAATTATTTCCTAAAAGACAACACACTAAACGAACTACCTCAAAATGTCCTTTTCTAAAAAAGAGAAGTCTCATCACTGGAAAATATTTCCGTACATCACTAGCAACGCTCGATCAGCGTAGCTATAGTCAGTCCTGCAATGTCCGATAACATTTTAAGTATTTAAAACAAATCGCTGGCGATCTCAATACGAGGTGTGCTACAAAATAGTGAGACTGATGACACCAAAGCTGCGAACAATTCTAATTTTCAAGGAAAAATCTCGAAAAATGTGTTACAACCACTATGTTGGCCTGATATGGTACTAAGTGATTTTTTATGTTTTATTTAAGTCAAATTTAGCTTAAACACTGAAGGCGTTTAACGCTGTGAAAGAAAAACGTCCAATAATGTTTTATGGTACCAAAGCTGTGAAAAATTCTACTTTTTAAAGGAAAACTCTC

					GAAATATGTGTTTTAAGTAACCGCTATGTTGACCAGATATGGTTCTAAGTGATTTTTTAAGTATTCTTTAAGTCAAATTTGGCATAAACATTGCAGGCTTTTATGGATGTGAAAGAAAAACGTCTAGTAATGTTTTATGGTACCAAAGCTGTGGAAAATTCTAATTTTCAAATGAAAAATCTTGAAAAATATGTTTAGATAACCTCTATGTTGGCCGGATATGTTCAAATATAGCGTAAACATTGAAGGTTTTTAACGCTGTGAAAGAAAAACGCCCAATAATGTTTTACAGTACCAAAGCTGTGGAAAATTCTAATTTTTGAAGGAAAAACTCGAAAAATGTGTTTTAAGTAACCGCTATGTTGACCAGATATGATACTAAGTGATATTTTATGCTTCCTTTAAAGACAACTTTGACTTAAACATTGCAGGCTTTTAACGATGTGAAAGAAACACGTCCAATAATGGTTTATTCAACACAAATTTCGCCTAAATATCTATAATTTCGATAGTTTAGAGCATCGTTGCACAAGCTCAAAATCGGTAAGGAACCGATTGTTGTAGCCGTTATGTTGACCAGATATGATACTAAGTGATATTTTATGCTTTCTTTAAAGACGACTTTGACTTAAACATTGCAGGCTTTTAACGATGTGAAAGAAACACGTCCAATAATGGTTTAATCAACACAAATTTCGCCTAAATATCTATAATATCTATAGTTTAGAGCATCGTTGTACAAGCTCAAAATCGGTAAGGAACAGGCCAAGAGGCCTAATATAAGAAGAAGAAGAGCATCGTTCTCATTATTTTATAACAACACCTTATATATACATAAATATATCAAGGGCTGTTGTACAAAAACAGCGTTTTAACAAAAAATATACATATTGTAAATAAATCTTCCACAGACGTAGATTCTGTTGGTTTACAAAAATGTTACTAAGCATATTTGATTTTTAGACCATATTTTATATGAGTAAAATAAATAAGAGATGAAACAAGAAAAAAAGACTTCTTGTCTACTTCATTTTGCAGTTTTCTTCTTCGCCGTCTGACATTGCCAAGCCTTCCCACATCGATAGTGTAAATATTGTTTGTAGATGGCAATGCATTAGTTCAAATATACTTAGTTAAAGTATTT

					CAAAAGTCCTGAAGGGCACCAACGTTTAGTCAAAGAGAGGCTTAAAACTTTTAAGAAAATTCTGTTCCAAATTAAGCAGTTTTTAAAAATAGAACTAACAGACTGTGAGGGAAGACTGTGCGTATTTAGTATCCCACACGAAAGGCTAACGTAAAAATACGGTGTGTGAGAGTTCTGAGCAGTTATTCCTACCTAAATCAGGATACACATGAAGGACTAAGTTGAACATTCAACATCAAAATTTAAATCATTAATGTACTTAAAAAACACCGAAAAAAATGCCAGACTAGTAATCAGCAACAAAATTGACTGAGTTGAGCTCTTTCATTTGATTTAAAACTCTACGACAAGAAAAACACATATTAGGAAATATAACAGCCCCCTGGAACTTACATCGTAGATGTCGCCAGTGTAGATCACTTACATTGACGGGTTTCATCGAGTAGTTCAAATATCACACAGAGGAGTTCAAATGCCACGTGGTGTCTTAATATAAATTATCCAGCTCACATTGCTGAGATTTCCACGAAAGTAGTATAAATACGTTACGAAGAGATCGAATAATTACAAAAATAAAGTTACGCTTGCAAATCACAAGAAACAAATAAAAAGGAACTTTCACGACAAGTCAGTCTAGTAGTGAAGATCAATTTATATACTCAAAATAACAGAGATCAAAAGAAAATTTTAGCAGACGTACCAAATAAAACAAGAAGGGCATAAAACGTTGTAAAAGGTAGGAGAAATTAAAGAAAATGTATAGAATAAAACAAAACAATCCAAACAGGCAAAAGCAGCACATATCACAGTTTAACAAAATTTTCTGTCTACATTAAAACCAAATAAAAACATACCAAGGAGTAGTACTACTTAATGACATTGCTCAAACTCTCTTCCACTAACAAACTGGTCTAGCACATCCCAAATTAGATTAATTTCATACGGAACAGAATTATAACTACATCAAAATACAATAAGATTTGTCGTAATAACAATAGTAGAAAAAACAAAGTGGTTTTATAATGCTCATAGAAAGATTGATGTGCTGTACGAGGCAAGATTTCTACATACATGTATAGGACATGAAATATGTAATTTGCTTCATGCTGATGGTATGACAGGTAGTTTTGTC

					CCCCTCCTAATCAGGTAACGCCCATTTGATCACTGTAAAAACATTTTGTTTTTCTACTAACAAAACAGTATTCACCCGAACTATAATAAAACAGTCTAAACAAAACACGTCAAAATATAATAAATTGCACAAAAATCGTGTTTTGCTAATTTTTTAAAACTTATCGGTTTTAAGCCCAATAATTGCGATAATCGTGTAACCTGCCACGATAGTGGTGATGTCATGCTGTCATTTGTCAAAATTATCAAGCAAGATTATTCCGTAATAGGTACTTCAGAGGGGAGTTAAGGTACCTTCATACATGATAAAAAATTGGGAATGGTTGAAGATACAGTTTGACAAACGAAAGAGCAAGTTTGACAAACTGTAGAAGTAAAAACAGACCTTAATAAGAATTTTGCGAAAATAGTTGAAAACTATTAGCAATTTACAATATTTTGTTGAGAATAAGCCACAATTTTCTTTCAGAATTAGGTTTATGTGACTTTTCCATTTCCACTTCGGAAATTTTTCGAACTTCTCGAATGATTTCGGAAGTGGAAATATAAACATCAAATAAAATGAATTTCAAAGTTAAACATTCCAGCTCTTTTAACGGTCTTGAGAATAATTAAGCATAATATTTATATGCTACGTCTTTATTGTCCTCCTCTATGGAGTAGAGTCATATAGAGCTGGAGATCTATATATAAGCTATACATATCTACTTCCTCCTCTAGTGTACTTATTACGGAATAAACTATTGACTATTTTCTGAGATAAGATTGTGTGATTCTGTAACCTGTCTGTATGAATTGTCGATGGTTTTATTTCAAACTAATTGAAGAATTAAAAATTAACTCTGTACAGAATTACCACGAATAAGTAAAGAAAAATTGGCAGCTTGACGTCACACTAATATCGCGCATAAAAAAACGAACTCAAAGCGATAGTTATTTAAATGTATAGTGGACTCTGTGTATTCAACTAGTTGTTATTTCTAAAAGTAATTATTTCCAAACACCCTGTAGGAAAACACAAACTTAAATAACAAAAAACTAATGAAAAATCAAGCTACCGTAAACGAATAACGCCAAAACTTTAATACAATAACATACCGAACTACCTGATTAGTCATACTTTCAAGAAACAATTACCCTGTAT

					GAATATTGTCCCAAATTCTTTATAACATACAAAACGAGAAGAAAATAACATTCAACAACTTTTCAACTTCAACGGTGTTCGGCAGGGAACACCCTCTAAGGCCACTTCATGTGACTGTGTATAACAATAATTTTTTAATAAAAAATTTGAACACGCCAATTCCTAGGCCGCAAAAAAATTATACTGATCTTTCATCTTGACCTCTTTTAATAGAGTTCCTGATACTAGTTAAAATATTTTTAAAACCCTGCGAAAACGAATATCAAATATACCGTTGCACTTGTTAAATTTTAAGTTTTTTTGCTTCTCACAAATTCATTGGATGCCATTTAACCATTGTTTCAGTTTGCTGTATGGTCTCAGTTGGCTGCACTAGCAAGTGACATTTGTTATATGTCAATTGTCATATTTGTCTTGAGGATATGTACGATGTAAAATTGATACCAAATATCCACAAACTAGCTAGGAACTGGCAAACAAATTACTGAACAAATATATTAAATACTCGATAATAAATAGTCGTGTTTTCTACAGGGTGTGTCACGTGTGATTTGTACATAGGTGAGCAAAAATGTTTAAGAAAGGAAATCATAATCGAAGAGGTCCGCCAAGCCTTCCGTCGCATCTAAGCTGAAGTTGTACTCTGGCTGCATTAAAGGCTCCAAAAGGACCAGCTCACTGCTCAAAACAGGATCCATAATTCCT **(5,677)**
MSTRG.39053.1	(1) No hit	Higher	(1) No hit	(1)181-26 MLSPFKDDTIVNINKTMGNFIILEIRQSPHTFYGLNTYTYVYYRKINVRFQ* **(52)**	TAAATCTTGATTATCTTATCGTATCTTATTGAAATCTCACATTGATTTTTCTATAGTATACATAGGTATATGTATTAAGACCATAAAAAGTATGTGGTGACTGTCTAATTTCCAATATGATGAAATTACCCATAGTTTTATTGATATTAACAATAGTGTCGTCTTTAAAAGGACTTAACATAGATGATAATGATGATTTTCCAGGATACAATTATATGAATCTAAGTTCAGAC **(233)**
MSTRG.40933.1	(1) Uncharacterized protein LOC111058130 [Nilaparvata lugens] (55%;51%)	Lower	(1) No hit (2) No hit	(1)766-407 MLAIIMTIFTLSAAAQKSCIDQVVLNQVLRFFNQDVLLLPGPRFPNIFPCRMACRRAYLDSFRIMCPKYSNSRFDGGQYFSVLLHSSKALLIC	TTTTCAATCTTTACTCTGAAAGAATATTTATCGAAGCTTTGCACGAAACTGAAAAAGATATTCTACTAAACGGGTACCGGCTAAATATCATCAGGTATGCAGATGACACCATAGTATTTGCGGACACCCTAGAAGACCTACATATAAACGTAAAGACCAATATAAACGTA

	(2) No hit (3) Endonuclease-reverse transcriptase [Lasius niger](94%;46%) (4) Endonuclease-reverse transcriptase [Lasius niger](98%;63%)		(3) No hit (4) No hit	DPISPWDFKNFILRLLRRRKLSLVWP* **(120)** (2)543-301 MVVSTSRFFSILLRPSSFVTRSVHGILRISFYGSYGAVNYRLSGLRLTLIPRERLWFLKMAPIRLKVDLAFPMRALTSCL* **(81)** (3)3-212 FNLYSERIFIEALHETEKDILLNGYRLNIIRYADDTIVFADTLEDLHINVKTNINVKKTKLMIVSKQKR* **(70)** (4)576-779 MRNESRYALLQAILQGKIFGKRGPGRRRTSWLKNLRTWFNTTWSMQLFCAAADKVKIVMMIANIRHG* **(68)**	AAGAAAACAAAGCTTATGATCGTCAGCAAACAAAAAAGATAACAGAAGGTCAACTCTATATCAACCAAACCCCTGTAGAAAGAGTGAGGCACTACAACTACCTCGGCACCATAATAAATGAAGAATGTACCTACAAGCAAGAGGTAAGAGCGCGCATCGGAAAGGCTAGATCAACCTTCAACCGTATGGGGGCCATTTTCAAGAACCACAACCTTTCTCTTGGTATTAAAGTAAGTCTAAGGCCAGACAAGCGATAATTTACGGCGCCGTAAGAGCCGTAAAATGAAATTCTTAAAATCCCATGGACTGATCGGGTCACAAATGAGGAGGGCCTTAGAAGAATGGAGAAGAACCGAGAAGTACTGACCACCATCAAATCTCGAGTTGGAATACTTTGGACACATTATGCGAAATGAATCCAGATATGCCCTCCTACAAGCCATCCTGCAAGGAAAAATATTTGGAAAGCGAGGTCCAGGAAGAAGAAGAACATCCTGGTTAAAGAACCTCAGAACCTGGTTCAACACAACCTGGTCTATGCAGCTTTTCTGCGCTGCTGCAGATAAGGTGAAGATTGTCATGATGATCGCCAACATTCGTCACGGATAGGCACATCAAGAAGAAGATCAGGAATCGTGACTCCCCCCTCCAAATTCCCATATGAAATTCTTCTCCTAGTTAGGCTGGAGAGCGTGAGACGCTATAATCCTGCTATCATCTTAAATGAAATATTATCATCATTGTGCTTTTGCTTGCCCGGGCGTCGAATCCCCTCTCCAAACTGGGTCCATTTCGGCTACTCAGAGCTTAAGATTTTTTTTGTTAGAAGAGGCCAGAAGCCGTTTTGTTTGTTTTTATATTTTTTGGAGGGTGGATATGTCTAAATCTATGTATTTATTATTTATGCTACCTATGCTTGATGCCCGATATAGGTAAAGTGCCTCTTTTCTTGCAATTTACCACTACATATAAGGAATTATTTATGTATATGTATGCCTATCTAGATTCTAAAATTGTGAAAACTAGCATTAAGTTGTTGTAATATTTCGTAAATATTGTACATATACGCGTATGTATTGTTCGGTTTGTAAGATGTTTAT

					GCCTTGATATGATACAATACTAATTAAAAATACAAATTTAATGTTTT **(1,317)**
MSTRG.42718.1	(1) THAP domain-containing protein 1 A-like [Athalia rosae] (29%;33%)/ PREDICTED:repressor of the inhibitor of the protein kinase-like [Vollenhovia emeryi](30%;40%)	Lower	(1) THAP-type zinc finger superfamily (IPR038441)/THAP-type zinc finger domain (IPR006612) GO:0003676 nucleic acid binding	(1)1-843 FFCDFSVKMSRCIVKECVYNKTKVCRRDKRNFNIHLFTFPMDNERRESWRLALNLNSEDLFKYSRVCHLHFNNDAFDYEKSPFSLSLKKNAIPSERVALADLQCSVPDIRPSISTCYYEEPNRELPSTVQKKPPNSPTIKTDSVMDKEVKLEIKEDIGEYTLRYLKNQLSTSIDFENCKNEPEEANYSVMEDKVKCKEEFEEHEHRCMESQLATPINLKDFKDEPEEANYSVMADEVKEEFEEHEHRCMENQLSTSRDPEDCKNKAEEINYSGEINNGMK* **(281)**	TTTTTTTGTGATTTTAGTGTCAAAATGAGTCGATGTATTGTAAAAGAATGTGTATACAACAAAACTAAAGTATGCCGACGTGATAAAAGAAATTTTAATATTCATTTGTTTACTTTTCCAATGGACAATGAAAGACGGGAATCATGGAGACTCGCTTTAAACCTAAACAGTGAAGACCTATTTAAATATTCACGTGTGTGTCACCTACATTTTAACAATGATGCCTTTGATTACGAAAAATCCCCGTTTTCTCTATCTCTGAAAAAGAATGCCATACCATCTGAGCGAGTTGCTTTGGCGGATCTTCAATGTTCTGTACCTGATATAAGACCATCCATCAGTACTTGTTATTATGAAGAACCAAATAGAGAACTACCATCAACTGTACAAAAGAAACCTCCGAATTCACCTACCATAAAAACTGATTCAGTCATGGACAAGGAAGTTAAACTTGAAATTAAAGAAGATATTGGAGAATATACACTCAGATATTTGAAGAATCAGTTATCCACCTCAATAGATTTTGAAAACTGTAAAAACGAACCTGAGGAAGCAAATTACTCAGTTATGGAAGATAAAGTTAAATGCAAAGAAGAATTTGAGGAACATGAACACAGATGTATGGAGAGTCAGCTAGCCACTCCAATAAATCTTAAAGACTTTAAAGATGAACCCGAAGAAGCTAATTACTCAGTTATGGCAGATGAAGTTAAAGAAGAATTTGAGGAACATGAACACAGATGTATGGAGAATCAACTATCCACCTCAAGAGATCCTGAAGACTGTAAAAACAAAGCAGAAGAAATCAATTACTCAGGTGAGATTAATAATGGAATGAAGTAAACATAACACT **(853)**
MSTRG.45015.1	(1) No hit	Higher	(1) No hit	(1)244-77 PMVFLSKKFTFFSSLIVFTSTSTLLTSNHRRRFEFLLIKCETTIFYYFIYSSNLA* **(56)**	GAGACCTTATGGCAAGTGATACCTCGTTTGAAAGGTATTGAAAATACCTATTCAGTCATACTAATTTTGTTTGAGTTTAAGCTAAGTTTGATGAATAAATGAAATAATAGAAAATTGTAGTTTCGCATTTAATTAATAAAAATTCAAACCTCCGCCTATGATTACTTGTCAAAAGGGTTGACGTTGACGTAAAAACTATT

					AGAGAACTGAAAAACGTGAACTTTTTTGACAAAAAAAACCATAGGC **(245)**
MSTRG.48586.1	(1) No hit (2) Hypothetical protein TcasGA2_TC002606 [Tribolium castaneum](54%;44%)/PREDICTED:ATP-dependent RNA helicase p62-like [Diaphorina citri] (51%;49%)	Lower	(1) No hit (2) No hit	(1)1392-1120 HQRLRSRNPPIRSARIIGDSYDIQRQWSTRWMPTIAADYIQISTLTQGFIGSGLPRSTWGGLIAYVPDILCSNGVVRKVQSAIADHLDRL* **(91)** (2)1315-1070 MVHKMDANNSSRLYSDIHPNPGFHRIGSAPVHLGRLNRIRTGHSLFKWGRAESPECDCGSPRQTISHCVSDCLNRAYRGNL* **(82)**	ACCTATTTTAACCTCAGCAATCTAAGGTTAAGCTATGGCCCATTATTTACCAAATACCCTGTATATTTTTGTGTTGGTCTTTGTGGTCAAAAAATGTGTTGTTTATTTGTTTGAAACTGCGTATAATTTGTTTAGAACAGTAACATCTTTCATGATTTCTGTTTTGTTACTAACTAAATATAGTTAGTAATATAGTTACTAACACTTTGTTTTTGATTTTGTTATGGATTTGCCAGTTCTACCTTCTTTGTTGTTTTTTGTGGACAAAGCTGTTCATTTGGAATAAGTTATTTTGAAGAAGAAATCCAATCAGGGTTCCTCCTCTTTCGTTGGTCTTTATCTCTTTATACGACACCTTGTCAAATACCTTTTCTAAGTCAAGGAATACTGCACTTCAATAAAACCAAATTTAAATAATATTTTATTTATTTCGAAAAGAATATAACTTCTACTAATTGAAAAACATTTCTGAAATCAGATATCATTGCCCATTCTTTCAAAAAAACGTTACTTTCTAGTGCTTCAGACTGATTACGTATTCCGCAAAATTTTAAGCTGCAATTTGGCCTATTCTACAAACATTATTTCCTCAAGTAATAGGTAATCGTACATTAGAAAGTAACTGAAGATAGGCCAGGATCCCGCGTACCAAAAAAGTTCATTATTAGCAAGCTGAAAATTTGTTAATAGCTTAACGGTGTCTAGTCTGGCAAACTTTCATGTATGGGAATACTGGAACAGGGGAAGTTTTAATTGTGGGACGTGATTTTAATTGTGGAACTTTTCATCCTGACAAGTTTATGATTGTGAAAACTAGCAGGTTGTTTTTAAGTTTATTCAATAGAAAACTTTATATAACATATGAAGAAAATGTTTGTCCGACAAATATGTTAGGCATTTTAATTTATTTATTGTTTTATTTATTTAGCGTATGGACTTTCACAGTACGATAAATACACAAATATAATACATATATTATTCAAACACTAAAATATAATGATTGAACCTAAATATTAATGTCCAATTTACATAGCCATTCAATTGCTTCTGGGGAGCATTCCACAAAGTCCTAGAGGTTTCCACGGTAGGCA

					CGATTTAGGCAATCTGAAACACAATGACTTATAGTCTGTCTAGGTGATCCGCAATCGCACTCTGGACTTTCCGCACGACCCCATTTGAACAGAGAATGTCCGGTACGTATGCGATTAAGCCTCCCCAGGTGGACCGGGGCAGACCCGATCCGATGAAACCCTGGGTTAGGGTGGATATCTGAATATAGTCTGCTGCTATTGTTGGCATCCATCTTGTGGACCATTGCCTTTGTATATCATAGGAATCACCAATTATTCGGGCAGATCTGATTGGAGGATTTCTAGACCTCAGTCGCTGGTGC **(1,393)**
MSTRG.97619.1	(1) No hit (2) No hit (3) No hit	Higher	(1) No hit (2) No hit (3) No hit	(1)2094-1903 MHWLNILLLKYRGILRILGFLTKFYKSCPCQSCCFSDFHTFVLFVEFGLGRYIHGLVLSHCHL* **(64)** (2)2778-2945 MPRIKILIKILHFTCNICKCNKISYNFVIRLTMLRLLYIFYCLTRWIIVFLYCYH* **(56)** (3)2320-2159 MYKMDIVLRTEGPFDFGNFYCDISFLYFILSSRFSFYLTVEYLELLFPLPFLL* **(54)**	TCACGCTTCGTCACTGGATACTTCAGTCTTAACTGTCTAATGTTGCGTTTCTTAATCAATATTTTTCTCACAAGGAGGAATTTCCTGTAACTGGTTGTATACCATTAATTACAAGTAAATTTAACGAACAATTTTTTTTCTTGGTAAAAGGTATATTTATTTAAAAACTATTAAAAGGGCCACCAATATCACAACAAAACGTTTTCGCTCTCTAAAAAAAGCATCATCAGTGTTACAAGCCTAACATACTGAGCCACCCAAAAATACAAATTAAGATCCTTTAAAAGTTGACAATTATTAATTAAATAAGTTATGGAATCCAAAGGATAGATATAATCCTTATGGATAAGGCCCTAGGGTAACATATGACTCCCACGTGGTACGTGGGTAGCTAGGTAATAATTAGGTTACCACATTGAGAGATGTGAAAGGCAACTAAGAGGTGAAAGAGTTCAACTGAAGTCTCCTCTCCTTGATTTGCTACCTGAGTGACCTTCGTGGTGTCAGATATTTCTGTACTCTTGTATATCTTTCGCAACTGGGTAGTAGTATCGGTCTTAATTTGTTTTATTTTTTAAATTTTACTAAACGCCACGAATTTCATTTCATTTTTGACAGATTTAGTTATAATTTTATGTAACATGTCGACAGCTTCCATAACATCTAATTATGACAGTTGTTAAACAAGTTAAGCTCAAAACGTCTCAACCTAGCATTTTTAGTAAGAAAATATTTCTTTTTTTATGTTAAAAATAGTACTCGTAGTATGAACTGTTTCTTAACCAAAGTATAAAGTTTGGATCATTGGTATAAACTGAATGTGAAATTATT

					ATATTTGATAAAATAACGTCCATGGTCTAAATTTTAAAATAGCTTAAATATGAAATTTTACTACACATATTTGGAGCAAAATATCAGGAGTGATGTAATGGAAACTTATAAACGTCAGCATCAGTGTAAAGTTATTTAATGCAACACCTGGTATATGGTTTTAATTTTTAAAATTCAACATTTTTCTTATCTGTTCTTATTAGTTTATTTTGACTCTTATCTAGTACTGATTAAAATAGTAATTAGATACTCTTTATAACAAATTTTAAACAATGACTTGTGACAGTTGGATTTGTCACTAAATCGTGGGAAATTCGCTATCCCGATAGCCTTATAAGCTCTGCCCACTAGCGTCATTTTTCAGGAAACTTTAGAACAGGTCAGGAAGAGATCACGTGTTCAATTATATGCTAGACTTGTTCTAAAAACAATTTAACCAATATTCGGACGCAGATATCAAGATATACTTTTCAAATGGTTTGTGCGCCGAATCCGAATGTGTGCTTCAAATTGTCAAATTGGCTCTGGTTTCTGAGATATCCTAACCTAAAAGTGCAAAAATAGAGGTTTTTGAGGTTATGTAGCGTCGTGATATATTTTTCTCCCAGAAATTGTTATAACTATTTTAAAGTGTAAGCATCGATCTTTTAAATGACGTTAAATTTATTCAGATATCTTCTTTTTTCCCTGAAATATCGCATTTTAACATTTTACGCATTTTATACATAATATGTAATGAAATCGCAACTATGATAGTACAACTAGACGAAAGTACAAATCCCATTCCTATTAAGAGAGGAGTTAGACAAGTAGACGTAATATAGCCAACGCTCTTTAAACTAGTTCTAGAAGACGTCTTCAAAACTACAAACTGCTCAATATATTGTTAATCAACGATTAACGTTAATGGCAACAGTTAAACCACCTCAGGTTTACTAACGGCATCGTGACTATAGCAAGCACATTCCAGGAACGGCAAATTATGATGGAAGAACTCGCAGACAGCTCCCAATGCGTCGGCCTAAAAATGGCAAAAACAATATCAAACACAGACGACACCAGATGTATATTTTATAAATGGCAGTGAGATAGAACAAGTCCATGAATATATCTGCCTAAGCCAAACTCGACAAAGAGAACAA

					AGGTATGGAAATCACTAAAACAGCAAGACTGGCATGGGCAGGATTTGTAAAACTTAGTTAAAAACCCTAAGATCCGCAAAATACCCCTATACTTGAGGAGCAAAATGTTCAACCAATGCATCCTTCCTATCGTGACATATGGATGGCACCTGGACCCTAACCAAGGCAAATATGAACAAAACTAGTCACAACAGAAAGGGTAATGGAAAGAGTAATTCTAGATATTCGACGGTCAGATAAAAGGAGAAACGACTGGATAAGATGAAATACAAAAATGAAATATCACAATAAAAATTACCAAAGTCAAATGGACCTTCAGTTCTTAATACTATATCCATTTTATACATAAATTGGAAAAGTATCGTTAAAAAACTAATGATTAATAATTTGGAACTTTACATGTATTTATTATATTATATTATTATGCTGAACCTCAAATTGTAAGATCCAAAAATTTCAGGTGAAGGTGCTAGGTGGCGCGTCAGTCATGCTCAATATAACCTCAAAAATAGCCAAAAATAGCTATTTTGCACTTTTAGGTTAGGATATCTCAGAAACCAGAGCAATTCGGTTATTTGCAGATTCGTATTCAGCACACCAAAAACCTTTCTGTTTTGTGGATCTCAGGCTTGCCAACCTGCATTATTGTAGAGAATGTTGTCAGAGGGCGACAGTAATGCAATTGATTTTTATCACATTTTACAGTGAAAATATAGTGGCTTTGCCAGGTTCCTTTTATCCAACCTCATATTCAGTTAAATATTATCTATCCTATATCCTATAGTCATTTTATTAAAATTATGGATGCCTCGTATAAAGATATTAATAAAAATTTTGCATTTCACGTGCAATATATGCAAGTGTAATAAAATTTCATACAACTTTGTCATTCGGCTTACAATGTTGCGGCTACTTTACATTTTTTATTGCCTAACACGATGGATTATAGTATTTTTGTACTGTTATCATTAGGTGTATTTTTTATGGATTGATTTTGTTGGTTTAGTGTAGAGAAACTTAGGAACATGCAGTGACTCACACTTTTACAAAGAATAGTCAAGCAAGAAAACATTATATAGTAGACATTTTTAAGGTTTTAATAATTTTATTTCCGTGCAAAAATTTTGAGAAAGTATTAT

					GACACTAGCAGTTTTGTTGATGTGATTTTTGAATGGTTTTTGTTTTGGGTTGACACGCATGTCTCAACATTTTTGTTTAATCTAATACTGAATATTATATACGTTTTTGTAAAATAATGTTGTGAATCGAACATACCATAGAAACTTTTCTATAATTTAATAAATACCTACTAATGCTGTGAGCTGAAGAAATATTGTTTAAATCTAACAACTTCATAAAATTTATTTAGAATACTTTGTTTTGGTCAGAGAACAAAACCTTGACCATGATTCCTATGAACATATATTGAGCATTAAGTTCAATTTTAGAGCACATATTGAACAACATAGGGCTCATAGGTAAACTTTGGAAACTCACATTTACTTGACACATGTCGCTGGTCCGGAAAAAGAATGACGTAACTTTTGTCAATTCCTGTTTATTGCGTAATTAACTTCTAAAATACTGTGTACAGATGATACAAAAGCGACATAACTGTAGCTATGTGCTGAGCCACTACAGGGTAGTTGCGTCGTTATTGAAATACACGCTATTTTAGACATTGTTTCAGATGAATAATGACGTAACTGTTAATAGGGTTGAAAATGGGGGGAATTAAATTAAGATAATGAAATTCGGACCAATAGGGATGAAAATAAAAGCCATCACTGTAAGAATAAACGGCTTTCTAAATATTTAAAAATCTTTTTTGTAGAGAAAAATTTTAAGATGAAGAATGACGCAGCTGTAGATAGGGTTGAAAATGGGGGGATTAAATTAAGATAATGAAATTCGAACCAATAGGGATGAAACCAAAAGCCGTCATTGTAAAAATAAACGCCATACCGATGTTCCTGGACGGTTACTCTTTATTTAATCACTATTTTAAATATTTAAACAAATTTAGATGAATAATGACGCAACTGTAGATAGGGTTGAAAATGGGGTGATTAAATTAAGATAATGAAATAATTCGAATCATTAGAGACAAAAATAAA **(4,090)**
MSTRG.2650.1	(1) Acaloleptin A [Anoplophora glabripennis](86%;44%)/Coleoptericin B [Tenebrio molitor] (58%;55%)	Higher	(1) Coleoptericin family (IPR009382)	(1)600-313 RLTMKFKHGSTFILIFALIVLTGAEDDNEQRIKRSPKPDWEVNPGANRDDDGNTNAGVQVKNYGNDHDFEAG	TGGTTTATCATCAAAAATACTTGAAATGTTACAAAAATTGCATATTCTTTTAGCAAAAAATTATCACATGAGTTGTTTGGAGTATAAAACTGTCCATATTAGTTAATTGAATTGGATAATATAATTTTATCTATGCAAATTAACAA

			GO:0042742 defense response to bacterium GO:0005576 extracellular region	WSKVVSGPDRAKPTWHVGGTWRF* **(96)**	TATTATCTACTTTGTTATTATTGCTACCAATTATTTAATTACTTGACAAACTAAGGAAAAACTAAAACTAGGAACTCGATTTAATTTTTTATTAACAATAAATTAAATAAATAGTACAAAATACGAGAATATTTGTATTTCCTAATATTCCTATTGCTATAGGATTCTAGAATCTCCAAGTACCACCTACATGCCATGTTGGTTTAGCTCTATCGGGTCCACTAACTACTTTGCTCCATCCTGCTTCAAAATCGTGGTCATTTCCATAATTTTTCACTTGGACGCCAGCATTGGTATTACCATCATCATCACGGTTAGCTCCTGGATTCACTTCCCAATCTGGTTTGGGCGATCTTTTAATTCTTTGTTCATTATCATCTTCGGCGCCTGTTAAGACTATTAATGCGAATATTAGAATAAAAGTTGATCCATGTTTGAACTTCATCGTTAATCT **(600)**
MSTRG.19832.1	(1) Dynactin subunit 2 [Anoplophora glabripennis] (99%;78%)/Dynactin subunit 2 [Leptinotarsa decemlineata](99%;78%)	Lower	(1) Dynamitin family (IPR028133) GO:0007017 microtubule-based process GO:0005869 dynactin complex	(1)3-449 SLYEWAEHLSATASLLDSAQLDHIEGRLGALAQKLESIAEKKKEVQPDEEKDSMILELYDLVKNTEGITQLLPQTIERLKSLEQLHNKAADFAKTLTQIEVTQAEMMSNVQNNKMLLQGVQESFAVNLNEINATVVSLDARIKALKNK* **(149)**	GTAGTTTATATGAATGGGCTGAACACTTGAGTGCTACAGCAAGTCTTTTAGACTCTGCTCAATTGGATCACATTGAAGGCAGACTAGGAGCGCTGGCGCAAAAGCTGGAGAGTATCGCAGAAAAAAAGAAAGAGGTACAGCCAGATGAAGAGAAAGACAGCATGATTTTGGAGCTCTATGATCTGGTAAAAAATACAGAAGGTATTACACAGTTGCTTCCACAAACTATAGAACGACTAAAATCTTTGGAGCAGTTACATAATAAAGCTGCCGATTTTGCTAAGACTCTGACCCAAATAGAAGTAACACAGGCAGAAATGATGAGCAACGTGCAGAACAACAAAATGCTTTTGCAGGGCGTTCAAGAAAGTTTTGCAGTGAATCTTAATGAAATTAACGCTACAGTAGTTAGTTTAGATGCTAGAATTAAAGCTCTCAAAAATAAATAAATTTTTAAATTACTAACTAAATTAATTACAAGAAAAGAATATGCCTAGACTTTTTTATTTTGATTGTGTTTTTTGGTATTCAGTGAAATTGTTGAAAGGTATTTTGTATGTATGTATACTTCCATTTCAATATTCTTGGTGAGTATTTTTCGTTTTGAATATGTTTCAGACTGTCTTTTCTGTCAATTTTTTATAGGACTTTTATTTGTTCTGTAGATTTTCTGTGTAAGACT

					ATAATTTATGGGCATATGCATCACATTGTATGATTTTTTTCTCCTCCTTAGAACTACAGTGACCTACAAAACACTCTAGCACACATACTATATCCCCTACATCCTCTGTATCCAAACTGCCTTGTTTCTCACTTTTCTTTCCATGTATTCCACTAAATTAGAGAACATACTGTGTTTCCCTCCTAAACACTTAACAGACTTAAGACTTCTTTACAATTTCCATAAGTTTTTTTTTAATTGTAACATATAAGCGGATTTTTTTACAAAAATCTTTAGTCTGCATCTGGTACACCTAGAATTATTTCTTTACTACTACACTCAAGCTTTTTAGCATCTCAACGTCTGCTAGTAAGCATCATTGAATGCGCTAACCTACATGCTTTGTTTTCTACTCATTTTCTACGCTTTTCAGCCATTTTTATTAGCTACAATGAATGTTGACAGCTGTCAACAAAAATCCTTAAAAGGTATAATACTATTAATTATTTGTGAATCACACTGTACATTTATCGGTGAAAGCAAAAATCACAATTAAAATCGGAATATATCTTCTAAAGGTAATATTGTCACATTATAATCCTGTCCAGAAATTTTTAACTATACTCGTATTATAAAACTGTCTTTGAGACAAGCAAATTCCTTGATGGCAATTTAGAACTTTTTTATATAACATAATGTTTAATCTAAAATAATAATAGTTTTTATGTTGTGGTGATTTATATTTATTTTGTTGTCTTTTAACGCTAGTAAATTATTTACACAAATTA **(1,449)**
MSTRG.23764.1	(1) No hit	Lower		(1)213-103 ILPREKLVSMLHYCRIDIIDDFVERHRSIVSGRLYY* **(37)** (2)96-40 MNNATSNTIGFIFLLFLK* **(19)** (3)1-48 LNGTIKRTKGANMLL***(16)** (4)62-106	CTTAACGGAACAATAAAGCGCACAAAAGGGGCGAACATGTTACTTTAGAAAAAGCAGAAAAATGAAACCAATTGTATTGGACGTCGCGTTGTTCATGAATCCCTAATAATAAAGCCGGCCACTCACGATACTGCGGTGTCGTTCGACAAAATCGTCGATGATATCAATTCTGCAGTAATGCAGCATAGAAACCAGTTTCTCTCGTGGTAAAATTG **(215)**

				MKPIVLDVALFMNP***(15)**	
MSTRG.65003.2	(1) Nuclear factor NF-kappa-B p110 subunit-like [Leptinotarsa decemlineata](89%;74%)/Relish protein [Sitophilus oryzae] (87%; 68%)	Higher	(1) Rel homology domain (RDH), DNA-binding domain superfamily (IPR037059)/p53-like transcription factor, DNA-binding superfamily (IPR008967)/NF-kappa-B Dorsal family (IPR000451)/Rel homology domain (RHD), DNA-binding domain (IPR011539) GO:0006355 regulation of transcription, DNA-templated GO:0003677 DNA binding GO:0003700 DNA-binding transcription factor activity GO:0005634 nucleus GO:0005737 cytoplasm	(1)3-350 APSATLHFVEQPTDRFRFRYKSEMAGTHGSLTGINSDKSRKPTYPTVELRNCGNHDKVVIRCSIYQANANPKGFYPHAHRLMMKRGREEFDDPHDVEVGHEDGFRAVAQLSKNYI* **(116)**	CAGCACCCTCTGCAACACTACACTTTGTAGAACAACCAACAGATCGGTTTAGATTTCGCTATAAGTCAGAAATGGCGGGAACCCATGGAAGTCTTACTGGTATTAATTCCGACAAATCGAGGAAACCAACATATCCCACAGTAGAACTAAGAAATTGTGGCAATCACGACAAAGTTGTTATAAGATGTTCAATATATCAAGCAAATGCAAACCCTAAAGGTTTTTATCCTCATGCTCACAGATTGATGATGAAAAGAGGGCGTGAAGAGTTCGACGATCCTCATGATGTGGAGGTTGGGCATGAAGATGGCTTTAGAGCCGTGGCCCAATTAAGCAAAAATTATATTTAAAATTATTTCCGCCCCCTAACCCCCAAAAAAGCCATTAAAAAAATGTGTATCTTATGAGATCCATTGGACAGATAGGTCTTGGAAGCGGTATCCTAAGAGATACATTGGGCACGACAAACCACTATTACATGGTGGGAAAATGAGTTACAAATAACATAATTTTCCTGTATAATATTTGTGTAATTAAAAAAAAGTTAA **(547)**
MSTRG.75310.1	(1) No hit	Higher	(1) No hit	(1)3-224	GTGAATGGAAAGAATACAGTTTTTTTGGTTTTATGATGTCGCTGATAGTATTTGTGG

				EWKEYSFFGFMMSLIVFVVKYAIPEDMKKADMNKLCEEFNSGRELEYEVRLDEKMMEIKYKTIFNHMVEYNFL* **(74)**	TTAAATATGCGATTCCTGAAGATATGAAAAAAGCTGATATGAATAAATTGTGCGAGGAGTTTAATTCTGGTAGAGAACTTGAATATGAAGTACGACTTGATGAAAAAATGATGGAAATTAAGTATAAAACAATATTTAATCACATGGTGGAATATAATTTTCTGTAAATATTAGGTTTGTTCCAACTCGATACAAAATAGTTCTTATATAAATAGAACGGTTACGAGTATGCGCAGTAACGAAAAATGTGTTACTGCACATAATTACCCGTTATTGCGCATGCGCGTAACGATTCAAGAACGGTTTTGTATCGTGTTGGAACAAAGCTATTAATAATTGCAAAATTTTTATGTTTTTGTAAATAACAAAACATCAACTTGTACTATAATATTACTAATTCTGTAAAAAAGTAACAATTTTTCATTTTTTATGTTCATTTTGTGTAACTTCTCCTGTCTGCTGTGTAGACCAATTATGTCAGTTGTCCCATTACAAAGACGACTGCAAGGCCTCTTCCCAGAAATATAATATTAAAAATAAATAAACATTTTCAATTCCGAATGCAATACGAAACAACAGCCGCATTATATTTAAGTTCAATCAGGGAGTGCGGCAAGCACCACTACCGATTTCGAGACTTGTTACGCGCTCGTCAGAAGGTGCATATGCTGCTCTGTCTGACTGAACCAGAATAATCCCCGGCGTCCAGTCTCGAATTGCAACGAACGAAATGGTAGTGATGCCCTAGCGACACCTGCTAGAAAAAAGTCTAAGTTTTAATCTAATAGCAAATAAAACAATATTTAAATATTATTTTACATTCCACCACATTGAAACTATGTTTAAAACGCCGCAGTACTTCTCAACACCATGTCTGTACAATGTAATGCACACTAGTAATAAAGAAACTCGTATTCACGATAAAAATAATAATAGACAAAATATCCCCAGCAGCCTATTACTGGATGATAAGTATTAAATGCCTGCCCTAATTAAATTTTTTTTTCGTCGGTTTTTTACTAGTGCTATTTCTGACAATTCGACATAGCGTGGCACTTATTGCTAATTAAGTGGTCTAATTAAGGATCTTACATGACTGACACTCACTTAAAAA

					CCACATTCTTTAAGGAAATTTGCAATAAACTTTATATTTAATTTCTTT **(1,219)**
MSTRG.3101.1	(1) P450 6k1-like [Leptinotarsa decemlineata] (96%;39%)/P450 6k1-like [Anoplophora glabripennis](96%;35%)	Higher	(1) Cytochrome P450 superfamily (IPR036396)/Cytochrome P450 family (IPR001128) GO:0055114 oxidation-reduction process GO:0005506 iron ion binding GO:0016705 oxireductase activity, acting on paired donors with incorporation or reduction of molecular oxygen GO:0020037 heme binding	(1)864-1 MSFLNSSWLFSLATFCIGIIFLGYKYFTREFNYWKKRGVYTPKPIPFFGNLYDVATLKLTLYEYVQKIYDETEEPYFGMFIFDKPVLLIKSPKLIKDILIKDFNVFCDRTMANVTHHNLISKFIYQQKYQTWKSTKTKMSSVFSSGMMKTFFTNLELINKKFTEYLENISGPVDAKYIAGHFGTEMIARCFFATDPRCFEREPSKFRHFVHRIFQYSLRNKFIQTGYFFKPNLVKFFKLNFIEDSVVQYFEQTFLEAMECRKGYSGKPVSMVDVVNDLEKACDGDFPG **(289)**	ACCAGGAAAATCTCCATCGCATGCTTTTTCCAAATCATTGACAACGTCAACCATACTGACCGGTTTACCACTATATCCCTTTCTACATTCCATGGCTTCCAAAAAAGTTTGTTCAAAGTATTGCACTACTGAATCTTCGATAAAGTTTAATTTGAAGAACTTTACCAAATTGGGTTTGAAAAAATAGCCAGTCTGGATAAATTTGTTCCTCAGACTATATTGAAATATACGATGAACAAAGTGTCTGAACTTCGATGGTTCTCTTTCAAAACAACGTGGATCAGTTGCGAAAAAACAACGCGCAATCATTTCAGTGCCGAAATGACCCGCTATGTATTTAGCATCCACTGGACCAGAAATATTTTCTAAATATTCAGTAAATTTCTTATTTATTAATTCTAAATTCGTAAAAAACGTTTTCATCATTCCAGAACTAAATACTGAAGACATCTTTGTCTTTGTACTTTTCCATGTTTGATACTTTTGCTGATAGATAAACTTCGATATAAGATTATGGTGAGTAACATTTGCCATGGTTCTGTCACAAAACACATTAAAATCTTTTATCAAAATGTCTTTAATTAACTTGGGTGATTTAATCAGCAAAACCGGTTTATCAAAAATAAACATTCCAAAATATGGTTCTTCAGTCTCATCGTAAATCTTTTGTACATACTCGTATAAAGTGAGTTTTAACGTGGCAACATCGTAAAGATTGCCAAAAAATGGAATTGGCTTTGGAGTGTACACACCTCGTTTTTTCCAATAGTTAAATTCTCTGGTAAAATATTTGTATCCCAGGAATATTATCCCAATACAAAATGTTGCAAGGCTGAATAGCCATGAAGAATTCAAGAAAGACATTTATCT **(870)**
MSTRG.3860.1	(1) Peptide transporter family 1-like [Anoplophora glabripennis] (97%;77%)/Peptide transporter family 1-like	Higher	(1) Proton-dependent oligopeptide transporter family (IPR000109)	(1)2-388 LVIFGLGRPTYKIKKPEGNVIVQVTKCIVCGIKNKFKSKDKKEHWLDYAEEKYGEKLVNEVKATLHVLVLFLPLPIFWALYDQQGSGWTLMAVRMDGNIGFYTILPDQM	TTTAGTCATCTTCGGCTTAGGAAGACCAACGTATAAAATCAAAAAGCCAGAGGGCAACGTTATAGTACAGGTTACAAAATGTATTGTGTGTGGAATAAAGAATAAGTTCAAGTCCAAAGATAAAAAGGAACATTGGCTTGATTATGCAGAAGAAAAATACGGAGAAAAACTAGTAAACGAGGTTAAGGCAACACTCC

	[Leptinotarsa decemlineata](98%;75%)		GO:0055085 transmembrane transport GO:0022857 transmembrane transporter activity GO:0016020 membrane	QVVNPLLILAFIPLFTYYXX **(130)**	ATGTTTTGGTTCTCTTTCTTCCGCTGCCGATTTTCTGGGCTCTCTATGACCAGCAAGGATCAGGATGGACTTTGATGGCAGTGAGAATGGATGGAAACATTGGATTCTACACAATTTTGCCAGATCAGATGCAAGTCGTCAATCCATTGTTGATTTTGGCTTTTATTCCACTGTTTACCTACTACGTNNNNN **(388)**
MSTRG.29792.1	(1) Peptide transporter family 1-like [Anoplophora glabripennis](98%;79%)/peptide transporter family 1-like [Leptinotarsa decemlineata] (99%;69%]	Higher	(1) MFS transporter superfamily (IPR036259)/Proton-dependent oligopeptide transporter family (IPR000109)/Major facilitator superfamily domain (IPR020846)/PTR2 family proton/oligopeptide symporter conserved site (IPR018456) GO:0006857 oligopeptide transport GO:0055085 transmembrane transport GO:0005215 transporter activity	(1)342-947 MNKKEEMEKIPYPKSVFFIVSNEFCERFSYYGMRTILILYLTNILLFSESQSLVTYHSFSMAVYFFPIIGAIISDSFLGKFNTILYVSMIYASGSILLALTASDPIGLPKVGFSVLGLLLIAVGTGGIKPCVAAFGGDQFRLPQQEKDLERFFSLFYFSINAGSLISTFITPILRNDVHCFGNESCFPLAFAVPGILMIISV **(203)**	TAGTCGCACCGCTGTCAGTCACGCATCAGAATATGGTCAGTGTAGTTCGAGTACCATAATACAGCGCGCTCGATGAACTATTAACTTTATTTTAACTAACGAATCGTCTATTAAATGTTATAATTGTTTGGAAAGTTTCTTTGACACACATTGCGAATAAAAATGTTGCAATTACGTCGGTGATATATGCGTATTAAATAATAGTGCATTAAATCAAAAATCTTGTTCGAAATCTGTGATATATATTTTATTTGAATTTTTGTTGTTTTTTTTTTTGTTAAAACGGGCTGTGTATATTGTGTTTTTTTTATAAAACTTTTACTAGACATAATCATAATTAAAATGAATAAAAAAAGAAGAAATGGAGAAAATTCCTTACCCGAAATCAGTATTCTTTATAGTCAGTAATGAATTTTGCGAACGATTCAGCTACTATGGCATGCGAACTATCCTCATCCTGTATCTCACGAATATACTACTGTTTAGTGAATCACAATCCTTAGTAACTTACCATTCGTTCTCCATGGCTGTATATTTTTTTCCAATCATTGGTGCCATAATTTCAGACAGTTTTTTAGGAAAATTCAATACAATCCTCTATGTTTCGATGATATATGCTAGTGGAAGTATATTACTTGCACTAACAGCTAGTGATCCCATAGGGTTACCCAAAGTTGGCTTCTCAGTATTGGGCCTATTACTCATAGCCGTGGGCACTGGTGGTATTAAACCATGCGTCGCAGCCTTTGGAGGAGACCAATTTCGCCTACCCCAACAGGAGAAGGATCTAGAGAGGTTTTTTTCATTATTTTACTTCTCCATCAATGCTGGAAGTTTGATATCAACTTTTATTACTCCC

			GO:0022857 transmembrane transporter activity GO:0016020 membrane		ATTTTAAGAAATGATGTACATTGCTTCGGTAATGAGAGCTGCTTTCCTTTGGCTTTCGCAGTGCCTGGAATTCTAATGATAATTTCTGTAGG **(949)**
MSTRG.29796.1	(1) Peptide transporter family 1-like [Anoplophora glabripennis](98%;56%)/peptide transporter family 1-like [Leptinotarsa decemlineata] (95%;43%]	Higher	(1) Proton-dependent oligopeptide transporter family (IPR000109) GO:0055085 transmembrane transport GO:0022857 transmembrane transporter activity GO:0016020 membrane	(1)2-640 RTLPYTDTDVKYTLKGKSININSGNTSAKEFSSPGHWSINVGKKQFNKTVNLELGGTYAVMLNKNQMEMAYTIVTKPNSVHIAWLLPQYFIITAAEIMFSITGLEFSYSQAPASMKSLLQACFLLTTAFGNLIIVIIESMEIFEKKSNDFFLYCGLMVADMLIFSFMAMRYKYIKKEESPPISEIEPIATKENQNGGIDNPSFVKSSNNVNA* **(213)**	TAGAACGCTACCTTATACTGACACAGATGTTAAGTATACCTTGAAGGGGAAATCAATTAATATCAACTCAGGAAACACTTCTGCAAAAGAATTTTCCAGTCCTGGTCATTGGTCAATAAATGTAGGAAAGAAACAATTTAACAAAACTGTAAACTTGGAACTTGGTGGAACATATGCCGTAATGCTTAATAAAAACCAAATGGAAATGGCTTATACGATAGTGACAAAACCTAATTCAGTCCATATAGCTTGGTTACTTCCTCAATATTTTATTATAACTGCTGCAGAGATTATGTTTTCCATCACTGGATTAGAGTTTTCGTACTCTCAAGCCCCGGCATCAATGAAGTCTTTACTGCAAGCTTGCTTTTTATTGACCACTGCATTTGGAAACTTAATTATTGTTATTATAGAATCCATGGAAATTTTTGAGAAGAAGAGTAACGACTTTTTCCTATATTGTGGACTGATGGTCGCCGATATGTTGATCTTTTCGTTCATGGCAATGAGGTACAAGTATATAAAAAAAGAAGAATCACCTCCAATATCAGAAATCGAGCCTATAGCAACTAAGGAAAATCAAAACGGGGGTATCGACAATCCATCCTTCGTAAAAAGTTCCAATAATGTTAATGCTTAAGAAAAACAACTCGAATTTTCAATTGAGAAAATTTAATTTGTTTGGGGGCCACATTAACAACAAGTGTACTGATCTTTTAATAATCAAGAAATCAAGATTTAGATAACATACCGTTAACATAAAATTGGAGTGATCTTGTACAAGATAACAGATTATCTAGCTTACCCTCTTTATAGTACCTATCCCACTTAATTTTTCTTGTAGTTATTTATTTTATTTATTAGTTAAAAGCATTTGACTATAAAATATAGAACACCTTAGTACATATTGTATAAATATCAGTTTACACTACCCCCAGTATTGAAAGAAATAGAGAAATGTAAATATTTTGAC

					TGACTTTATTTATTTATTGACGTTAATGCAACTAAATGACTATCTTTAAAAAATCCAAAAATGTTTATTTCTTTTTAAGATGTGTAATTTTGGTATACTGTTGGTACCTACTTTATTTCTTAAAAGACCTTAAAAGACTGTATATAGGTTCCAATTGGAGATTTTCTATATTTATATAATATTCCAGATTGAAAACATTTGTAAATTCTGAACAATAGCATTATGTGCATTAAAGAAAGTGTACCTATATAAAAAATTATAGAATTTAAGAAAATTTTGTTAAAATATATATAAAAATAGATTTATAAATACTTTATAACATGAAATTCTTTTGGATAAAGTTCTTTTCAGTAGCATTTTTCAGTGCGTCACAAATGATAGAAAAAAAGGTAAGTCCGTG **(1,373)**
MSTRG.43015.1	(1) Carboxypeptidase Q-like [Anoplophora glabripennis](95%;61%)	Higher	(1) Peptidase M28 domain (IPR007484)	(1)65-1501 MWLSTIAVLVCASLSNALSCNLSSDLLKEIRSYQGTVDQIINATTQGLFKGKTYDELAYFVDKFGARQAGSQVLEDSIDYLLDLMQSTGYDLDNVHGENVTIPHWIRGTQTCEMLSPRKANIPVLTLGGSVSTLANGFEAEAIVVKDFDELDRVSDKVKGKIVVYNNEYITYGVSVAYRSKGPSKAAKYGAIATLIRSVTPFSLNTLHTGQTAYEDSIPKIAAASITREHANMFQRMQDRGDKIVLKLNIQTQNLDPVTSRNVVAEIKGSRDPEKVVLVSGHIDSWDVGVGAMDDGGGAFISWYALRVLKALGLKPKRTLRSVLWTAEEPGLIGVQAYGQAHKDELDKHIFVMESDEGVFTPLGIEYVAGDEGGCILEEILKLLTPIDATQAKLVEFAGSDITIWRNILPTANLLSRNENYFWYHHSEADTMDVLDTAALDKATALWASVAYILADLNKDF	AAATCTCATTATCTAAATAAACAGTATAACAATCTCCTTCCTGTGTAATCCATTTGGTCTGATTATGTGGTTGTCAACAATTGCCGTGTTGGTGTGTGCATCACTATCTAATGCACTTTCCTGCAATTTGTCTTCGGATCTGCTTAAAGAAATTCGTTCTTACCAAGGAACAGTTGACCAGATCATAAATGCAACTACACAAGGACTATTCAAGGGCAAAACCTACGATGAACTGGCGTATTTTGTTGATAAGTTTGGAGCCAGACAAGCAGGAAGCCAGGTATTGGAAGATTCAATAGATTATTTACTGGATCTGATGCAATCGACAGGATATGACCTAGATAATGTTCATGGAGAAAATGTTACCATTCCGCATTGGATTAGGGGAACTCAAACATGTGAGATGCTGTCGCCAAGAAAAGCTAACATTCCAGTACTAACCCTCGGTGGTTCTGTGTCTACCTTAGCCAATGGATTCGAGGCAGAGGCAATAGTTGTAAAAGACTTCGACGAATTGGACAGAGTTTCTGACAAAGTAAAAGGCAAGATTGTGGTGTACAACAACGAATATATTACATATGGGGTATCTGTAGCTTACAGGAGTAAAGGACCAAGTAAGGCAGCTAAGTATGGAGCAATAGCGACCTTGATAAGGTCTGTAACACCGTTTTCCTTAAATACACTCCATACTGGTCAAACTGCATACGAAGACTCCATACCAAAGATAGCAGC

				PRQVPKLNIVLPSVLHV* **(479)**	AGCTTCAATAACAAGAGAACATGCTAACATGTTCCAAAGAATGCAGGATCGTGGTGACAAAATAGTATTAAAACTCAACATCCAAACCCAAAATTTGGATCCAGTTACATCAAGAAACGTCGTTGCAGAAATTAAGGGATCAAGAGATCCTGAAAAAGTAGTTCTAGTATCTGGCCATATTGACAGTTGGGACGTAGGTGTAGGAGCTATGGACGATGGAGGGGGTGCTTTTATTTCTTGGTATGCTTTGCGCGTACTTAAAGCTCTTGGTTTAAAACCAAAAAGGACTCTAAGATCTGTGCTTTGGACAGCTGAAGAACCGGGATTGATTGGTGTCCAAGCCTATGGCCAAGCCCACAAAGACGAATTGGACAAACATATTTTTGTAATGGAATCTGATGAAGGAGTTTTTACACCTTTGGGTATAGAATATGTTGCTGGTGATGAGGGAGGTTGTATTCTGGAGGAAATACTAAAATTGCTGACTCCAATAGACGCAACACAGGCCAAATTAGTCGAGTTCGCAGGATCTGATATTACAATCTGGAGGAACATTTTACCAACTGCAAATTTGCTGAGTCGGAATGAAAATTACTTTTGGTATCATCACTCTGAGGCCGACACCATGGACGTTTTAGATACCGCAGCCTTAGATAAGGCCACAGCATTATGGGCTTCCGTAGCATACATACTTGCTGATCTGAACAAAGATTTCCCAAGACAAGTACCAAAATTAAATATAGTGTTGCCATCAGTACTGCACGTTTAGATTTAGTTTAATTTATTTGTATTATTTGTATATCATTCATCATCATCATCAATGGCGTTACAACTCTTCGTGAGTCTTTGTCGCGTTTAATATTGTCTTCCATGTTTGTCTGTCCTGTATATCATTAACCCCCTATTAAAAAATATTACCTCACTCTTGAGACTTTTTTTATTCAGTCATTCATGTTGAGTCTGCCAAATGCCTCAAAAAATATGGGCCTGCAAGTAAACGAGGAGAAAACTAAGATGATGGCATCAACACCCAACAATAGAGCCACAAACATCGGTCACCAATTCACGGTTGATAACTCTACCTTTGAAGTGGTGGACCAATTCACATACTGAGGCTCCTTGATCACCAA

					GGAGAACGTCATTATTGCGTTTATTAAATGGATGAACATCCATTTATTAATATATTATAATACTTTCATTATGTATACCATAATATCACTTTAATGATATTACGAACACTGTTCACTGAGTCAACGAACTCTATTCAGTGAAACAACAACGTCGTTAATTGACCGACGAAGACTATTCGTTATGTCAACAAGAGTGTTATTTCTCCTAACGTATACTGCTTCATGCATCCAATAAATTTCGTTTATTTCTACAGTTCTTTCCGTTTATTCTTACAATTAATTCTGTTCATTCCAACAATAAATACGGTTATTCTGACAAGCAACAAAAATACTAATTAGTTTTCCCAGGATTCGAAAAAAATGAATACGATAATAGATACACGAAAACTTCCTTCCAGTATGGACTACATTTGAAAACGAAATGAAATTATTCGGCACTTCGGCAGAGGTAACATCATTGTTTAC **(2,327)**
MSTRG.18102.1	(1) Leucine-rich repeat protein SHOC-2-like [Leptinotarsa decemlineata](99%;80%)	Higher	(1) Leucine-rich repeat domain superfamily (IPR032675)/Leucine-rich repeat-containing protein 20 family (IPR037384)/Leucine-rich repeat (IPR001611) GO:0005515 protein binding	(1)338-979 MRPPTQYPQDIAQEAEAESEPDPRMGAMMICTRLAGRAVIRVIGRCNDAKENENLDLSDCQLMQVPDAVYHLMRHTELKTCDLSDNVITKIPPKFAAKFNQITELNLSHNQVSKLPDECVSLGALERLDISHNTFIELPDCIFKIPKLRHLNASNNSIVDLDVDCLKDAPSLESVDLTNNPLAPRIYEQLSRLSDLRILLTPREKEDWEDLTI* **(214)**	CCACTCATGTATTTTAAAAAACAAATAAAAATAAAACACTTAAAAAATAAATTAAAGCTAGATCAAAAACAAAAACACGCGGTGATCTGTTCGAAATCCGCACGTTGCTCCTCGCTAGCGCTGCTTTTTGCGTCTCTACCGCGACGCACCGTCGTCTCAGGTCAGACGCAACGGCGCCCCCCGGGGCAAGGGGAAAGTATAAACAAAGCCAACGAGAGTGTATAAAAACCTCTCTGCGCGTCCAATAACAAAACATTTGATTCTAAACCGCTCCAAAGCAAAAGTGATACCAAAAGTGCATTATTCCGCTCGTTGGTGATCAGTTTGTGACGAAAAGATGCGCCCTCCTACACAATACCCCCAAGATATCGCCCAAGAGGCCGAGGCCGAAAGTGAACCCGACCCCAGGATGGGGGCGATGATGATCTGCACCAGGCTGGCTGGAAGGGCTGTCATCAGGGTCATCGGAAGGTGCAACGATGCTAAAGAAAATGAAAATCTTGATTTATCCGATTGCCAGTTAATGCAAGTTCCTGATGCAGTGTACCACCTGATGAGGCACACCGAGCTCAAAACCTGTGATCTCAGTGACAACGTCATTACAAAAATACCTCCAAAGTTTGCCGCCAAATTCAACCAA

					ATCACAGAGCTCAACTTATCTCACAATCAAGTGTCGAAGTTGCCTGATGAATGCGTAAGCCTAGGTGCGCTTGAGAGACTGGATATATCGCACAACACCTTCATAGAATTGCCCGATTGTATTTTCAAAATTCCCAAATTACGGCATCTTAATGCCAGCAATAATAGTATAGTTGATTTAGATGTAGATTGTTTAAAAGATGCACCATCGTTAGAATCAGTAGACCTAACAAATAACCCATTGGCACCGAGAATATATGAACAATTATCTAGATTATCAGATCTCCGAATACTGCTCACTCCCAGAGAGAAAGAAGATTGGGAAGATCTCACCATTTAATATTTACGTAATATATTTTGTGGCAAATGCTATAGACTGAAGACAGCTAATTGATAGGTTCAGTTATAGCGGACTACTTCCTAAATTGTGTTCCCTCAGAGACGTATCTCGATTGTAGCTGTAGATCAGAGTATGTAGTCGAATTATGACTAATAATGTAATGCAACATATAAATAATATGTTACAAAATATACAAAGGTATAATCTCCCTTTTTTGTAGTCTTTAATCTCAATTACTTGCAGTGAATACTTATTTCTTTGGTAATTAATAAAAAGTATTTCAAAAGGTACATCAAAAGTCTCAGCGCCCAGTATTTTTTTATATTATAAAAATGTCTAGTGATTGTAAACTCTTTTGGTTTTTTAGATGTTGCATTAAAAATTGCTGAGGTGTACATATGCCGAGTGCAAAGTACAGATTGTCATGATGATCGCCAACATCCGAAACGGATAGGCCCTACAAGAAGAAAAACATTTTAACATAATATGGCACGCCAATTGAACAAGTGTATTCTTACCAATACATTTCTGGGCCACTATTTATACTAAATTTACAATCAAGATGCAGTAGAAATAAACAAACCAAGACACGTTAAATGCTACTATTAGCACTCCCGAATCATAATTTACAATGTATAAACTTTGGAAATCATGATTTGGGATTTACAATGTATTATTAAGCTCTCATTAGATCAGCATCTTATTAATTCTATTAATTAATGAATTATTTAAATTGCTACTCATGAAAACGAAACCAAAATTTAATAAAACTTTCCAATAAAAATATTCTCAGTGCTAATT

					GATTTTAATGTATTACCTTTAGTTTGTGGCTTCTAGTATTTCTCGTTGCTTACTTTATCCAGGACAAAACACGGAAAATAAATATACTCAAAATCATATAAATTTTTTATAACTATTATTTATTTATATACTATACCATAAATATACGATTCAAAATGTATGCTAAACTTTATTCTGTTGTAAACATTTCTTATCTAATAAAAAAATCTTTAATTCTACTATCTCCTTTTTTGAACCAAAACTTATTTAAATGATTCGGTAGACTGTTCTTATTATTATATAAAAAAACAAAATTTAATTTTCACTTTTTAAATGGATTACTTATATCTTCTATGAATTTACGAATGAATAAATTATGCTGTAAAACTGTTCAGTTGACAAAAACAAATATGGTGTGTAATATAAAACAACTCTCTCTGTTCACAAATAATCTGACTAACCTTTTCTATCTTCTTTACTTCTTCTCATGGATTGTGATGTCCTCGGTTCTCCCACAACGTGCTCCTCGGATGCTCCGACTGTCCTTCTCCTTCAAACTGTTAGCAAACAAAAACAGCACTCGTTCGAATTCTCTCCTCAATTAAATCTCTGACTCGATACAAACAATATCAATCTTTATAATTCCAAGATTTCTTCTCTCAGCTCGATATCTCGTGCAAGTTGATATAAACCGGCCACTCGTTCCAGACAAAAACTGGAATCTATTCGGACACAAGGAGTTTGTACTTCTCGACTTGATCACGATTTCATCTCAACATGAATCTGCTTCCACGGCCACCAAATTAACCACTTTACACAAAAATACTACTTTCGAACTGGACTGGTTGCTTCCGATCTTAATTACACAGTAATTTCTTTTGCTTGCTTTCCTCATCAATCCGAAAATCAACCACTCTATTCTCCCTCCATCGGTCTCCTCGCCAATCACAAGCATTCTCCATACATCATATCACTACTTTTTTTCTTAAGAACAAATAGTATTGTGTACAAATTTTATGTCTTGTCAATTTCCAGGAGATACTAAAATTAAATTTTACTTACATTTTAGAAAAACCCTCCATTCTAAACTAAACAAAATTGTTTACAATTGTTTCTTTCTACGAAACCATTTAGAAACATGGTCTATTGTCCATTCCAAAGCGGCACATTAAC

					TTTCTAAAACTACCGTTTTCTAGTTCATTGTTTTGAAATGTATTAATCTGTTCGTAGAAACTTTACCACTAGACTTTGACTCTTCCACGAAACACTGCTTACGGCTAAATTATTTTATTTACAAATTTGGGTCATATACAAGGCGATAAAAATTTACGATCTCGTGGTCTTTAACACAAAATGAATTCTCTAAATTCTCCCCATAAAAATTATTTAACAGTATATACATTGTAAATTATGATTCGGGTGTGCTCCTAGTAGCATTTAACGTGTCTTGGTTTGTTTATTTCTACTGCATCTTGATTGTAAATTTAGTATATATCATGTTAGGAACAGACAACCAAACAACATACAAACAACAACACATAAACACAGAGTATGACTAGCATGGGTAGCTTATGGAAAACTGAGGGAAGTGTTTAAATCAGATATTCCCATGTGCTTGAAAAGAAAGATTTTTCCCATGTGCACCAGAAAAATAATAAATAAAATACAAGTAGCACAGAGGGCCAAAACAATGGAGAGGATAATGTTGAATATATCTCTCATAGATACATTTTCAAATCAAATAGAAGAAAAACTGATGTTATAGACGCAGTTAACTGAACTAAAATGCTGGAATGGAACTGGCAGGCCATGTTACCAGACACAGAGATGGAAAATGGACCAAGAAAATTTTAGTATAGAGATCTAGACACGATGCTTATCGTAAACGAGGATTTCCTTACAAGATGGTCGGACAACATCAAGTGCATCAAGAACCACTGGATTAATTCAAAGTGCTCAAGACCGAAAGCAACAGAATTAACTAAGGGAGCCTATGTTCAGCAGTGGACTCAAAATTGCTAAGAATGAATAATAATGGATGATGAATTGTAGAATATTCATTCTGCCAGTTGTTATAAAATACCTATGTGAAAAACATATTAAAAGTAAAGGTTTTAAATCAGGAAACTATCGAACAAATTACAGAAATAAGTATACTGAAAGAGATATGTTTGTCCTGAAATATTTTTAAGATTATGGACAGAAAAATAATATACCAGAGAAAGAAAAAAGTTGATTTCTTGAATTAGTGAAACACTACATAGTGTTATGTGACATACCTACAGATTTTAAACAGTTTTTTTTTATAATCATT

					TTGTTGTAAAACGAAACAAGAGCCGTCTTATATTTCAGTTTGTTCAGAGAGCTTCAGCACCCTGACCGGATTCAATCCTCATTATGATATCATCAGAGAGTGCATATTTGATTATCTCTGTACAAATTAAAATTCCGGCTGCCAGTATCGATTCACAACGAAATAACATGATGGTGTGGATGTCGTGGCGACATCTGCTAAAGACAAGCGAAAGTTTTGCTTTAATAAAAGCATTTTTATCTAAACAATAGGTCCTAGATATTAGAAATTTGACAAAATACATCTGAAGGAACACAAGCTAGGAATGCTCTCTATATGGTGCTGCATATCTAGGTCTACTTACTAGACAACGTTTTGTCAAGATATTTGTATTTTTATATAAAGGTATTTATAGTAGATAATTTAAAAATGACTAATTTTTCAGGTACTTATTTTTGAAGTACTTATGTGTGAATATTTTTTGTACTGACTTCCTGTTGAACTGTAATAATGTACTATTTGACATTGGTAATGGTTACCATCTAGTCATATATTGTGATATGGTTCTATATTTAGTGATTGGATGCTCTGTTTACAACTGTCAAATAAAGAGATCTAGTAAAACAGTCTTTTTTTTTAAAATAACATTTAGTCCTGTCGGGTGTTAGACGAATA **(4,727)**
MSTRG.43013.1	(1) No hit (2) No hit	Higher	(1) No hit	(1)184-41 MMFLKQIVLGSTTKKIITSLMGLYLFSYSCRVRQLFYFGKFSGEGVL* **(48)** (2)260-352 MLNQTKLHQKRVLFRRSFCIYSPVNDHFPA* **(31)** (3)98-12 MSSQTTFLFRKIFGRGRFVNIEVTLKKI* **(29)** (4)333-383 MTIFPHNFLSLHRFTF* **(17)**	GTATTAACTAACTAAATTTTTTTGAGTGTAACCTCTATATTTACAAAACGCCCTCTCCCGAAAATTTTCCGAAATAGAAAAGTTGTCTGACTCGACATGAATAACTGAATAAATAAAGTCCCATGAGGGAGGTAATAATTTTTTTAGTAGTAGACCCAAGGACTATCTGTTTTAAAAACATCATCTTGCGGTGGTAAATTTACTTTTTTTGAAGATTTACTTTTTGATATACATATAGTATGTGTAGTTCATATGATTCATGTTAAATCAAACGAAGCTACACCAAAAAAGAGTTCTTTTTAGACGATCCTTCTGTATCTATAGTCCAGTCAATGACCATTTTCCCGCATAATTTTCTGAGCCTGCACCGATTTACTTTTTGAGTAATTCGCAAAAACCCCTTTGAAAAATGTTTTTTTTTTAAATATATTTAATTCTCTAATGACATTTTTGCAAGAAT

				(5)261-217 MNHMNYTYYMYIKK* **(15)**	ATGATATCGATTTTAAAAACTGCAGGAGACCGTCCTA **(497)**
MSTRG.60092.1	(1) No hit	Higher	(1) No hit	(1)209-3 MNHFYCCTYLYVFKLHKYTLSLKYYLTYIHFYLIKLLNCLFVKFLSDENRSGLAGLPGYRGPTYRGSTV **(70)**	AATACAGTGGAACCCCGATAAGTCGGCCCCCGATAACCCGGAAGTCCGGCTAACCCGGACCGATTTTCATCAGACAAAAATTTAACAAATAAACAATTTAACAATTTTATCAAATAAAAATGTATGTAGGTCAAATAATATTTGAGAGATAATGTGTATTTGTGTAATTTGAACACATATAAGTATGTACAACAGTAAAAATGATTCATGCACACGGCGGCAGGCAGAGCGACCGTCTCAGCTTATCGGAAAGAACAGGCACCTGTCTGTATTCCTTTTCCGTTATTTATGTCAAACTGTCTTAG **(305)**
MSTRG.65069.1	(1) Reverse transcriptase [Tenebrio molitor](86%;39%)	Higher	(1) Reverse transcriptase domain (IPR000477)	(1)3-1214 KNIDMNRGVKQGDPLSPYLFNMVVDELICKLEEDMQGLPVVDGRKVSVLGSADDLILLSDSFNDGNKQLRTAVGFFERRGMSINAGKSAAITVNVDRGNKHSYCVTHSLFSVGNDRIKQLKPSEMFKYLGQRYNALGQTKVAFQDLQTQLDRISKSGLGPAQKLNLVKTYLLPRYIDKLQSPTITLKALKGFDRTIRIAVRKFLRLNRTCADAYIHAPTREGGLGVMTMVMHVPAILRRRLAKLMISATQATADILSLPYISRLWEKLVKWTSNNGGSSTFIARELSAKLETGYSGNGLAQGSCHPESSAWIHNPPPYWSGRDYVKAIQLRGNLLPTKGIPSNPPQERMCRTGCGRSESLSHVLQKCSIAHWQRCRRHDQLVTSLRKSCERKGWICEVEPRIRL **(405)**	CGAAAAACATCGACATGAACAGAGGAGTTAAGCAGGGCGACCCGCTTTCTCCTTACCTGTTCAACATGGTGGTCGACGAGCTAATATGCAAGCTCGAGGAGGACATGCAAGGCCTACCAGTGGTAGACGGCAGGAAAGTCTCAGTACTAGGATCTGCTGATGACTTAATTCTGTTGTCCGATTCGTTCAATGATGGGAACAAGCAACTCCGGACAGCTGTTGGATTCTTTGAGAGGAGGGGGATGTCGATCAACGCTGGTAAGAGTGCAGCTATTACGGTCAATGTGGATCGTGGTAATAAGCACTCTTACTGCGTAACGCACTCGCTCTTCTCGGTCGGCAACGATAGAATTAAACAGTTGAAACCAAGTGAGATGTTCAAGTACCTAGGACAAAGGTATAATGCCCTGGGACAGACCAAGGTGGCTTTCCAAGACTTGCAGACCCAGCTCGATCGTATTTCGAAATCTGGTCTGGGGCCAGCTCAGAAGCTGAACCTAGTAAAGACGTACTTGCTACCGAGATATATAGATAAGCTGCAGAGTCCGACAATAACGCTAAAAGCTCTGAAAGGCTTTGACAGGACCATACGCATAGCCGTGCGGAAATTTCTGCGTCTCAACAGAACATGTGCGGATGCCTACATTCACGCGCCTACTAGAGAGGGTGGTCTGGGCGTCATGACCATGGTCA

					TGCACGTTCCGGCCATCTTAAGAAGGAGATTGGCTAAGTTAATGATCTCAGCGACGCAGGCGACAGCTGATATACTGTCATTGCCGTATATAAGCAGACTCTGGGAGAAACTAGTAAAATGGACTTCGAACAACGGAGGCAGTTCGACATTCATAGCACGTGAGCTGAGCGCGAAGTTAGAAACTGGCTATAGCGGTAATGGTCTTGCTCAGGGTTCTTGCCATCCAGAGAGCTCTGCCTGGATACATAATCCACCGCCCTACTGGTCGGGAAGAGATTACGTAAAAGCAATCCAGTTGCGAGGAAACCTTTTACCAACCAAGGGTATCCCGTCCAATCCTCCACAAGAACGGATGTGTAGGACGGGATGCGGTAGGTCCGAGTCTCTGAGCCACGTACTACAGAAGTGTTCAATAGCACATTGGCAAAGATGTAGGAGACATGACCAGCTCGTGACCTCTCTACGAAAATCCTGCGAACGTAAAGGGTGGATATGTGAGGTAGAGCCGCGTATCAGACTA **(1,214)**
MSTRG.78713.1	(1) Cathepsin L1-like proteinase [Diabrotica virgifera virgifera] (98%;58%)/ digestive cysteine proteinase intestain [Leptinotarsa decemlineata](95%;47%)	Higher	(1) Papain-like cysteine peptidase superfamily (IPR038765)/Peptidase C1A family (IPR013128)/Peptidase C1A, papain C-terminal domain (IPR000668)/Cysteine peptidase, cysteine active site (IPR000169)/Cysteine peptidase,	(1)1-648 GVHVADPNVKLASSVDWRSKGAVLPVRDQASCGSCWAFSTAAALEGQLAIHKNEKIPLSPQNLVDCSTQNDGCDGGDQVLAFKFIKSSGISSEADYPYVGVDQKCHKNVHKTVSTISGYKHLSANENALISALSSVGPISVSVDASVWSLYAGGLFDERDCGTDINHAVLAAGYTDEYILVKNSWGTDWGEEGYIRLARGHNICQINEDNSYPIL* **(216)**	GGGGTTCATGTCGCCGATCCAAATGTTAAGTTGGCATCCTCTGTTGATTGGAGGAGCAAAGGAGCAGTATTGCCTGTAAGAGACCAAGCTAGCTGTGGATCATGCTGGGCATTCAGTACCGCAGCTGCTTTGGAGGGACAACTAGCAATACACAAAAACGAAAAAATTCCTTTGAGTCCACAGAATCTTGTGGACTGCTCTACACAAAATGACGGTTGTGATGGTGGAGACCAAGTGCTGGCTTTCAAATTCATTAAATCAAGCGGTATTAGCTCCGAAGCTGACTACCCATACGTAGGAGTCGACCAGAAGTGTCACAAGAATGTCCACAAAACTGTTAGTACCATCTCCGGCTACAAACATCTAAGTGCAAATGAAAACGCTTTGATTTCTGCTCTTTCTTCTGTTGGACCAATCTCCGTTTCTGTTGATGCCAGTGTTTGGTCACTATACGCAGGTGGTCTTTTCGACGAAAGAGATTGTGGTACTGATATCAACCATGCAGTACTCGCTGCAGGATATACCGACGAATACATTTTAGTCAAAAATTCTTGGGGCACAGACTGGGGTGAGGAAGGGTATATCAGA

			asparagine active site (IPR025661) GO:0006508 proteolysis GO:0008234 cysteine-type peptidase activity		CTAGCAAGAGGACATAACATATGCCAAATCAACGAAGATAATTCTTACCCCATTTTGTAAATTGTAAATCTGACATTACCTTGTAAATGTAGACATATTTTTTTTATTTTAAACAAAAAGAATACACTTAATCTACAAGATTAATCA **(735)**
MSTRG.17015.1	(1) Maltase 2-like [Anoplophora glabripennis](95%;51%)/Maltase A1-like [Tribolium castaneum](98%;46%)	Higher	(1) Glycoside hydrolase superfamily (IPR017853)/ Glycosyl hydrolase, family 13, catalytic domain (IPR006047) GO:0005975 carbohydrate metabolic process GO:0003824 catalytic activity	(1)206-1933 MWKLTIFFYLWICCLQSSKAYHLSTDDEWWKTATFYQIYPKSFKDSDGNGIGDLQGVIEKLDYIKDLGVTGVWLSPIFKSPQADNGYDISDYRDIDPQFGTLEIFLELLKEAHKRGIKVVLDYVPNHTSDQHEWFKKSENGEKPYDEYYIWKDGKNGSKTEPPNNWLSVFGHSGWTWSEKRQQFYYHAFLKEQPDLDYRNPLVRQEMKDVLSFWLDTHNVDGVRMDAVSKLVEDAAFLDEPKSNAPGVADFMYDYLTHTYTENQPEGYDVVYEWRSHLESISKKKESSRICMAEDGANFTLTLPYYGTLNGSVLGAHFPFNFFFLPLNTTSNGGQIANIINEWLIRLPKIYTLNWVLGNHDLHRIASRVGKEKVDALNMLTAVLPGIQITYNGEEIGMEDGEVTCEQGDDLKSNCTLYPSVSRDFERTPFQWDSSEFAGFTNGTSTWLPVSSKKDNCNVADQLKDDRSHLSIYKSLQKLRKTLNSRSEIEVNAQGNDKNVLEVARFNKVNGSNTDLVEFICNL	CCTATATAAAGTCTAATCTTTATCATAATGCATAAAATCAATGATTTACGAGTATATATAATTTCAACTTGGAATGATTATTTGTCAATTATTTTACTGTCACAGTAAAAAATGTGCTAGGTATGTACGCTCATAGTATCATTTGAACAAGATAATTATAGCTGTATTACGATTTAGTTTTTAGAAGGTATATGAAATTGAGAACATGTGGAAATTAACAATTTTCTTCTACCTTTGGATTTGCTGTTTACAATCTAGTAAGGCATATCATTTATCGACCGACGATGAATGGTGGAAGACAGCTACATTTTATCAAATCTATCCAAAATCCTTTAAAGATTCTGATGGTAATGGGATAGGTGATCTACAAGGTGTGATCGAAAAGTTGGATTATATTAAAGATCTAGGAGTCACTGGCGTTTGGTTGTCTCCTATTTTCAAATCTCCACAAGCTGATAATGGATATGATATAAGTGACTACAGAGATATTGATCCGCAGTTTGGGACTCTGGAAATATTTTTGGAGCTATTGAAAGAAGCACATAAACGAGGGATAAAAGTTGTTTTGGACTATGTTCCCAATCATACGAGTGACCAGCATGAATGGTTTAAAAAATCTGAAAATGGAGAGAAGCCTTATGATGAATACTATATTTGGAAAGATGGAAAAAATGGATCAAAAACTGAACCCCCAAATAATTGGCTTAGTGTTTTTGGACATTCTGGGTGGACTTGGAGCGAAAAAAGACAACAATTTTATTACCACGCATTTCTTAAAGAACAACCTGATTTGGATTATCGCAATCCATTGGTCAGACAGGAAATGAAAGACGTTTTATCATTCTGGTTAG

				GNTAADVSLLENNNVGYKVLISSKNSKRKPGDIVDNKSLVLDPYEALILGEA* **(576)**	ATACTCATAACGTCGATGGTGTCAGGATGGATGCAGTCAGTAAACTAGTTGAAGATGCTGCATTTCTTGATGAACCTAAGTCTAATGCACCTGGTGTAGCTGACTTTATGTACGACTATCTAACTCACACTTATACAGAAAATCAACCAGAAGGTTACGACGTGGTTTATGAATGGAGAAGTCATTTAGAAAGTATTTCTAAGAAAAAGGAAAGTTCAAGAATATGCATGGCTGAAGATGGGGCAAATTTCACACTAACATTGCCTTATTATGGTACTCTTAACGGATCTGTATTAGGAGCCCACTTCCCCTTCAATTTCTTCTTTCTGCCACTAAACACCACTTCTAACGGAGGGCAAATAGCGAATATAATAAACGAATGGTTAATTAGACTTCCAAAGATATATACTTTGAACTGGGTGCTAGGTAACCACGATCTGCACAGAATAGCTTCAAGAGTAGGCAAAGAAAAGGTTGACGCCTTAAATATGCTCACAGCAGTTTTACCAGGCATCCAAATAACTTACAACGGTGAGGAAATTGGTATGGAAGATGGAGAAGTGACTTGTGAACAAGGCGATGACCTGAAAAGTAATTGTACTCTCTATCCTTCTGTAAGTAGAGATTTTGAAAGAACTCCCTTCCAATGGGACAGCAGCGAGTTTGCCGGATTTACCAACGGAACATCTACTTGGTTGCCTGTCAGTAGCAAAAAAGATAACTGCAATGTTGCCGATCAACTTAAAGACGATAGAAGCCATTTGAGTATTTATAAAAGTTTACAAAAATTGAGGAAGACATTAAACAGTAGATCAGAAATCGAAGTAAATGCCCAAGGAAACGATAAAAATGTATTGGAAGTAGCAAGGTTTAACAAAGTTAACGGTTCAAATACTGATTTGGTTGAATTTATTTGTAATTTAGGAAACACTGCGGCTGATGTTTCTTTGCTTGAAAATAACAATGTTGGATATAAAGTGCTTATAAGCAGTAAAAATTCAAAACGAAAGCCAGGTGACATTGTTGACAACAAAAGTCTGGTGCTGGATCCATACGAAGCGCTTATTCTCGGAGAAGCTTAGTTTGTTGTTAGCATAGCTTTAATATATTAGTTTTTAACTGTAAATTGTAT

					AAATAATATCTAAATTAAATTATATTTATTAATTGCATT **(2,022)**
MSTRG.25208.2	(1) PREDICTED:Glyoxylate/hydroxypyruvate reductase A-like [Tribolium castaneum] (99%;51%)	Lower	(1) NAD(P)-binding domain superfamily (IPR036291)/D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding domain (IPR006140) GO:0055114 oxidation-reduction process GO:0051287 NAD binding	(1)119-1084 MHSVISVLSRIKNIVPELQNALPNLTFHEVSNAELDKQFKESHIIVADYDLLTPHMYSLPQAKWVQGTWAGVNDLMAKVTQPPPFSLSRFTGRHFGALMSEYVVANIINFERNAFETHQNQKMKQWIVDGKIEEHRAIFDLTVGILGLGNIGDRVARTLNYMGAVVFGYGRRPHLNLEDNPHISKYFSNQMLPQLLRECDYVVNTLPETQESKWLLNGDILENCKDKQAVFINVGRGTIISEEALIKALENKWISGAILDVFEQEPLPTESALWQMPNVIITPHVSASCRAKDIAQQMKDNLEYYRQNLPIPATVDFSKGY* **(322)**	CTCTAACTGGTTCAACCTAATTTGGCAACGTTGCTGTATACTGTATAATCAGCAAAAGTAAACATAACCTATAATGGATATATTTTTAATTTGCAAATCATACTTTTAAGTTAATAAAATGCATTCGGTAATATCTGTGTTAAGTAGAATAAAAAATATTGTTCCCGAGCTTCAAAATGCTTTACCAAATTTGACATTTCACGAAGTCTCTAATGCAGAATTGGATAAGCAGTTCAAGGAATCCCACATAATAGTAGCAGATTACGACCTACTAACACCGCACATGTACAGTTTACCTCAAGCCAAATGGGTACAAGGAACATGGGCAGGTGTTAACGATTTAATGGCAAAAGTTACTCAACCTCCACCATTTTCACTTAGCAGATTCACCGGAAGGCATTTTGGGGCGTTAATGAGCGAATATGTTGTTGCTAATATTATAAACTTTGAGAGGAATGCATTTGAGACTCACCAGAACCAAAAAATGAAGCAGTGGATAGTAGATGGAAAAATAGAGGAGCATAGAGCCATTTTTGATTTGACTGTTGGCATTTTAGGATTAGGGAATATTGGAGATAGAGTGGCTAGGACGTTGAACTATATGGGTGCTGTAGTTTTTGGCTATGGTAGAAGACCGCACTTAAACCTTGAAGATAATCCTCATATATCGAAGTATTTTTCGAACCAAATGCTTCCACAGCTTTTGCGTGAATGTGACTATGTTGTTAATACTCTGCCTGAAACTCAAGAATCGAAATGGTTGCTAAATGGAGATATTTTAGAAAATTGTAAAGATAAACAAGCTGTATTTATAAATGTTGGTAGAGGAACAATCATATCAGAAGAAGCATTAATAAAAGCTCTAGAGAACAAATGGATATCAGGAGCAATTTTAGATGTCTTTGAACAAGAACCATTACCGACTGAGAGTGCCTTGTGGCAAATGCCTAATGTGATAATTACCCCACATGTGTCAGCTAGTTGCCGCGCAAAAGATATAGCTCAACAGATGAAAGATAATTTAGAATATTATAGACAAAATTTGCCCATTCCCGCTACTGTAGACTTCAGTAAA

					GGTTACTGAGAACAATATATCCAAAGATGGACAGCTGAAATATCTTTTACAAACAAAGTGTGATATTTTTACCATGTTACGTTTAAATATATCTATAAATATACATTTATCATATAAA **(1,193)**
MSTRG.27946.1	(1) Multidrug resistance-associated protein 4-like [Anoplophora glabripennis](99%;63%)/ABC transporter C family member 3 [Dufourea novaeangliae] (99%;48%)	Higher	(1) ABC transporter type 1, transmembrane domain superfamily (IPR036640)/P-loop containing nucleoside triphosphate hydrolase (IPR027417)/ABC transporter type 1, transmembrane domain (IPR011527)/ABC transporter-like (IPR003439)/AAA+ ATPase domain (IPR003593)/ABC transporter conserved site (IPR017871) GO:0055085 transmembrane transport GO:0005524 ATP binding GO:0016887 ATPase activity	(1) 145-4179 MDIGYKLKAENPKQNANIFSKIFFGWMIPLIRRGTKQNLEINDLYKTLKKDQSKRLTDALEKNWQKQVDKAKKKGGKPSVLMAISRTFAFEFMMYGILWAIQNVVLMSLKPILIAQLIELFTDDTSTRFREMYFFSTSLILVSLLIVFFFHHTNFGLQAIGMRIRVATSSLIYRKITRLNQKSLGETATGQIVNLLSNDVQRFDMVVVPLHALWVMPLQVAILMFIIWNQVGISSLAGVISMAIIALPVQGYMAKLMGMLRQKVSGKTDTRVKLMNEVIGGIQVIKMYAWEKPFEKVIKQARSSEIGDITKASYLRGVFSSFIVFLDRVALFFTVMTYVLLGNVISADIVFSLAQTFNILQTAMAIWYPVAISVGAEALVSAKRIQNFLIMEEREEASIEKIDKPGIILSNVFASWTTKGRTLQDISFQVPPGTLCAVVGPVGAGKSSLLQLLLGELPLKHGRVQLGGEVSYSSQEPWLFQSTVRNNILFGSPYEKRWYEKVVKVCALERDMEQFPQGDKTIVGEKGVSLSGGQRARINLARAIYRQADVYLMDDPLSAVDTHVGRHLFDQCILHHLRGKTRILVTHQLQYLKKAGLIVVLNDGKIEAQGTFEELMDSKMDFTKLLVAADET	TATATCTATGTTTGTTTAATTTTTTTATAATTAACATAATTATCATTGGTAAAGGAAGCTTTGTCATTGCTATTGGGAGCAGTTTAGTTTTTAGTTAGTGGTGAGGTTTAGTTATGATATGATTGTGTAGATATTAGTGACAATATGGATATAGGGTACAAATTGAAGGCAGAAAATCCCAAACAAAATGCAAATATATTTTCAAAGATATTTTTCGGGTGGATGATACCACTAATAAGGAGAGGAACTAAACAGAATTTAGAAATAAATGACTTATACAAAACTTTAAAAAAAGATCAATCAAAAAGACTAACAGATGCTTTGGAAAAAAATTGGCAAAAACAGGTTGATAAAGCGAAGAAGAAGGGAGGAAAACCCAGTGTACTTATGGCTATATCAAGGACGTTCGCTTTTGAATTTATGATGTACGGAATACTATGGGCCATTCAAAATGTAGTTCTAATGTCTCTAAAACCAATATTGATTGCACAATTGATCGAGTTATTCACTGACGATACTTCTACCAGATTTAGAGAAATGTATTTCTTCAGTACATCATTAATTTTAGTGTCACTTTTAATTGTATTCTTCTTCCACCACACGAATTTTGGTCTGCAAGCAATTGGAATGAGGATAAGAGTTGCGACTTCATCCTTAATCTACAGAAAGATTACTCGGTTAAATCAAAAATCTTTGGGCGAGACTGCTACAGGACAAATTGTCAATCTACTATCAAACGATGTCCAGCGATTTGATATGGTGGTGGTACCGTTACACGCGTTGTGGGTGATGCCGCTTCAGGTGGCCATACTTATGTTTATAATCTGGAATCAAGTTGGCATTTCGTCTTTAGCAGGTGTTATTTCGATGGCAATCATTGCTTTGCCCGTACAAGGTTATATGGCAAAGCTCATGGGTATGCTTCGACAAAAGGTTTCCGGAAAAACCGACACCAGAGTGAAACTAATGAATGAAGTCATTGGTGGTATAC

			GO:0042626 ATPase activity coupled to transmembrane movement of substances GO:0016021 integral component of membrane	GEKHDKQEDADPEPVDFTRKFSSTRRFSVLSDASGEISLSMRSVDMTSDKNGEEEESAGDGKPFKDYLFATKNICFVIFVCVLMIMAQAFVVGVDLWLTFWTSQEAIRHENGTIVESTSPTVEIIPLHGDNFSYSYNYNYSYIPENNTNSFNNTKSFNINDIFDTVNVDGQLKKIIKTNWALYFYSGLIGLAIVFTLTRSLLFFKGCMMASVNLHSSMFHMLLKAPMRFFDTNPSGRILNRFSKDMGAIDELLPMGFLDTMQIMLALCGILVNITVSNAYIVIAIAILAAVFLKFRSWYISSARVLKHLEGITKSPVFSHINATLNGIITIRASNAQDVLIEEFDENQDANTSAWYLTIACMNSFGLWLDFLAIIFLAIVTFCFVILRKFTDVNGSLVGLAVSQCSALTGMLQFGMRQTAEIINQLTSVERVMQYTKLDTEGPFDTPEENRPRGVWPKRGQIEFRNLSLKYVENDPPVLRNLNFMITPGQKIGIVGRTGAGKSSLISALFRLAPLEGAIYIDGVNTKNLGLTDLRRKVSIIPQEPVLFSASLRYNLDPFNEFDDDKIWDALEQVELRDSVDSLDFHVAEGGGNFSLGQRQLVCLARAVLKNNKVLVLDEATANVDPRTDALIQATIRKRFKDCTVLTIAHRLNTIMDSDKVLVMSFGNMIEFDHPHKLLQIPDGHFHKMLLETGPVMSAQLKDVAMRAYQQE* **(1345)**	AAGTGATAAAGATGTATGCCTGGGAGAAACCATTCGAAAAAGTCATAAAACAAGCTAGATCATCGGAGATTGGTGATATAACAAAGGCATCCTACTTGAGAGGTGTATTTTCTAGCTTCATCGTATTTTTGGATAGAGTGGCTCTATTTTTCACTGTTATGACCTACGTTTTACTAGGTAACGTTATTTCCGCTGATATAGTTTTCTCATTGGCCCAAACCTTCAATATTCTACAAACAGCCATGGCCATTTGGTACCCAGTTGCAATTAGTGTTGGAGCGGAGGCTCTAGTTTCAGCTAAGAGAATTCAAAACTTTTTAATTATGGAGGAAAGAGAAGAAGCGTCTATCGAAAAAATAGATAAGCCCGGTATAATACTATCTAACGTGTTTGCTTCTTGGACAACTAAGGGACGTACTTTACAAGATATTTCATTCCAAGTTCCACCAGGTACTTTGTGCGCTGTAGTAGGACCAGTAGGTGCTGGAAAAAGCTCGTTGTTACAGCTCCTTTTGGGAGAGCTGCCACTAAAACATGGAAGAGTTCAACTGGGAGGAGAAGTTTCCTACAGTTCGCAAGAACCTTGGCTTTTCCAATCAACTGTACGGAACAACATTCTCTTCGGAAGTCCCTACGAAAAACGCTGGTATGAAAAAGTGGTTAAAGTGTGTGCATTGGAACGCGATATGGAACAGTTTCCACAAGGAGATAAAACTATTGTTGGAGAAAAGGGTGTTTCACTTAGTGGAGGACAAAGGGCTAGAATAAATTTAGCACGAGCAATTTACAGACAAGCTGATGTTTATTTAATGGACGACCCGTTGTCTGCTGTTGACACACACGTTGGACGACATTTGTTTGATCAGTGTATTCTTCACCATTTGAGAGGTAAAACTAGAATCCTAGTAACGCATCAGCTACAATATCTGAAGAAAGCTGGTTTAATCGTTGTACTTAATGACGGCAAGATTGAGGCTCAAGGCACCTTTGAAGAGCTAATGGATAGTAAAATGGACTTTACAAAACTCTTAGTTGCTGCCGATGAAACTGGTGAGAAACATGACAAACAAGAGGATGCTGATCCAGAACCTGTAGATTTTACAAGAAAGTTTTCTAGTACTAG

					AAGATTTTCGGTATTGTCCGACGCCAGTGGCGAAATATCGTTGAGTATGCGCTCAGTAGATATGACTTCGGATAAAAATGGTGAAGAGGAAGAAAGTGCTGGTGACGGAAAACCATTTAAAGACTATTTGTTTGCCACTAAGAATATTTGCTTCGTTATTTTTGTATGCGTGCTGATGATAATGGCGCAGGCTTTTGTTGTAGGTGTAGATTTATGGTTAACATTCTGGACCTCTCAAGAAGCAATACGGCACGAAAATGGAACAATAGTTGAATCAACATCTCCAACTGTAGAAATAATTCCATTACATGGAGACAACTTCAGTTATTCCTATAATTATAATTACAGTTACATACCAGAGAATAACACAAACTCATTCAATAACACGAAATCATTCAATATCAATGATATATTTGATACTGTTAACGTCGATGGCCAGTTGAAAAAAATAATCAAAACGAATTGGGCGTTGTACTTCTACAGTGGTCTAATAGGACTGGCTATCGTTTTTACGCTAACTAGGTCACTGCTGTTCTTTAAGGGTTGCATGATGGCTTCAGTTAACTTACACAGCAGTATGTTCCATATGTTACTTAAGGCTCCGATGAGGTTTTTTGATACGAATCCCAGCGGAAGGATCCTCAATAGATTTTCCAAAGACATGGGTGCTATAGATGAACTTTTACCTATGGGTTTCTTAGATACGATGCAGATCATGTTAGCATTGTGTGGAATTCTGGTAAATATTACTGTTTCTAACGCCTACATAGTTATAGCCATTGCCATTCTTGCAGCAGTTTTCCTAAAATTCCGATCATGGTATATATCCTCAGCTAGAGTGCTTAAGCACTTAGAGGGAATAACTAAGTCTCCTGTTTTTTCTCATATTAATGCCACACTAAATGGAATCATCACAATACGAGCTTCAAATGCACAAGATGTCCTAATAGAAGAATTTGACGAAAATCAGGACGCAAATACCTCAGCATGGTACTTGACAATTGCCTGTATGAATTCCTTTGGATTATGGTTGGACTTCTTGGCTATTATATTCTTAGCAATTGTTACATTCTGTTTTGTGATTTTAAGAAAATTCACCGATGTCAATGGCAGTTTAGTAGGTCTAGCTGTTTC

					CCAATGTTCAGCTCTTACTGGCATGTTACAATTTGGAATGAGACAAACTGCAGAAATTATTAACCAGTTAACCAGTGTCGAAAGAGTTATGCAATATACTAAACTTGATACAGAAGGTCCATTTGATACACCAGAAGAAAATCGTCCGAGAGGAGTATGGCCAAAACGGGGTCAAATTGAATTTAGGAATCTATCTTTAAAATATGTTGAGAACGATCCACCAGTACTCAGAAATCTTAACTTTATGATAACGCCAGGACAAAAGATTGGTATAGTTGGCCGAACAGGGGCAGGAAAATCCTCTCTTATCTCAGCTCTCTTCCGTCTGGCTCCACTTGAAGGTGCCATTTATATAGATGGAGTAAATACCAAAAATCTAGGATTAACTGATTTAAGAAGAAAAGTTTCCATCATTCCCCAGGAACCAGTACTGTTTTCCGCTTCTTTGAGATACAATTTGGATCCCTTTAACGAGTTTGATGATGACAAAATTTGGGATGCTTTAGAACAAGTGGAACTCAGGGACAGCGTAGACTCCTTGGACTTCCATGTAGCTGAAGGCGGTGGTAACTTCAGTTTAGGCCAAAGACAATTAGTATGTTTAGCAAGAGCTGTTTTGAAGAACAATAAAGTTTTAGTTTTAGATGAAGCTACAGCAAATGTTGATCCTAGGACTGACGCACTAATCCAAGCAACAATTCGAAAAAGATTCAAAGACTGCACGGTTCTAACGATTGCCCATAGGCTGAACACCATCATGGACTCCGATAAAGTGCTGGTAATGAGTTTCGGAAACATGATCGAATTCGACCATCCTCATAAACTCCTTCAAATTCCTGACGGACACTTCCACAAGATGTTACTAGAAACTGGACCAGTGATGTCGGCGCAACTCAAAGATGTGGCCATGAGGGCATACCAACAAGAGTGAAGACAAGCATAGTATAGGAATCTTTATTTATTTCTTTAAAATACCTTTATTTTCTAATAACACGTCACACTACATAAACGTTTTTTTCGGATAAATGTTAAATATAAAAAAGTATCTTAAAAAGGATTTTACTTAATATGAAGATAACGTTGAAAGCGTTGAAATTTTTCTTTTATAGTAATTATGTTTTATAAATACGG

					TTTACTACATATTTTATAGTTTTATTCTATTTTCTATTTCCTCGGTAAATTAAGCTTTAATAACTCTAATTGCGTCATATAAGTACTCTCTCTCTCCTACAGCGTTACAGCCCCAGTCGGGCCATGTATCCGCCTCCAAGTATCTCTGTCCCTAGCTGCTCTCCTCCAGTTATACACCTTTAAGATCTCTTTAGCATCGGTTCTTCGTCTATCCACCTCCTCCTTTGTCTTCATACTGGTTGACGTCCCACCATAGTTCCGCTAAGCGTTCTATTAGGTGTTCCGTCATTGTAGGTTATGTTATGAGGTGACGTGCTTAGCGCAATCTTTGTATTTTTGCATAATTTGCTATAGAGTGTCATATAAGTA **(4,748)**
MSTRG.2797.2	(1) Beta-hexosaminidase subunit beta-like [Aedes aegypti] (99%;51%)/ Beta-hexosaminidase subunit beta-like [Anoplophora glabripennis](96%;54%)	Higher	(1) Beta-hexosaminidase-like domain 2 superfamily (IPR029018)/Glycoside hydrolase superfamily (IPR017853)/ Beta-hexosaminidase family (IPR025705)/Beta-hexosaminidase eukaryotic type, N-terminal domain (IPR029019)/Glycoside hydrolase family 20 catalytic	(1)249-1868 MKFKIQLLSTFLCTSLVYAYIEEPGPRYPPTKGELWPKPYHQIKNHSFFTVRKEHFNFKIINNTCSIVEEAIKNYESIIFSGYTLMQENLNLSNHHLEKKPWLSNPKYLGILDVLEISLDIHCNGKEMPSDHMEEAYTIIVSEDVKRLKAFSVWGILRGLESFSQMIYMTNEGLSLRINKTSVEDRPRFSHRGLLIDTSRHFIPIKNILLTLDAMAYNKLNVFHWHIVDDQSFPYVSRKFPELSLKGAYTSYYTYSYKDIQNITEYARVRGIRVIPEFDTPGHTRSWGVAHPEILTACEGDLKGKYGPIDPTQNKTYTFLDDFFEEISNTFADAYIHLGGDEVEFECWSSSTIIKNFMKKNGINDFKALENFYLQKLINMVAKRNRKYIVWEEVFTNGVKLPNNAIVQVWKTYWHSVLLEVTNSNRTGILSSCWYLDHLNTGGDWIQFYNCEPLSFSSNPKNQL	AACGATAATACGAAACGATATAGCTACTTCTTTATTCTCCAGGAATGTTTTTACATAAATTACAAAAATATTATATTACCATGGAACCATCAAAAAACAAGCGTGAGTAGAAGAGGCTGTGAAATTGTCCCGTTTCTAGAGAAATGTACAATTATTAGTTCAAAAATAGAAGAAAATTACAAATTCTATTGTTTTTAAATTGTAGTGAGTTCACCGTTTTCAAGTAACCTCTTGAAATTTCGCACAAAATGAAATTTAAAATTCAATTGTTATCAACGTTTTTGTGCACCAGTTTAGTTTATGCATACATAGAGGAACCTGGTCCAAGATACCCACCAACCAAAGGAGAGCTTTGGCCAAAACCATACCATCAAATTAAAAACCATAGTTTCTTTACAGTCAGGAAGGAGCACTTCAACTTTAAAATAATCAATAACACGTGTTCAATAGTAGAAGAAGCAATTAAGAACTACGAATCCATCATTTTCTCAGGATATACTTTGATGCAAGAAAACTTAAACCTATCCAATCATCATTTAGAAAAGAAACCGTGGCTAAGTAATCCCAAATACCTGGGAATATTAGATGTTTTAGAAATTAGTCTCGATATACACTGCAACGGAAAAGAGATGCCTTCAGATCACATGGAAGAAGCATATACAATAATTGTTTCTGAAGATGTAAAGCGATTAAAGGCATTTTCTGTATGGGGCATTCTAAGAGGCTTAGAGTCATTTTCTCA

			domain (IPR015883) GO:0005975 carbohydrate metabolic process GO:0004553 hydrolase activity, hydrolyzing O-glycosyl compounds GO:0004563 beta-N-acetylhexosaminidase activity	LVVGGEACMWAEVVNQNNIMSRVWPRASATAEKLWSQRDDNYDLLKVRKRLEEHTCRMNRRGIEAQPPNGPGFCY* **(540)**	GATGATATATATGACCAATGAAGGACTATCGTTACGTATTAACAAAACTTCTGTGGAAGATCGGCCACGATTCTCTCATCGTGGACTGCTTATAGACACCTCAAGACATTTTATTCCTATAAAGAATATTCTACTTACACTAGACGCGATGGCTTACAATAAACTTAACGTTTTTCATTGGCATATTGTAGACGATCAGAGTTTTCCTTACGTCAGCAGGAAATTTCCTGAGTTAAGTTTAAAGGGTGCCTACACGTCGTACTATACATATTCGTATAAAGATATTCAAAATATAACGGAATATGCAAGAGTAAGAGGTATAAGAGTAATTCCAGAATTTGATACACCAGGACACACGAGATCTTGGGGTGTAGCTCATCCAGAAATACTAACCGCTTGCGAAGGAGACCTAAAAGGAAAATACGGACCTATTGATCCAACTCAAAATAAAACCTACACCTTTTTGGACGATTTTTTTGAAGAAATTAGTAACACATTTGCTGATGCATACATCCATCTTGGCGGTGATGAAGTTGAGTTTGAATGTTGGAGTAGCAGTACCATTATTAAAAACTTTATGAAGAAAAACGGAATCAACGATTTTAAAGCTTTAGAAAATTTTTATTTACAGAAACTTATTAATATGGTAGCTAAACGAAATCGTAAATATATAGTTTGGGAAGAGGTATTTACAAATGGCGTTAAACTACCCAACAATGCAATTGTTCAAGTTTGGAAAACTTATTGGCACTCAGTTCTATTAGAAGTAACAAACTCAAACAGAACAGGAATACTTTCATCTTGTTGGTACCTAGATCATCTCAATACCGGAGGTGATTGGATACAATTTTACAACTGCGAACCACTTTCCTTTAGTAGCAACCCCAAGAATCAATTACTAGTTGTTGGAGGTGAGGCTTGCATGTGGGCGGAGGTCGTAAATCAAAATAACATCATGTCACGAGTTTGGCCAAGAGCTTCAGCTACAGCTGAAAAGCTTTGGTCACAAAGAGATGATAATTACGACTTACTTAAAGTAAGAAAACGACTGGAAGAGCACACGTGCAGAATGAATAGGAGAGGCATAGAAGCACAACCACCAAATGGTCCAGGGTTTTGTTACTGATTTTA

					TTTTTTATAATAGTTAAAGTTATAATATTAATTTAATGACCTTTTATATTTCTATAAGCTTAATATTTATCTTAAAACATAGTGAATTGATTAAATTTTTCATAAATCTA **(1,983)**
MSTRG.7894.1	(1) Uncharacterized protein LOC111507202 [Leptinotarsa decemlineata](83%;27%)	Higher	(1) Transcription activator MBF2 family (IPR031734)	(1)43-441 MTEIYLFSKAIFFFKTKMFSTVFKMFLLVAVLILVTLSPSSADNYNKCPETSHERYLIYQNTLKGRVIHVRIPGTGFFHAPITCLQVTDINESFSTPVIEEGGYGKEYVVLRIDPVQSGEQLQYDVQIYVDQ* **(133)**	AAGTATATATACAACATACAACAACTGCCATAATATATTGTGATGACAGAAATATATTTGTTCTCTAAAGCAATTTTCTTCTTCAAAACCAAAATGTTTTCAACTGTTTTCAAAATGTTTTTGTTGGTTGCAGTATTAATATTGGTTACCCTTTCACCATCCAGTGCAGATAATTATAACAAATGTCCAGAAACCAGCCATGAACGATACCTAATTTACCAGAATACTTTAAAGGGGAGAGTTATCCATGTACGCATTCCAGGAACGGGTTTCTTTCACGCTCCAATCACTTGTCTTCAGGTAACCGACATAAATGAGAGTTTTAGTACACCAGTTATAGAAGAAGGTGGATATGGAAAGGAGTATGTAGTTTTACGAATTGACCCAGTTCAATCAGGAGAACAACTGCAGTACGATGTTCAGATTTATGTTGACCAATAATCAAGTTATCTTTAAATAAATTTTTTGGTCTGTA **(475)**
MSTRG.24813.1	(1) P450 6k1-like [Leptinotarsa decemlineata] (100%;38%)/P450 6k1-like [Anoplophora glabripennis](100%;40%)	Higher	(1) Cytochrome P450 superfamily (IPR036396)/ Cytochrome P450 family (IPR001128)/ Cytochrome P450, E-class, group I Family (IPR002401) GO:0055114 oxidation-reduction process GO:0005506 iron ion binding	(1)3-1328 MLLTSSPFLDGLIYLSILCIAAYCYATRDFNYWKRRNVQFLKPVPFFGNLYDVMMFKTTTQECIKKIWDGINAPYFGMFIFDEPVLVLKSPKLIKDVLIKDASTFCNRRVATPSHPNMAHGMFFLKYNEWRKVRKMLSPVFTSGMLRYLQPHIIEINQTMLDFVHKNCGIFDVTNIGEDFAIEFLVRCFYEANPRCFNEKPSVFKKCIHTMFAFNFRNGVVQNLFFLKPALADALKLNFVAKNCMKFFEDVFKRIMTARESYDGKPRSMVDVANKAIREKKRGEKDALGFETIMSNVLLFLIAGRDSTTTIISFTLYEIAKNQEIQDKLRKEVKLN	AGATGTTGCTCACCTCCTCCCCGTTTCTTGATGGCTTAATATATTTAAGCATTTTATGCATTGCTGCTTATTGTTACGCTACAAGGGACTTCAACTATTGGAAAAGAAGAAATGTTCAATTTTTAAAACCCGTCCCTTTCTTCGGCAATCTTTACGATGTAATGATGTTTAAAACTACTACCCAAGAATGTATAAAGAAGATATGGGATGGAATCAATGCTCCCTATTTCGGGATGTTCATTTTTGATGAACCAGTTTTAGTTCTAAAATCTCCCAAACTAATCAAAGACGTGTTGATTAAAGATGCTTCAACATTTTGCAACAGAAGAGTTGCTACACCTTCACATCCCAATATGGCTCATGGAATGTTTTTCTTAAAATATAATGAATGGAGAAAAGTAAGAAAAATGCTTAGTCCAGTGTTTACCTCGGGCATGTTAAGGTATTTGCAGCCACATATAATCGAAATAAATCAAACGATGTTAGACTTCGTACACAAGAATTGTGGTATTTTTGATGTTACAAACATTGGAGAAGAT

			GO:0016705 oxireductase activity, acting on paired donors with incorporation or reduction of molecular oxygen GO:0020037 heme binding	VEKHGSICFEGVQENKYLEMCINETLRKYPTLPFLDRTPIDDYQFKDTDLKVEKNTSILIPLFALNRDEHIYPNATLYNPDRFLSDQINSDGLNFIPFGEGPRICI **(443)**	TTCGCAATAGAGTTCCTAGTTAGATGTTTTTATGAAGCCAATCCTCGTTGTTTTAATGAAAAACCATCAGTATTCAAGAAATGTATACATACGATGTTTGCTTTTAACTTTAGGAATGGAGTTGTCCAGAATTTATTCTTTCTGAAACCAGCATTGGCAGATGCTTTAAAATTAAACTTTGTGGCAAAAAATTGCATGAAATTTTTTGAAGATGTTTTCAAACGCATAATGACAGCTAGAGAAAGTTATGATGGTAAGCCGAGAAGCATGGTAGATGTAGCAAACAAAGCTATTAGAGAAAAGAAAAGAGGAGAAAAGGATGCTTTAGGATTTGAAACGATTATGTCCAATGTCCTGTTATTCTTAATAGCTGGACGCGACTCCACTACTACAATAATAAGCTTCACTTTATACGAAATTGCTAAAAATCAAGAAATTCAAGACAAATTAAGAAAAGAAGTCAAATTAAATGTTGAAAAACATGGATCGATTTGTTTCGAGGGGGTCCAGGAGAACAAATACTTAGAAATGTGCATTAATGAAACTTTACGAAAATACCCAACTTTACCATTTTTGGATCGAACACCTATCGATGATTACCAGTTTAAGGACACAGACTTGAAAGTGGAAAAAAACACATCAATACTAATTCCATTGTTTGCCCTTAACAGAGATGAGCACATTTATCCTAATGCTACATTATATAATCCTGATAGGTTTCTAAGTGATCAGATTAACTCAGATGGTTTGAATTTTATACCATTTGGAGAAGGCCCAAGAATTTGTATTGG **(1,330)**
MSTRG.50645.3	(1) No hit (2) ABC transporter G family member 20 [Anoplophora glabripennis] (88%;88%)/ABC transporter G family member 20 [Leptinotarsa decemlineata](84%;85%)	Higher	(1) No hit (2) No hit	(1)608-291 QHFYQYSPNILFSYSMFCCILLFQLLFPCPQSCLNHSTRGWVSSSSHSACTRALHSLHSVFGSILWTVDVLEAAFPHLHPPNRAQELVAPPDHPLSYPQLLTLFL* **(106)** (2)302-565 MLITEGTTMGDRVEPQVPGPDLVGVNVERPPLVHQQSTVWNRRQNAVSVRHA	AATAAACTCGGGTAGCACCAAATATTGCAACTCCTCACCAGCCAGTCCGTTTTTAAGCTCCTTGAGTGACCACTTGCTGAGTCAAAATAAGTGTGTTGTGCGCGCGGCGAATGAAAGTTGGCCTATTAATTGTTTCGCGTGTCGTACGATATCAAGGTATAGTTTGGCGATATTATGCAAATTTCTTGTAAAAATTAATCATTACAAGTAACTATGATGTGTGATAGTAAGTAAAAAAGTGAAAGTTGTGGGAACTTTACGTGAAGTAACGGCAACACTTGATAATCCTTTTACAAAAACAATGTTAATAACTGAGGGTACGACAATGGGTGATCGGG

				YKHYGSKKKPNHVLSDLNMTVGKGTIIEIIKYNKT* **(88)**	TGGAGCCACAAGTTCCTGGGCCCGATTTGGTGGGTGTAAATGTGGAAAGGCCGCCTCTAGTACATCAACAGTCCACAGTATGGAACCGAAGACAGAATGCAGTGAGTGTAAGGCACGCGTACAAGCACTATGGCTCGAAGAAGAAACCCAACCACGTGTTGAGTGATTTAAACATGACTGTGGGCAAGGGAACAATAATTGAAATAATAAAATACAACAAAACATAGAGTAAGAAAACAATATGTTGGGTGAATATTGATAGAAATGTTG **(608)**
MSTRG.89601.1	(1) RNA-directed DNA polymerase reverse transcriptase domain [Lasius niger] (69%;56%)	Lower	(1) No hit	(1)2-301 KYVVMDMLKHVKVRKQANKANYASGCLRDVIRRNKDMRLEGKVRIYKSCVRPMTYAIETRCDTAESKRTLRTSEMRTFKVNNCENTERQNTERQNKRSL* **(100)**	GAAATATGTAGTTATGGATATGCTAAAGCATGTTAAAGTCCGAAAGCAAGCAAATAAAGCCAATTACGCGTCAGGATGTCTGAGGGATGTCATCCGGAGAAATAAAGATATGAGGCTGGAAGGGAAAGTACGCATATACAAATCATGTGTGAGACCGATGACTTACGCGATAGAAACAAGATGTGACACAGCAGAAAGCAAGAGGACACTGAGAACATCAGAAATGAGAACTTTTAAGGTCAATAACTGTGAAAACACTGAAAGACAGAATACCGAACGACAGAATAAGAGATCTCTGTAACATACTACAAGATATAGTACGGCGGGGAAGACAGAGAAGACGAGAGTGGAATCAGCATGTGACGACAACGGACAGCGAGAGAATAGCCCGTATATCTAGAGATTTAAAAGGTAACAGACAAGAGACCAATAAAAAGGCCCTTTAAAAGGTGGCGAGATAGCTGGCAGTCAACATCACAGCTACGAATGCAAGCTTAAAATCGGTTAAGAACAGGTCAAGAGGCTATTATAAGAAGAAGAAGAATTTACAGCTCCACAATATGTATTTATATTATGCTAAGTTCAAATTGTGGTCGCCAAGAATGTCAGGTGACGACGCTAGGTGTGGCGTCAGTCATGCACGGGGCGAATATCTAGGAATATCCTAGATTCTAGGTGTTAAAGGGTAGTAAACAGTAAAAAAATAGTAAACTTTTTATTTTTATAAAAATTCTCTATTTCAACAATAGATAACAAAATATCATAATTATTCGAATGCAGAGAAAATGGTAAAATTTCCCTGAGATGCATTCAAAATATCACAATTTTACAGTTTTTTTAA

					TAATAAAATTTACGAAAATAAATACAAAA ACGTTCGAGAGCAGTCAAAATAGTGAAA AATAAATGCAACTCTTCGATAGGTATCC AGTTTGAAGACAATAGTGACTTATATCTA AACATTACTCTACCACAAGATGCGCCAG AATGAACAAGTTACATGGCTGACTGACC GACAAATTCTCGTTAAAAAGACTGCCAA CAAATTACATCGAGTATTACATTACGTCA ACAGTATCTTTGCAGATACAGCGCCGGC AAAAAATCTTTGGAAAAGACTGTAAGAC TTGTACACACTTCTAAGTAGGTCAAAAC GGCAAACAAGTGCATGTTCTCAAAAAAA TTGATAGTGTATAAAAAAGTTTTATTATC AGCTAAGTACTTTTTGTTTTTAAAAGAAT TGTGATAACTTATATACACGTTAACATTT TACTTCAACATTAATAATAGTAATTTTTTT TAAATTTAACTTTAAAATTTAGTATCTTAA CTTAAAATTCGTTTAACCTATACATGGCG TTTTAGTCATTTTCAATTTTGATTAATTTT TAATTATTATTTACGAATATAGAGGTCGT ATAAGATTATGGTTCCTTCTTTATCATTT TAATGAATGAAAGTCCTCCTCAGCTGTT CACGTGGGCTCAAAATGGTTTGACTCAG CCATGTTGTCGTTTTAAAATAAAAAAGAA ATTAGATGTGAATTTATTCATTTTAAGGG GTTGTTATACCCGATATCTGTGGCTTTTA CCCAGAATCTATGTTTTTTATTGTGTCGT TTAGCAATTGCTCTCTATGAAGGTTTTAT AAGAGGACATAAGTTTTTCAATCTTTCTT TTTATAAAAAATCTTATCTTAAATGTCCTT TTAGGAAGCTCTGATGGTGGCACGTTAT GTGTTAAAAGTACTTAGCTGATAATAAAA CTTTTTTACACACTATCGATTTTTTTAGA ACATACACTTGTTTGCCGTTTTGATCCAA AAAAAATCTTTACATTTCAAAATAAATCA CTAATTTAGAAGAAAAATTGCATGCGTTC TGTCTGAGCCTGTTTAGCGTTTGAGGGG AGAGATGATGACGTACTTGTTTCGGCAG GTTCCTGTAGTTTGCTGACTGCTTATTTT CTTTAGTTTATTCTGTGCATTTGTACTGT

					ACATACAGTTAGCTTTATACAAGTAGTCAATGTGAAACTTCTTGAAAAATTGAAGTAAAAACCATGGGGCGAAAGAAACTCAGAAATGAAGAGAAAGTTCGTGCTTCAACGTTACTTGTTGAGAAAGGGGGCTCTGTAATTACCATATCACGTGATATTGGTGTTTCAAGAGATTAAATTCATCAATTGAAACGGTCGAATGCGTCGTAGCCTCTAGGACTGTTCCGGAAAGAAAACCTGGTTCTGGAGCCCCTAAAAAACATCATCTAAGACTGACACCATCATCAGGCATGTAGTTATGTTGAACCCTTCCATAACTGCCACAGAACCCAAAATTAAATATGGTCATAAAGTACTATTTTTTTAAAATCAAAATAATAATTATTATCCTGATTTTTATGCGTTTCATTCACTTTGTAAAGATTATTTTTCTGTCGACACTGTAAAATTTTTACAGTACTGAACCAAGGGGTGGTCATTGAACATTATGGTTTAAATAATAAAAAAATGAATGTAAGTAGATAAGTTACTTTTCTACATATCACGCCTATCTTCTTTCAATTTTAATGAAATAGTTGTATAAATATGATGACGACACAGTGCAGTTACATTCAAATTTAATTAAAAAGCTAGTTAAACCAGGGCGCATCTCTAAAAATATTAGTACATTTGGGGGTTGAGAGGTGACTCATATTTTTTTGCAGAAATTACTTAAAAATAACTCAAATAATAATGTTTGAGTTATCCTTCCTCTCAAAAAGGTCCAGAACATTGTTTAAATAATCAAAATGTCAAAAAATTAACGACAAACTCCATTTTTTCTTCGTTTTTCGATTATAACTTTAAAAGTATTCATTTCCGAGAAAAGGTGTATGGACATAAAAGTTGCGTAATTAAATTTTTACAATAGAGGATTAGTTAAATATTTTAAAAATTGTCACCCTTTTTGCAAAATAGCAATAATTGCGAAAAAAAAAACAAGTAGTCCCATTTTACGTTTTTCATCGACTTATGCTACACTTAAGACCTTCATATTTTAGCCAGAAAAACTTATATAGTCAAACAACACTGTGAATTTCATTAAGATCGATTCAATAGATTTTGCAAAATAAATTTTGCAATCCAGCTTTCGCAGAAAAAATTAT

					TTTTTCAAAATGTTGCAGGACTGAAAATAAAGCAGAAAGCAAGTTGAATTTCTTTTTTACATATAGAAAAATACTGCACCTTTCATTTGCAATTTGAAAAATTAAAATCGGTTAACCACCACGGCGTCAGAAATTTTTTTAAATAAACATTAATTTATAATCAACTATTTTCAATGGGAAATAAGCCACAATTTTATCAAAAAATTATCTTATTAACGTTTTTACTGATTTTCTCTCGTGATTTACTATGGAATCTCTAGCGCGAGAATTTTATTGCCACCGTTGCATTTGGTTGTCTTTTTAAAGACAGATCACATGCTATGATTTTTTGTGGCGGATATTCTTGAATTGAGGTTGATTTCATGTAATC **(3,506)**
MSTRG.1766.1	(1) Myrosinase 1-like [Leptinotarsa decemlineata](96%;75%)/glycosyl hydrolase [Chrysomela lapponica] (99%;66%)	Lower	(1) Glycoside hydrolase superfamily (IPR017853)/Glycoside hydrolase family 1 (IPR001360)/Glycoside hydrolase family 1 active site (IPR018120) GO:0005975 carbohydrate metabolic process GO:0004553 hydrolase activity hydrolyzing O-glycosyl compounds	(1)51-1544 MKVFIFALLLGVCLAQNADTNPRRFPASFKLGVANAAAQIEGAWEEDGKGEHIWDRWSKVRPEMISDRSTPAVAADSYHKYKEDVRLIKEMGLDVYRLSISWARIYPTGYPTAEPNAAGVQYYKNLLAECKQNGIQVMATLYHWDLPQQLQDDFGGWLNETVVDLFAAFADVSFKLFGDDVTWWITINEPKQVCHAGYGDGYFAPGVVSSGVGEYTCARNVLLAHAKAYHNYNDNYKASQGGKVSMVIDTLWFEPGSDSDADKDAAERLLQFGFGLYGNPIFNGDWPKLVKDRVAMRSEKEGFKQSRLPAWTQEEIDYIKGTGDFVALNHYATHMANGTNEAPIGNPSFGSDISAMEWARPEWPKGDGDWFSIVPWGLRKLLVWLKDTYNDQEIIITENGLSDNTGVLEDDHRVDYFRDYISNCLDAIYEDNVNLSTYIAWSIIDDWEWGGGYKSFLGMYKVDFNDPERPR	TTTCTATATAAACTTGCAAAACTAGTAAAATATTGAGTGAGTTCATCGCAATGAAGGTGTTTATATTTGCCTTGCTATTGGGCGTTTGCCTTGCTCAAAACGCCGACACCAACCCAAGACGTTTTCCCGCCAGTTTCAAACTTGGTGTAGCCAATGCTGCGGCTCAAATAGAAGGAGCCTGGGAAGAAGACGGCAAAGGAGAACACATTTGGGATCGTTGGTCTAAGGTTCGTCCAGAGATGATTTCCGATAGGTCTACGCCTGCTGTAGCCGCTGATTCATACCACAAGTACAAAGAAGATGTACGTTTAATCAAGGAGATGGGTCTTGACGTTTACCGTTTATCCATCTCGTGGGCTAGAATCTACCCAACAGGATACCCAACTGCTGAACCCAATGCAGCTGGTGTACAATACTACAAAAACTTATTGGCCGAATGCAAACAGAACGGAATCCAAGTAATGGCTACCCTTTACCACTGGGACTTGCCCCAACAGCTCCAAGACGACTTCGGAGGTTGGCTCAACGAAACCGTCGTCGATCTATTCGCCGCCTTCGCCGACGTTTCCTTCAAACTCTTCGGTGACGATGTCACGTGGTGGATCACCATCAACGAGCCCAAACAAGTGTGCCATGCAGGTTACGGAGATGGTTACTTCGCGCCAGGTGTTGTTTCCAGTGGCGTTGGAGAGTATACCTGTGCCAGAAACGTGCTTTTGGCTCACGCAAAGGCTTATCATAATTATAATGATAAC

				IKRKSADYFTQIVKNRCLVDADKCVD* **(498)**	TACAAAGCATCACAAGGAGGAAAAGTCTCTATGGTAATCGATACACTTTGGTTTGAACCCGGCAGTGATAGTGATGCAGATAAAGATGCAGCTGAAAGATTGCTACAATTTGGTTTCGGTCTATACGGTAACCCCATCTTCAACGGAGATTGGCCCAAACTCGTCAAAGACCGTGTAGCCATGCGCAGTGAGAAGGAAGGATTCAAACAGTCGCGTCTTCCAGCTTGGACCCAAGAAGAAATCGATTACATCAAGGGCACCGGAGACTTCGTTGCTCTGAACCACTACGCAACTCATATGGCTAACGGAACCAATGAGGCACCCATTGGAAATCCCAGCTTTGGATCTGATATCAGTGCTATGGAATGGGCTAGACCAGAATGGCCAAAAGGCGATGGAGACTGGTTCTCGATTGTTCCATGGGGATTAAGGAAACTTCTTGTTTGGTTAAAGGATACCTACAATGACCAGGAGATTATCATTACTGAAAATGGTTTATCTGATAACACTGGAGTTTTGGAAGACGACCATAGGGTTGACTATTTTAGAGATTACATCAGTAATTGCCTGGATGCTATCTATGAAGATAATGTCAATCTTAGTACTTACATTGCCTGGAGTATCATTGACGATTGGGAATGGGGAGGTGGATATAAATCATTCTTGGGAATGTACAAAGTTGATTTCAATGATCCTGAAAGGCCCAGAATCAAGAGAAAATCCGCCGACTACTTCACACAAATCGTAAAGAACCGTTGTTTGGTTGATGCAGACAAATGTGTGGACTAAATATATTTTCTGTGAAAATTGTGACCTTTATTTTATAAATAAACCTTAAACATTATG **(1,601)**
MSTRG.12896.1	(1) No hit	Higher	(1) No hit	(1)227-403 MKFKHGSTFILIFALIILTGAQDDNEQRFKRSPKPDWEVNPGANGDGNGNTNAGVEIRN **(60)**	ACAAAAATATAACACGCTACTAAAAATAAGTGATTAAAAATTATTGTTTAATAATAAAGTAAAGTCCCGTGTTGACATGTTTCTATGGGTAAATGGTAAAGTACTAACATCTTGGTACTCTCTCAATATTTTTGGGATATAAAATGAATACTATGATATGGAATCAACAGTTCGAAATCTGTATTAGACAAGAAAGTACTCCGTTGGAAAATAGAAAAGATTAACGATGAAGTTCAAACATGGATCAACTTTTATTC

					TAATATTCGCATTAATAATCTTAACAGGCGCCCAAGATGATAATGAACAAAGATTTAAAAGATCGCCCAAACCAGATTGGGAAGTGAATCCAGGAGCTAACGGTGATGGAAATGGTAACACTAATGCTGGAGTAGAAATAAGAAATAA **(405)**
MSTRG.22086.2	(1) Heat shock protein beta-1 [Anoplophora glabripennis] (98%;83%)/Heat shock protein beta-1 [Leptinotarsa decemlineata](98%;82%)	Lower	(1) HSP20-like chaperone superfamily (IPR008978)/Small heat shock protein HSP20 family (IPR031107)/Alpha crystallin/Heat shock protein family (IPR001436)/Alpha crystallin/Hsp20 domain (IPR002068)	(1)236-859 MSNRNIPIKMGDFSVIDTEFSSIRERFDAEMRKMEEEMNKFRSELTSREANNFFRSTTSMSYESETVTGGNKSSSTSSSTTQQSSTGSDLAHRAPSGDVRTWYDDLNSPLIQQDGNEKSLKLRFDVSQYAPEEIVVKTVDNKLLVHAKHEEKTESKSVYREYNREFLLPKGTNPEHIKSSLSKDGVLTVEAPLPAITSGEKLIPIQH* **(208)**	CAAGATTCGGTATCCGTGGATCTCGAATCTCGAATCGCAGAGGTGTAGAAGAGTTGCGCAAGACTCGTCTGTACCCCCTCACGAATTCTATTTAAAACCGTCCCATCCCCGGTTCTGCGCGCTAGTAACATTCGGTGACAGACAAGAGGCAGCTATTATTAACGACACACCGCTCTCTCGTTAGTGTTCATATTTTACGTGTAGTGTAACAGAAAGTGCAGTTTTTTTATTCACCATGTCTAACCGCAACATCCCTATCAAAATGGGTGACTTCAGTGTTATCGACACGGAGTTTAGCAGCATCAGGGAAAGGTTCGACGCCGAAATGAGGAAAATGGAAGAAGAAATGAACAAATTCAGATCTGAACTTACCAGTAGGGAGGCGAACAACTTCTTCAGAAGCACAACCAGCATGTCGTACGAATCTGAAACGGTGACTGGTGGAAATAAGTCTTCATCGACGTCCAGTTCAACGACACAGCAAAGCAGCACAGGATCAGATTTAGCCCACAGAGCACCAAGTGGTGATGTCAGAACATGGTACGACGACCTCAACTCTCCCCTAATCCAACAGGACGGTAACGAAAAGAGCCTAAAATTAAGATTCGACGTTAGTCAGTATGCTCCAGAAGAAATTGTAGTCAAAACTGTTGATAATAAACTCTTGGTTCACGCCAAGCACGAAGAGAAAACAGAATCAAAATCCGTATACAGAGAATACAATAGGGAATTCTTGCTGCCTAAAGGAACAAATCCCGAACACATCAAGAGCTCATTAAGTAAAGATGGCGTCCTCACTGTCGAAGCACCTCTCCCAGCTATCACCTCAGGGGAAAAATTAATTCCAATCCAACATTAAGTAATTTAAAATTCCTTGTAAGCCTTCGAAGCGTTTATGTCCGCTAGTAAATACTCATCGATTAATTATTTAAAATGTAACAACTCATG

					TGACTAACAAAATTTTTATTTTATTTCATTTTTAAAACCTGGCAACGTTGTCTGGCTTGTTTAGGATAAGTCACAAATTTAGTGTTGGCTCTAAAGTACTTACTGTCTACACAGCACAAGTCACAAATCGTTAAATACACCATAAACCTCATGCATCGTTGCCGGATGGTTCAAAAGCTCATACTATTTGTGACTATCTTCTTGATGGCGGCCGTAAACTTGAAGGTTGATTAACATCCTTTCACAAAGCTTAATTATGCAATGAAAATAATTTTTAACAACTTTATTTGTGACAAAAAAATTGAAGCTAATGTAAAATTGTTTGGTTAAATTCTTGTGAAGGTCTATGGTTCGATGTTCAATAACCAGCAATTTCACCGTAGGCGTAGTGTAACAAATTGTATCATGTGTAGGATATTTACGAATAAATTATTTTTAATCTCGTATGTTTGGACTCTTATTTCTTTTATATAACTCTTGTTGTTTTATTGAAATCAAGTACAAAATTATTGTGGCATATGCTATTGTGTAATATTTGTTTAATAAAAGATGACATATACTTGGCA **(1,514)**
MSTRG.29667.1	(1) Uridine phosphorylase 1 [Anoplophora glabripennis](92%;93%)	Higher	(1) Nucleoside phosphorylase superfamily (IPR035994) GO:0009116 nucleoside metabolic process GO:0003824 catalytic activity	(1)337-723 MSISEEERDEYPDGSVRLRNPHIELMDQDILYHLALGSESHDLIEMFGDIKFVCMGGTPKRMENFAEYIMKEIGHKLPTGTQLMDISQYSYRYSMYKVGPVLSISHGMGAPSIGILLHEVIKLMYHAKC **(130)**	AAAGCATTTAACGACAACAATGAAATCTTATCTGTTTTGCAATATGTACTGTAATCAAAAATGATTCACCTAATCCACAGGAGTGGCGCATATCCTCTCTATTATTATTGGAGTAAAAAACCCGACAGTTCCAAAATACCCATCCCTATTTCCCCATCTCTAGCCGTTCAGTGTGGTCGATCGTAGTGGAAGGAGACGCACCCTTCTAGTTTATCTTTAGTTAAATAAAAAAATGTCTATTAGATTTTGTTAAAAATACCCTTCTAAACGGACTTTGTTAGTTCCCTTTCTAGTGACCATCCTTGTAAGTGTTTGTTTTTCAGGATTTCTCTCAAGATGTCGATATCAGAGGAGGAAAGAGACGAATACCCAGATGGATCCGTACGATTACGAAACCCCCACATCGAACTTATGGACCAAGACATTTTGTATCATCTAGCTCTGGGAAGCGAGTCTCACGATCTTATTGAAATGTTCGGTGATATCAAATTCGTGTGTATGGGAGGAACACCAAAGAGAATGGAAAATTTTGCCGAATATATCATGAAAGAGATTGGCCATAAATTA

					CCAACTGGAACTCAGTTAATGGATATAAGTCAGTATTCTTATCGCTACAGTATGTACAAAGTGGGGCCTGTATTATCTATTAGTCACGGCATGGGTGCCCCATCCATCGGTATCCTTCTTCACGAAGTGATAAAACTAATGTACCACGCGAAATGTA **(724)**
MSTRG.87888.1	(1) Laminin subunit gamma-1-like [Leptinotarsa decemlineata](100%;74%)/ Laminin subunit gamma-1 [Anoplophora glabripennis](100%;69%]	Higher	(1) Laminin EGF domain (IPR002049)/Laminin IV domain (IPR000034)	(1) 3-584 RCEENFFDFSSSGCKTCGCHPAGSFNNQPTCDPYNGMCQCKENVEGKQCNECKPGFFNLDEENAFGCTPCFCYGHSGQCSSASQFSKFVVTSSFFKGTERWNAEDEYQRQIEVKYEPISQSIGVHTVGDEAVYFIAPNRFLGDQRASYNQLLEFTLRIGDNRAVPTATDIILEGSGASVTNTIFAQKNAIPSMQ **(195)**	ATAGATGTGAAGAAAATTTCTTTGATTTTTCATCATCCGGATGTAAAACTTGCGGATGTCATCCTGCTGGATCGTTTAATAATCAACCCACATGTGACCCCTACAATGGAATGTGTCAATGTAAAGAAAACGTAGAAGGTAAACAGTGCAATGAATGTAAACCTGGATTTTTCAACTTGGATGAAGAGAATGCTTTCGGATGTACACCCTGCTTCTGTTACGGTCACTCAGGCCAATGTAGTTCAGCTTCACAATTTTCAAAATTTGTGGTGACCTCATCTTTTTTCAAAGGAACTGAAAGATGGAATGCTGAAGATGAATATCAAAGACAAATAGAAGTTAAATATGAACCTATCAGTCAAAGTATCGGCGTGCACACTGTGGGAGATGAAGCTGTGTATTTCATAGCACCTAACAGATTTTTAGGTGATCAAAGAGCATCATATAATCAACTTTTAGAATTTACTTTGCGAATTGGAGATAACAGAGCGGTACCAACAGCCACGGATATTATATTGGAAGGATCGGGAGCTTCTGTTACGAACACTATTTTTGCCCAAAAGAATGCCATACCGAGTATGCAG **(584)**
MSTRG.25345.1	(1) ATP-binding cassette sub-family G member 1-like [Anoplophora glabripennis] (99%;68%)/ PREDICTED:ABC transporter G family member 2-like [Nicrophorus vespilloides] (99%;64%)	Higher	(1) P-loop containing nucleoside triphosphate hydrolase superfamily (IPR027417)/ABC transporter-like (IPR003439)/AAA+ ATPase domain	(1)3-1799 SRVILDSINGDFSGGELTAIMGPSGAGKTMLLNILAGYTSKGVLGEKLINDKPRNELAFQRKSCYIMQDDDLQPLLTVSESMTIAASLKMSSKYTWKEKKNRIKEILESMGLYKHGKTRIGALSGGEKKRLSIALELLKNPDVMFFDEPTSGLDSVSSKQCVLLLKQMAISGKTVICTIHQPAAPIFEIFDHLYVIADSKCLYQGSVKGLLPYLEEVDLRCPTYH	GATCTCGGGTAATTTTAGACAGCATAAATGGTGACTTTTCTGGAGGAGAACTAACAGCTATAATGGGACCATCTGGTGCAGGGAAAACTATGCTTTTAAATATTCTGGCCGGATACACATCCAAGGGCGTTTTAGGTGAAAAACTAATAAATGATAAACCAAGAAATGAACTAGCATTCCAAAGAAAATCTTGTTATATAATGCAAGATGATGATCTCCAACCTCTACTTACAGTATCTGAGTCAATGACAATAGCAGCCAGTCTTAAGATGTCTTCTAAATATACATGGAAAGAAAAAAAGAATAGGATTAAAGAAATTTTGGAATCTATGGGACTCTACAAACATGGAAAAACTCGTATAGGGGC

			(IPR003593)/ABC-2 type transporter domain (IPR013525)/ABC transporter conserved site (IPR017871) GO:0005524 ATP binding GO:0016887 ATPase activity GO:0016020 membrane	NPADFLLEVASGEYGDYATILSEKSENGLNMEYRKQQRNSLQLESLEHIGRMMTSGKITPVHAPPIYFSKSPICCDKDIDISYLHSYKGSYPASFFTQLNVLIRRTFLVITRNKTLTVSRFLTHIVIGLFIGVLYFGIGIDASNMLNNFNYIFFSQMFLMMTAFNSVLTTFPSELPILTREHFNKWYSLKSYYLAISIADIPIQMAASTCYALLTYFMTQQPIEGFRVGQFLFICLLIAAVSQSFGLLISATMSINNGVIFGPFCFLPFTIFSGFFVQLTAAHPALQWIFHISFLKYGFEGLVLSIFGYERGKLPCETDYCHHVYPKHFLKDMDMENSTYSLAVIFLVSLFVALRIAAFIALHFKVKGHRQSR* **(599)**	CTTGTCAGGAGGAGAGAAAAAGAGACTTTCTATAGCCTTAGAATTATTAAAAAATCCAGATGTAATGTTTTTCGACGAACCAACAAGTGGTTTAGATAGCGTCTCTTCAAAACAATGTGTATTATTGTTGAAACAAATGGCAATATCGGGAAAGACCGTAATTTGTACAATTCACCAACCTGCTGCACCAATTTTTGAAATTTTTGATCACCTTTATGTAATAGCCGACAGTAAATGTTTATACCAAGGAAGTGTTAAAGGTTTATTGCCATATTTGGAAGAAGTAGATTTAAGATGTCCTACTTATCATAATCCTGCCGACTTTTTACTAGAAGTAGCAAGTGGAGAGTATGGTGATTATGCAACAATCTTATCAGAAAAATCGGAAAATGGGTTAAATATGGAATATAGAAAACAACAAAGAAATTCCCTACAATTGGAATCATTAGAACACATAGGAAGAATGATGACATCTGGAAAGATCACACCCGTACATGCTCCACCTATATACTTTTCAAAATCTCCAATATGCTGTGATAAAGACATAGATATTTCATATCTACATTCATATAAAGGTTCATATCCTGCCTCATTTTTTACTCAACTTAATGTCCTCATACGAAGAACCTTTTTAGTTATCACAAGGAACAAAACGCTTACAGTTTCTAGGTTTCTCACACATATAGTTATAGGATTATTTATAGGAGTTTTATATTTTGGAATAGGAATAGATGCATCAAATATGTTAAATAATTTTAATTACATCTTCTTCTCTCAGATGTTTCTTATGATGACTGCCTTCAACTCAGTTTTAACAACTTTTCCGTCCGAGCTGCCAATTTTAACCAGGGAGCATTTTAATAAATGGTATTCACTTAAGTCATATTATTTGGCCATATCAATTGCAGACATTCCAATTCAGATGGCTGCATCTACCTGCTACGCACTACTTACTTATTTCATGACTCAACAACCCATAGAAGGTTTTAGAGTAGGACAATTTTTGTTCATATGCCTGCTCATAGCAGCTGTATCACAAAGTTTTGGACTCCTAATAAGCGCTACTATGAGTATAAATAATGGAGTAATTTTTGGTCCTTTTTGTTTCCTACCATTTACGATATTTTCTGGTTTCTTCGTTCAA

					TTAACAGCGGCCCACCCAGCGCTCCAATGGATCTTTCACATATCATTTCTAAAATACGGTTTTGAGGGACTAGTTCTGTCAATTTTTGGATACGAAAGAGGAAAACTTCCATGTGAAACAGATTATTGTCATCATGTGTATCCAAAGCATTTCTTAAAAGACATGGATATGGAAAACTCAACATATTCATTGGCTGTGATATTTTTAGTTAGTTTGTTTGTTGCTTTAAGGATAGCTGCATTTATTGCACTGCATTTCAAGGTGAAAGGTCACCGACAAAGCCGGTAGTACATAGTTTATTGTGATTTTATTGGTTTTAACGGTACATATGAGGGTCATTTGTAACAAAAGGTTCCCTGTGCCACTGAGAAAGAATACGACGTGATAAGAGAAATCTGGCAACATTGCATTACGCATCAACTCTCTCTCTCTCTCGCTCTCACCCATCACTATCATCTCGCTACCCTTCTCAGTGTGGGCTTAGCAGCCTTCGAAGATGGAGTTCACGATCGCTGTTACCACCAGATACAAAATTGGTACTGCGATACGTTTTTAAATGCAAACGGATTTCACCTATTGACATTACTTATCAGTTAATCGAAGTTTAGGGGTAAAAGTGCATATCTGTTCAGCATTTTCGCAAATGGTGTAGAGAATTCAGTGAAGGCCGAACGGAAATGGACGATGAAGATCTGAGCGGAAGGCATTCAGATTCAGACGAATATTGATTGAAGATTAGAGGTTCACCATTAACGACCTTACTTACGTATTTCTGAGACTTTCCACACCAGAATTCATAAAAAATTAGGCTATCACAGAGTGTGTCTGCGATAAGTACCGCGACTGCTTACAGAAAATCACAAACAGCAACGGGTCGAGTGTGCCCAGCAATTTTTGCAAAAAGATGACAAGGAAGAATTTTTGGATTCCATTATCACACGGTAAGAAACATATGTGTTTCACTTCATCTCCAAAACTAAGCAGCAATCACGTGAAAGGCATTACTCAACTTCTCCGAAGTCGAAGAAGTGTAAACAAACTCAATCGCTGGGAATGTCATGACGACCATCTTTTGAGACAGGAAGAGCCTACTGTTAATCGACTTTTTGACTTATGGACCAAGA

					GTAGTTAACTCCAATAGATATTGGGAGACATTAAAAAGATAAGACGTGCGCTCCAGAACAGCCCACTAAGACTATTGCCCAGTGTTGTGAGACTTCTCCATGACAACGCTCGACCTCATGTACTCATGTCTCACATCAAACTGAAGAACTGCACTGCTGAGCGATTTTGGCTGGATTGTTGTGCAAACGACCCCCCTACCGTCCGTATCAAGCACCAAGTGATAATCACTTATTTCCAAAATCAAAGGAACACTTGGGTAGCTTACGCTTCAGTCCCGATGATGAAGTCAAGGAAGAAGTTACTCGATTCCTCAAAGGATTGCCGGTTGAATTCTATAACATGGGGATAGAAATGTTGGAGCATCATCTGCAAAAGTCTTTGGAAAAAAACAGCGATTATGTAGAAAAATAACGCAAGTTTTAAATTTTAAAATGATGTGCAATACTAAGCACAAAAATAAAGCTGTCTATTCTAGAAATTTATGGGAATCTTATTTTACAAATGACCCTTGTAAAATGATTGTTGTATAGAAATGACAATCGTATTTGTCGATATAATGTCGATTTGGTAAAAACATTTGATATTTGTACTAATAGGTGGGTTTTATAATTTTATTAAAAAATACATTGACTATTTTTGTAAATTTTTTTGGTAATTTTGAACTATGTATTTACAATTTTTTTTTTAAATTTGTGAACAGTGCAAAAGTGTATAAAGCATTAATAACCAAATAAATACACTGAGTGGCACAAAAAATGACCACCCCACAAAATGGGTAA **(3,417)**
MSTRG.31399.1	(1) Uncharacterized protein LOC111507003 [Leptinotarsa decemlineata](98%;76%)/PREDICTED:elongation factor Tu [Tribolium castaneum] (90%;74%)	Lower	(1) P-loop containing nucleoside triphosphate hydrolase superfamily (IPR027417)/Translation protein beta-barrel domain superfamily	(1)164-1534 MLTYSICRTFTKEIVKSKYPLKISVLDCVKHFSQFSQNKGNHSLPLPKLILNYCTDIKKNINVGTIGHVDHGKTTLTAAITKVLQKDGLAKYVSYDEIDRAPEEKARGITINAAHIGYSTKKRSYAHTDCPGHADFIKNMISGVSQMDGAILVVAATDGQMPQTREHLLLAKQVGVTKVIVFVNKADLVDQEILDLVELEIRELLEDF	CTGAAACAACATAAATTGTTCGAAAAAAATTGGGCGATGAATAGCCCTATTGACAATGATCTCAGCTTAGAACAGTTAAAAAAAACTGACTGAGAAGAAGTAACTAAAAATGTGGTTAATTTTTGTGAGGTTTTGTATTTAATTTTTAAAATTAAGTAGAAAAATGCTTACATACTCAATTTGCCGTACGTTTACTAAAGAAATAGTTAAAAGTAAATACCCTTTAAAAATATCTGTATTGGACTGTGTTAAACATTTCTCTCAGTTTAGTCAAAATAAAGGCAATCATTCTTTGCCATTGCCGAAATTGATTTTAAATTACTGCACAGATATTAAAAAGAACA

			(IPR009000)/TRanslation elongation factor EF1A/initiation factor IF2gamma C-terminal superfamily (IPR009001)/Small GTP-binding protein domain (IPR005225)/Transcription factor, GTP-binding domain (IPR000795)/Translation elongation factor EFTu-like domain 2 (IPR004161)/Elongation factor Tu domain 2 (IPR033720)/Translation elongation factor EFtu/EF1A C-terminal domain (IPR004160)/Tr-type G domain conserved site (IPR031157) GO:0003924 GTPase activity	GFDGTNTPFIFGSALEAMNDKETKFGIPAIKELIACLDSYIPDPQRDVTSPFMLPIDNAFTVPGRGTVVVGTIFRGVMKKLQEAELLGFDNQFKTTVTDIQVFKKSVAEAKAGDNVGTLLRGIKLKDISKGMLLCAPNSVKISNRFKASIYFLSSREGGRTKPITGKYCQQLFSRTWNVACRIDLGEEVKMILPGEHGSVDLTLLWKMVMLPGQQFTIRENNITVATGIITETLPSIAVTSSLGKLTV* **(457)**	TAAATGTAGGTACAATCGGTCATGTTGACCACGGAAAAACTACACTTACAGCTGCCATAACTAAGGTACTACAGAAAGATGGTCTTGCAAAATATGTTTCCTATGATGAGATTGATAGAGCTCCAGAAGAGAAAGCAAGAGGTATTACAATTAATGCAGCTCACATTGGTTACAGTACGAAAAAGAGAAGTTATGCTCATACAGATTGCCCAGGACATGCAGATTTTATAAAAAATATGATTTCTGGTGTGTCTCAGATGGATGGTGCTATATTAGTTGTAGCTGCGACTGATGGACAAATGCCACAAACTAGGGAACACTTATTATTGGCTAAACAAGTTGGAGTAACAAAAGTCATTGTGTTTGTAAACAAAGCTGACTTAGTTGATCAAGAGATACTGGATCTAGTGGAACTGGAAATTAGAGAGCTACTTGAGGATTTTGGTTTTGATGGCACCAATACGCCATTTATATTTGGATCTGCATTAGAGGCTATGAATGATAAAGAAACAAAATTTGGTATACCTGCAATTAAAGAACTTATTGCTTGTTTAGATAGTTATATACCAGATCCTCAAAGAGATGTTACATCACCTTTTATGCTACCCATAGACAATGCATTTACAGTTCCTGGTAGAGGAACTGTTGTTGTTGGAACAATATTTCGGGGTGTTATGAAAAAATTGCAAGAAGCAGAATTACTTGGTTTTGACAATCAGTTTAAAACTACTGTTACAGATATACAAGTATTTAAAAAAAGTGTTGCAGAGGCAAAAGCTGGAGATAATGTAGGGACATTATTAAGAGGTATCAAATTAAAAGACATAAGTAAAGGTATGCTCCTTTGTGCTCCTAATAGTGTTAAAATCAGTAACAGGTTTAAGGCTAGTATTTATTTTCTATCAAGTAGAGAAGGTGGAAGAACGAAACCTATAACTGGCAAATACTGCCAACAGTTATTTAGCAGAACCTGGAATGTGGCATGCCGCATAGATTTGGGCGAAGAAGTTAAAATGATATTACCTGGAGAACATGGTTCTGTAGACCTCACTTTGTTATGGAAGATGGTAATGCTACCTGGACAGCAGTTTACAATAAGAGAAAATAACATTACAGTTGCAACTG

			GO:0005525 GTP binding		GGATAATAACAGAAACTTTACCCAGTATAGCGGTTACTTCAAGTTTAGGAAAGTTGACAGTATAGCGATAATAGAACCATAATTGTTTGTAAATAAATTGTTTAAAGTTGATGTGTAAAATCAATTACCATAATTGTTAACTTGACCTTTTTCCTACAGGCTATTAGCTTCCCTAGTTGTATTTCCAAAGAATATAGACCTTATAGAAGGGTACTGCCCTGTAACGTTTCAGCATAGGATTTTGTGCACCAACTGAGTAGGTGCATGTGGCCTGACAAATGAGTAGGTACAGTATTTTCAAGGGACA **(1,776)**
MSTRG.38519.1	(1) Retrovirus-related Pol polyprotein LINE-1 [Zea mays] (99%;61%)	Lower	(1) Reverse transcriptase domain (IPR000477)	(1)3-449 WLAGLFNRIMEVGQMPDEWRSSILVPVYKNKGDIQQCTNYRAIKLLSHTMKIWERVIDRRIREETEISENQFGFMQGRSTTDAIFTIRQLMEKYRSKETNAHMVFIDLEKAYDRVPREILWWALNKKGVPGEYVKIVRDMYEGVTTSVX **(150)**	GGTGGCTAGCAGGTCTATTTAATAGAATTATGGAAGTCGGACAAATGCCAGACGAATGGAGAAGCAGTATACTGGTACCTGTTTACAAAAACAAGGGAGATATACAACAATGTACAAACTACAGGGCTATAAAACTGCTTAGCCACACCATGAAAATATGGGAAAGAGTAATTGACAGACGGATACGTGAAGAGACCGAAATATCCGAGAATCAATTTGGCTTTATGCAGGGTAGATCAACAACAGATGCAATTTTCACTATAAGGCAGTTGATGGAAAAATACAGGAGTAAAGAAACAAACGCTCATATGGTATTCATTGATCTTGAGAAAGCATATGATAGAGTTCCTCGAGAGATTCTGTGGTGGGCACTCAATAAGAAAGGAGTCCCTGGTGAATATGTAAAGATTGTGAGGGACATGTATGAGGGAGTAACGACTAGTGTTAGNNN **(451)**
MSTRG.38739.1	(1) Chitinase 10 [Anoplophora glabripennis] (95%;51%)/chitinase 5 precursor [Tribolium castaneum](96%;39%)	Higher	(1) Glycoside hydrolase superfamily (IPR017853)/Chitinase insertion domain superfamily (IPR029070)/Glycoside hydrolase	(1)232-1347 MKWCGIIVIFCVVLGAVSCAPTNFTRNVICYYTGSFGIKVAPPESIDTNLCTHLNYAFVKINENGTLIHNKYVDIKKEMYKRVASLKKMNPKLKILISIGDTPAAVFSEVAADPDKRHSLIQNTIDFLRLHGFDGVDVDWEKPYSKDEENFIHLLKEFKKALETKNYLLSVAVYPYPDAGYIVPKITENVDMINIMCYNFYGPWSIYT	AGCGTTGTTTGGAGAGAGAATTTTAAATTTGATGATAAAAAATGATAAAATTGTATCACCTATTTAAACCTCATCATCGGGTTATGATTATGTATAATATGTGAATTCTTATATTTAGGTATATAGTGGTAGTTATATACAACTATAAACAAAACAGTGGTAGTTCCCCAACAACTTTTGATACAAATACGAACCTCTGCTGGACGGTACCGTTATTTGAGTTAATTAACCATGAAGTGGTGCGGAATCATTGTGATTTTTTGCGTTGTTCTTGGTGCAGTATCATGTGCACCAACAAACTTCACAAGAAACGTAATATGTTATTACACAGGCAGTTTTGGAA

			family 18, catalytic domain (IPR001223)/Chitinase II domain (IPR011583)/Glycoside hydrolase, chitinase active site (IPR001579) GO:0005975 carbohydrate metabolic process GO:0004553 hydrolase activity, hydrolyzing O-glycosyl compounds GO:0008061 chitin binding	GHNAALFASPVESAYERNHLNTAMGLQNWLKAGATKEKVNVGIPFYGRTFTLADPNDHGFHAPITGSGKPSTATYRQICSNFANYTSVWDDTQKVYYKYYEDQWLTYEEERSVKEKAKYIRSQNVAGAMIWQIGQDDINGECGPKQGLLQVVNKYLHEDNNLC* **(372)**	TCAAAGTAGCACCACCTGAATCAATAGACACAAACTTATGCACCCACCTAAATTATGCATTTGTAAAAATAAATGAAAATGGAACCTTAATCCACAATAAATATGTAGATATTAAGAAGGAAATGTATAAACGAGTGGCATCGCTTAAAAAAATGAATCCTAAACTGAAAATTCTCATAAGTATTGGGGATACACCTGCTGCAGTATTTTCTGAAGTAGCTGCGGATCCGGATAAAAGACACAGCTTAATACAAAATACCATTGACTTCCTTCGTTTACATGGCTTTGATGGAGTAGACGTTGACTGGGAAAAGCCTTACAGTAAGGATGAGGAAAATTTTATTCATCTCTTGAAAGAATTTAAGAAGGCATTGGAAACAAAAAACTACCTACTAAGTGTTGCAGTATATCCTTATCCTGATGCAGGTTATATTGTACCAAAAATAACAGAAAATGTTGATATGATCAATATAATGTGCTACAACTTTTATGGCCCTTGGAGTATTTACACTGGTCATAATGCAGCTCTCTTTGCTTCGCCAGTTGAAAGTGCTTATGAGAGAAATCATCTGAATACAGCCATGGGTCTTCAAAACTGGTTAAAAGCAGGAGCAACTAAGGAAAAAGTTAACGTCGGAATACCTTTCTATGGACGAACCTTCACTCTTGCCGATCCCAATGATCATGGTTTTCATGCTCCTATTACTGGTTCTGGTAAACCATCAACGGCAACATATAGGCAGATCTGTTCAAACTTTGCGAATTATACCAGCGTATGGGATGATACACAAAAAGTATACTACAAGTATTATGAGGATCAATGGCTGACTTATGAAGAAGAAAGATCAGTTAAAGAAAAGGCTAAGTATATTCGTTCACAAAATGTTGCTGGCGCTATGATTTGGCAAATAGGTCAAGATGACATAAATGGTGAATGTGGCCCGAAACAAGGATTACTTCAAGTTGTGAACAAATATTTACACGAAGATAATAATTTATGTTGAAATTAATTTAGATTAAAATAATTATAGGTAGTTTCATAGTATCATAACTCATAGACTGCCTGTCATGACAGTATTCTAATTTATTAATTTAAATAATTAAACATTCATGTTCAAGTATTTCTTATATTTTTTTA

					CATTTAAAATATATATTACGTTAAACTAA **(1,510)**
MSTRG.88057.1	(1) Aldose 1-epimerase-like [Anoplophora glabripennis] (89%;59%)/Aldose 1-epimerase-like [Leptinotarsa decemlineata](82%;58%)	Higher	(1) Glycoside hydrolase-type carbohydrate-binding superfamily(IPR014718)/Galactose mutarotase-like domain superfamily (IPR011013)/Aldose 1-/Glucose-6-phosphate 1-epimerase family (IPR008183) GO:0005975 carbohydrate metabolic process GO:0003824 catalytic activity GO:0030246 carbohydrate binding	(1)108-383 MAKVILTEDKFGKITDGKGRTQIVRRFTWKNKNNVSAQVINYGGYITSIKVPGCNKEVEDITIGFNDIEGYLKPENRYLIVLVYTGCPRLI* **(92)**	CTTCCCTAATTATTTTGTTAACTTTATATAATGCACTCAATCGGTTAGTAACAGACAAGCAAACATTTAGTTTTATTTTTAATATACCTGTGTAGCAACACAAAAAAATGGCGAAAGTCATTCTAACAGAGGATAAGTTTGGAAAAATAACCGATGGAAAGGGGAGAACGCAAATTGTAAGAAGATTTACATGGAAGAATAAGAATAATGTAAGCGCCCAAGTGATCAACTACGGAGGATATATAACATCAATCAAAGTACCAGGTTGTAACAAAGAGGTGGAGGATATTACAATTGGTTTTAATGATATCGAAGGTTATCTCAAACCAGAAAACAGGTATTTGATTGTTCTAGTATATACAGGGTGTCCCAGACTAATTTAGCCACGCTATATCTCTTAAACGAATAGAG **(411)**
MSTRG.20829.1	(1) Alpha-tocopherol transfer protein-like [Anoplophora glabripennis] (94%;38%)/retinol binding protein pinta-like [Leptinotarsa decemlineata](90%;33%)	Lower	(1) CRAL/TRIO N-terminal domain superfamily (IPR036273)/CRAL-TRIO lipid binding domain superfamily	(1)250-1101 MKSKIIDAENLDSPPLLVINREGVRKYWGKSESDVCEIVKDLQEWIKEQNFPEMPTNHMIEFFLTNCKYKIDATKDVLNTYYTIRKQVPEIYEDSNPRLAEMGNSWNMGCYCPLPQLTDDLCRISIVKLTSNTSNFVASSYFANIMNIYE	ATAAAAAGAAAGTGTTGATAGAGAATAAAAGCCAGTAACAATTATTTTTTATGGCGCACTTTAAACACGTTGATTTCGTTTTCAATCTGTGTGTCGTGTCTTAAGAAATACTACAGATCTTACTTGCAACACGATCACCCAGTTAACCCGAAATTGTGCGACATACAAACGTGAAAGATCATTGAGTTAAATTGTAGTTAACCAATTGAATCGTAACCTTGATTTTACGACCTTTAATTATTCAAAATCATGAAGTC

			(IPR036865)/CAL-TRIO lipid binding domain (IPR001251)	LRIYEDLCLSEIIICDYSALSWGHVFKMDIFTVRKMAHIMNSLKNRVKQLHIVDSPSCINIIISLAKKLLNKKIADRIVVHKSYDSLYEHVPKDLLPSDYGGKGRPLEETIDMWKEKVKQYQERFDTLEAWSK* **(284)**	CAAAATAATAGACGCGGAAAATCTGGATTCACCACCGCTGTTGGTGATAAATAGAGAAGGGGTTAGAAAATATTGGGGAAAGTCGGAGTCCGATGTATGTGAAATTGTTAAAGATCTTCAAGAATGGATTAAGGAACAAAATTTCCCGGAAATGCCAACGAATCATATGATAGAATTTTTTCTTACCAACTGCAAATATAAAATTGATGCTACTAAAGATGTTCTCAATACATATTACACAATAAGAAAACAAGTACCTGAAATATATGAAGATTCTAATCCCCGACTAGCAGAAATGGGAAACTCTTGGAATATGGGGTGTTATTGTCCATTACCACAATTGACAGATGACTTGTGCAGAATATCTATTGTCAAACTTACCTCAAATACATCAAATTTTGTAGCTTCTTCATATTTTGCCAATATAATGAATATTTATGAACTACGAATATACGAAGATTTATGCCTTAGCGAAATTATTATTTGCGACTATAGTGCTTTAAGTTGGGGACATGTTTTTAAAATGGATATTTTTACTGTTCGAAAAATGGCACATATAATGAATTCACTTAAAAATAGAGTAAAGCAGTTACATATCGTGGATTCCCCGTCTTGTATAAACATAATTATATCATTAGCCAAAAAATTACTTAATAAGAAGATAGCAGATAGGATTGTGGTACATAAATCGTATGATAGTCTTTATGAGCATGTTCCAAAAGACTTACTTCCCAGTGATTATGGTGGCAAAGGAAGGCCCTTAGAAGAAACCATTGACATGTGGAAAGAAAAGGTAAAGCAATATCAGGAAAGGTTTGACACCTTAGAGGCATGGAGCAAATAGGACTGAACAAGGATCTCACCTTTTTATATAAATATTTGTTCATTTTTATATTTTTATAAAATGAGTGGTATATATTATACTATTTATTTATTTCTATTATATTTTTAATAAAGAAGACATTATAATTATGCG **(1,233)**
MSTRG.80801.1	(1) No hit	Higher	(1) No hit	(1)275-87 APTGSRAPAPAHRTYDNCARISCHNICNFTSNYINYGNLCKFIISYVKFHKLRKFQKLHKLH* **(63)**	AATTAGTGATGTGAGTTGTAAAATTACATAACTTACGTTACATAAATTACACGTAACTTACGGTAATATTACATGATACCCGTAACTTAATGTAATTTATGTAATTTTTGGAATTTACGTAATTTATGAAATTTAACGTAACTTAT

					GATAAATTTACATAAATTACCGTAATTTATGTAATTACTGGTAAAATTACATATATTATGGCAACTTATGCGCGCGCAATTGTCGTAAGTGCGGTGCGCCGGTGCCGGCGCGCGCGAACCAGTGGGTGC **(275)**
MSTRG.81903.1	(1) Facilitated trehalose transporter Tret1-like [Leptinotarsa decemlineata](98%;52%)/ Facilitated trehalose transporter Tret1 [Anoplophora glabripennis](95%;52%)	Higher	(1) MFS transporter superfamily (IPR036259)/Major facilitator sugar transporter-like family (IPR005828)/Sugar inositol transporter family (IPR003663)/Major facilitator superfamily domain (IPR020846)/Sugar transporter conserved site (IPR005829) GO:0055085 transmembrane transport GO:0005215 transporter activity GO:0022857 transmembrane transporter activity GO:0016020 membrane	(1)154-1539 MNILSILMQCKYTSFFIVITVNLLATTGDSTLSWTSPIFPKLMSNDTSSNPLGRPITKHEDSIIGSILNVGALIGPLIFNFITRRFGYKYTLLGLAIPHIVSFLVLAFARNIYLFYAARFLAGLSLGAGYSLFSLYVGEISDDSNRGGMIVITNIFWSLGNFLPLAIGPYTSIMSFNLILTVLPVLFFVLFFGIGVESPYYLIRQKEEEKAEEALMYLRGKNKKDITEELGKIKNFVEHSTEGRIQDIFTDKVLRKCILICILLLATQDLGGYCSILYHLTLIFKAAGSEISEDTAALIVGIGLFASSFLAPFLVDYFGRRPLLITSALGMGLSLGVLGLFFFLRNHHFNVESIKFLPLLSLICYIISYNLGINTVPWTLISELFPSSVKQEASTIGAFCCWFTTAVVTFSYNYLNDALGVYGTFWLFACWCLFSATFCFFFVPETKGKSFIEVQKMLYAQ* **(462)**	CGACAAAATTGCATGTCAAAAGATTGCCGCATTTGTTCCGTTCTATCTGACTAATTTTATTATTCTAAGATCATACCTTCAATAAATAACACGGTCGGTTAATTATCTAATCATTTTTAGCGAAACCAAGTGAGTGACTGACTTACCTTCAGGATGAATATTTTGAGTATTTTGATGCAGTGTAAATATACCTCGTTTTTTATCGTTATAACAGTTAATCTTCTGGCAACCACAGGTGACTCAACATTATCATGGACCTCACCGATTTTTCCGAAACTGATGTCAAACGATACGTCAAGTAACCCATTAGGAAGACCAATAACAAAACATGAAGACTCAATTATAGGTTCAATCTTGAACGTAGGAGCTCTCATTGGACCGCTCATATTCAACTTCATAACTCGTCGATTCGGCTATAAATACACCTTGTTAGGATTGGCCATACCGCATATAGTTTCATTTTTGGTTCTAGCATTTGCAAGAAATATTTACCTTTTCTACGCAGCCAGATTTTTGGCCGGACTTTCACTAGGAGCTGGATATTCCTTATTTTCCTTGTATGTAGGAGAAATATCAGATGATTCGAATAGAGGAGGGATGATTGTAATAACTAACATATTTTGGTCATTAGGTAACTTCCTGCCTTTAGCCATTGGACCATATACTTCTATTATGTCTTTCAATTTGATTTTAACGGTCCTTCCAGTTTTATTTTTTGTACTCTTCTTTGGCATAGGAGTGGAAAGTCCGTATTATTTAATTCGTCAAAAGGAAGAGGAGAAAGCTGAAGAGGCCCTTATGTATTTAAGAGGAAAGAACAAGAAAGATATCACGGAAGAACTTGGTAAAATAAAAAATTTTGTAGAACACAGTACCGAAGGTCGTATTCAAGATATTTTTACTGACAAGGTTTTAAGAAAATGCATATTGATTTGTATCTTATTGCTGGCTACCCAAGATTTGGGAGGATATTGCTCCATACTTTATCATCTAACGTT

			GO:0016021 integral component of membrane		GATTTTTAAAGCAGCTGGTTCAGAAATTTCCGAAGATACAGCTGCTTTAATAGTCGGCATTGGTCTATTTGCATCTAGCTTTTTAGCTCCATTTTTGGTTGATTACTTTGGACGACGACCTTTACTAATAACATCAGCTTTAGGCATGGGTCTTTCGCTAGGGGTATTAGGATTATTCTTCTTTCTTCGTAACCACCATTTCAATGTTGAGAGTATTAAATTTTTGCCTCTGCTCAGCTTAATATGCTATATTATCTCTTATAATCTTGGTATCAACACAGTTCCTTGGACTTTAATCTCTGAATTATTTCCGAGTAGTGTCAAACAAGAAGCCTCTACTATTGGCGCATTTTGCTGTTGGTTTACGACAGCTGTTGTTACCTTTAGCTATAACTACTTGAACGATGCACTTGGTGTTTATGGTACTTTTTGGTTGTTTGCTTGCTGGTGTCTTTTTAGTGCCACGTTTTGCTTCTTCTTTGTACCTGAAACAAAAGGAAAGAGCTTTATAGAAGTCCAAAAAAATGCTTTATGCCCAATAGACACTCTGCGTTAAAGTTATTTTAAAGTCAAATATATTTATGAATATTTACAATTCCACTTGACAATGCACAATTGTGCATTGAAAGGATACATGTACCTACGTCAGAGTTGGAGGTGATACAAACCACAATTTAAAAAAAACTAGCTTACGTAAACACCATCCATATTTTATAATATTGTGTCCTTAAAAGCAAACAAAACTACTCATATAATTATTATAGTTTGAAAACTATAAAATAATGCATAATTATTTGAGTAATACGAAATACTTGGTTATTGTATATCAAGAAACACCTCTAATAGATCCACAAATCCAACCTGACTGAAGATGGCAAGAATAGAAAAATTAAATACATAAACCTTCGAAAAATTGAAAAGTTTATATGTATAGCTATCGTGAACGATGTATAAACATTTCAGAAAGCGTAATGAAACAGTAAATAGACCGCAAAAAGAAGAAATAACCTACAATTGGATATGGTAATTGAGTCAATACTCGCAATCTTTAGTTTGTATTTTTTATTAGTTGCTATGTAATCATGGGGCAACCGGTTTCGAGTCTTACAATATATGACTCATCATCAGGCCCAGTACAAAAAGTCT

					TCTCTATACAAACTACAAGCTAAAAAACACAAAACGAGAGACATGTACACATATATATAAAACATGAAAAACAACTTTGTCTTGGTTTCAATCACATACAATAAAGCCAAGCAACTGTTTAGTATTGAACTCAACAGTCCATATCATGTAAAATGAGACATTATATCATTGGGAGCGACCAATCTGATGAAAAATACTTGGTATATAATTTGATATATATACTACCATCAATCCTTAACTAGTCAAGGGTCGATGGAGTCCTGGTAAGATAGTATGCGATCAAAAGACATAATACAAAATTTCTTTAGTAAACGGTATCTACTTACATAACAGCCATAGAAACTGTTCCACAGCTAAAGATGTACCTGGAAGTCACCAGCCCCATAAGAAGAGTTGACCAATCAAACAGCCCTTAGTCTCTTAAATTGTTAGTTAAGTGCAATTTGGAACCGTACAAGAAATTTTTTTTTACTGTGTTCCCAGTGGTGTGTGTTATTTCTCTTAAACAGTTGTTCTTGTCCAATTTAGCAGTTGTTTTTATGTTTTATGTAGAAAGAATGTACAAACATTTAATAATTATTAAAATAATGGGACATCACACACAAAATTTCACATGCACAAAAATTTTAAAAATTGTTTTTCGGTTGCCAGAGACTTTTTGATATTTTTTTAAGTCATTATTTGAGGTTGTGCTGTCAGATTTCCCAGAAATTTTTAAGATTGACATGTCTTCTACTTTCTATAAGGAAATAACCTTTTCAAACTGATCTTGATGCAAAGATACAAAGATGCAAAGATAGTAGGAAAATAGAGGAATTATACTCCATCCTATCGATATCCTACAGATATTGTAACTTGTGATAATATTTCTTGAGAAGGGCAGAGAAACACTGTTAAAGAACTTGTCCACGAAACAATGCTACTCAAGATCGTAGTTATCTATATTCAATAACTTTTACCATAAAAACGATTCCAGTTACCTATTTTGTTTATAGGAGAATAATGAGTTATTTTAACCCCTATTTGTTTAGTAATAGGGCATTCCAACATGCTATCAAAATTAAATCAATATGGCGGCTGGGAGGCACACATAGGCCTAAATGTTATTCTGTTAGTTCTCAATGTGTTTTAGATCATTTTAGTTG

					CGTGAAGTGGTAATTTAGTTTTATACAAGGAAAAATTTAACATTTTCACTGAAAGAATCTATTTAAAATGATAATATGCCTCATTTCCGTTATGTTGTGAAGTATGGAATGCGAGGTAATCATGATAAAGTTCAGTTTTATCGGTTACTATCACTACTAGCTACATTTACTTAAATCTTAACTGAGGCGCTCCGAGCAACAGTCGCCCAAGCCACAAATTGAGCATTTTTAGATTAATATATCAATAAAAGTAGCAACATTAAATCTTCGAATTAACAAGGGTCTACACAACCTACCTCTATACTTGACTAATAGGCGAGCGGGAGATGACCCCTAAAATGACCAGGTACTGACCACGGAGAGGTGAATGGCCAATTTTAGACATACTGTATGTTTTTGACAGTGCTGAAAACGAAAATGAGATTTATTTTGAATTTCATGTGGGGGGACATTGCCAAAATCGCAATTTTTCCCTAAAAATAAATAAAAATAAAATCATGTTTTTTGCGTTTACCTCGCTACAACTCGGTTCCATTTTAAAATTTTTTTTCTAAAATTGTTACAGTATATAGCTCTAACATTTCTAAAGACAACGGTACCTGTTTTAAGCTTTAATTCTCATTCTGATAAAGGTTATGAATTTTTAAAAGGAAAAGGTGCGTATTTGTGCATTGCAAAGTTTAATCGAAAAAGTTGAGTGACGAAATTTAAAATTTAGCCTTTTAATCACGTTTATGTTAAAATAGAGCGTACAAAGAAGTTTTCTGGAAAATTTTAGATCAAAATGTTTTATAGAAAAAAAAATAGTGCAACTTTTATTATCGACATTAGAAATCCCCAATATAACGGTTACTTTTCGAGATACTGACCATGGGTGGTGAATGGCTAATTTTGGTCTTAGATTATGTTTTTGACGGTGCTGAAAACGAAAATCAAATTTATTTTAAAGTTTATGTGGGGGAATATTGTCAAAATCGCAATTTTACCATAAAAATAATAAAAAAAATGAAATCACGTTTTTTGCGTTTAACTCGCTACAACTCTGGTAGATTTTTCCTAAGGTTTGTACACTATATGTTGTTCACTTTTCTAAGGACAACGGTATCTGCTTTAAGATTTTAGTCTTATTCTAGTAAAAGTTAT

					GAATTTTTTAAAGTACAAGTTGCAGATTCGTGAATTGCAAAGTTTAATCGCAAAAGTTGAGAGGCAAAATTTAAAATTTATCTTATTAATCACTAGGGAGGTGAATGTCTAATTTTGGTCTTATTTTATGTTTTCGATGGTGCTGACAATGAAAAATAGGTTTATTTTGAATTTTATGTGAAGGAACATTGTTAAAATCGCAATTTTAACCTAAAAATGAAAAAAAAGTGAAGTCACGAATTTTTACGTTTAACTCGCTACAACTCTGTTCCATTTTAATATTTTTTTCTAAAATTTTTACAGCATATATTTCTCACCTTTGTGAAGACTATGAAAGTAACTGTAGTATTTCAGTTTTTCTTTATAAAAGTTATGAATTTTTAAAAATAAAAGGTGCAGATTCATGATTTGCAGAGTTAAATCGCAAAAATTAAGTGAAAAAATTTAAAATTTATCTATGTGATTACGTTTATGTGAATCCATAGAGTTCAAAGAAGTTATATGGGGAGTTTTAGGTCTCGATGTGTTATAGAAAAAATATGGTGCAACTTTTAATTTTAAGAAAAACGTGGTTTAACTTTTTTTTATTTTTAGTGCAAAATTGCGATTTTGACAATTTTCTCCCACCTAAAATTCAAAATAAACTTCATTTTCGTTTTCAGCACCATCAAAAACCTTAAGACCAAAATTAGCCATTCACCACCAAGTATCAGTATCTCGAAAAATTAGCGTTATTTTGGGGATTTATAACGTAGATGTTAAACGTTGCACCATTTGTTTTCTATAAAACATTTTATTCCAAAACTTTCCAGAAAACTTCTTTGTACTCATGTTTTATTTTGAATTTGATTTAAAATCTATATTTCAAATTGTGTTAGTCAAATTTTGCGATTAAACTTTGCAATTCACGAATCTGCACCTTGTACTTTAAAAGATTCATAATTTTTACTAGAATAAGACTAAAAGCTTAAAGCAGAAACCATTGTCTTCAGAAAAGTGAGCGATATATAGTGTACAAACTTTAGAAGAAAAAAAATATTAAAACGGACCAGAGTTGCAGCGAGCTAAACGCAAAAAAACGTGATTTCATTTTTTTTTTTTTTAATTTTTAGGGTACAATTGCAATTTTGACAATATTCATCCACCAAAAATT

					TAAAATAAATTTTATTTTCGTTTTCATCACGGTCAAAAACATAATCTAAGAAGAAAATTAGCCGTACACCACCCATGGTCAGTATCTCGAAAAATAAAGGTTATATTGGGGATTTCTAATGTCGACATTAAAAGTTGTACTATTTTTTTTATAAAACATTTTATTTTAAAACTTACAGAATTTCTTTGTACTCTCTACTTTAACATAAACGTGATTAAGAAGCTAAATTTTAAACTTCGTCACACAACTTTTGCGATTAAACTTTGCAATGTACAAATCCGCACCTTTTCCTTTAAAAAATTCATAACATTTATCAGGATAAGAATAAAAGCTTAAAACAGGTACCGTTGTCTTCAGAAATATTGGAGCTATACACTGTAAAAATTTCAGAAAAAAACTATTAAAATGGAACAGAATTGTAGCGAGGTAAACGCAAAAAAGCGTGATTCATTTATTTTTATTTTTATGTTAAAATTGCGATTTTGACAATGTTCCCCTACATGAAATTCAAAATAAACTTCATTTTCCTTTTCAGCACCCTCGAAAATATAAAGTATGAATAAAATTAGCCATTCATCCCTCCGTAGTCAGTATCTCGAAAACTAAGCGCATTTTTGAGGGTATCCCGCTCGTGTATAAATACATAATAATACTTATTATAAATTATTTATTATACACATTACTATAAATTATTTATAGTGCCATCCCATAAGCATAATGTAAATACGAACGCAAAGATTACATTTATCTCAGAACTTCGTTTTTGGGGTTAGTCCACTGTTGCTCTGAGCGCCTCAACTGTTCTTTTTCCTGATGATAGTGAGAAATAAGTAATCATCACACTTTTAGATATGTATTAGATATAGTTTATG **(6,455)**
MSTRG.12727.1	(1) Zinc finger FYVE domain-containing protein 26 [Leptinotarsa decemlineata](99%;57%)/ Zinc finger FYVE domain-containing protein 26 [Anoplophora glabripennis](99%;53%)	Higher	(1) Zinc finger, RING/FYVE/PHD-type superfamily (IPR013083)/Zinc finger, FYVE/PHD-type	(1)453-4463 MEEISKLIEKITRQDSTNQNKHINLLYKKISEFKPQDKHDTGCLFEYILPKIYDLFQRDIVKRDVLYLSLIGAHNVDVLQIFLKYHEATLNASLENATRLYDYCVCKKKHWFNEILTTDNLFITNQKILNKILTLQLIGITNSSKFDTQHVK	AGAGTACCACCTTTTTCGTAGCAGATAGAAAATACACACCATAAAAGAACATATAAATAACCAAACCTTTTTATAGTGTTGTTCTGTGAATTATAAATATTTACAAATTAAACCTCAGATATGTGTCAAATAAATTGTATGGAAACCAAAAACAAATAAAACTAATATCTCTTGGACTCTTGGAAAAAATGTGAAAATGAGGATGAATCATCAATATCAATCATCTATTTATCACTCAGATGCTGTTTATATCCGCTTC

			superfamily (IPR011011)/Zinc finger FYVE domain-containing protein 26 family (IPR028730)/FYVE zinc finger domain (IPR000306)/Zinc finger, FYVE-related domain (IPR017455) GO:0000724 double-strand break repair via homologous recombination GO:0000910 cytokinesis GO:0032266 phosphatidylinositol-3-phosphate binding GO:0046872 metal ion binding	RLLENIDQGDIQPFWKKYFVVTEYFLNIMDYVKSNISSLNAHDVFCHINENAALETFSNYLPLKSSSLEQALQLVVQEENIFEIKNHHSTQFEAFIILRNLFNCITRIPNINITDEVSDIKERLLKIPDLSLQLELLENIFVTIFLERSHLSNKVNESKMVCEEKEVRLLLFLVKEVLDEVKLNNTPAKESVEYAKLSQLNKVVADTIWRMELIGDIKGSSKCEKNLLKYMLSSPESLIQMCLARSDFERAFQVIKIFSLEEPYLTSEIKFSENLISLRDTLKKTIKIKAIQKVNPKISITTLNVCVDKTIEIFFKKNSIVTNPKIDTTIDKLSQKYKFFNHFHSKNEMFMNILDLAITVSQDNENSEIILQLACENNSLDANICSNYSKFCKRLVDLYKEIGKEKNLSLGEVIVLPEYHLDLNVYTKEEEFFATFAQAFNDAMSDLTLSEPGYLNMRHLSHRTVLKLNSLCVDNSYSRVMENKYILKLFNYLKAFSRVLYIEQNTSDIVSRGKNSSYFDLLVFNRSELMGKLLFERNLDPSEFEKYFEKLKLDYLYHVVGNCFPTINLHIEENVAKDELYPENNLYVPNKSIITYIQKRNWLLAYILNKMYMVEGVSIDISEIRVRVFMNYLGLRKVQVLQRVYNENTIITALQNEISIQKVSDYINDRILLHERSSNLHLSHNSSDSLEAAEELGEDTLGYINWKSVYDLVACIPEDQCRKNRVCLSMTDMVLVSLIQDGVEPDYYRYVLLIGNRDMRI	TCAGTCATTATGTTTATTGTTATTGTACCATCTGCACTGCATTGTCTACGCATGATCGACTGACCTATTAAAAGTTATTTGTTTTTTATAGTGTATAAATATGTAATTTGCTGTGATATCAAGTGAAACCAACACAATTGTTGCATCTTAATTGTGATATGTAAATATACTGAAACAAATGTGATTTTACAGAATGGAAGAAATCTCAAAGCTTATAGAAAAAATAACAAGACAAGACAGTACTAACCAAAACAAACATATCAACCTGTTGTACAAAAAGATCAGCGAATTTAAACCCCAAGATAAACATGACACTGGCTGCTTGTTCGAGTACATCTTACCAAAAATATACGACCTCTTCCAAAGGGACATAGTCAAAAGAGATGTTCTATATCTATCTCTAATAGGAGCCCATAATGTTGACGTCCTGCAAATATTTCTTAAGTATCATGAAGCCACCTTGAACGCCAGTCTAGAAAATGCGACACGATTGTACGATTACTGTGTTTGTAAGAAGAAGCATTGGTTTAATGAGATTCTAACGACAGATAACTTATTTATTACAAATCAGAAAATACTGAACAAAATCTTAACCCTGCAGCTAATAGGTATTACCAATTCTAGTAAATTTGATACTCAACATGTTAAACGGCTGCTGGAGAATATCGACCAAGGGGATATTCAGCCATTTTGGAAAAAGTATTTTGTCGTTACTGAGTATTTCCTCAACATCATGGATTATGTAAAAAGCAACATAAGTTCCCTGAATGCACACGATGTCTTTTGTCACATCAATGAAAATGCTGCCCTCGAAACGTTTTCAAATTATCTACCACTTAAAAGTTCAAGTCTTGAACAAGCTCTTCAACTAGTCGTTCAGGAAGAAAATATTTTCGAAATAAAGAATCACCATTCTACACAATTTGAGGCCTTCATAATTTTAAGAAACTTATTTAACTGCATTACAAGAATACCGAATATTAACATTACTGACGAAGTTAGCGATATCAAGGAACGGTTATTGAAGATTCCAGATTTGTCTTTGCAGTTAGAACTATTAGAAAACATTTTTGTTACTATCTTCTTGGAAAGAAGTCATCTTTCCAACAAAGTTAATGAATCCAAAATGGTTTGCGAA

				SMILDHIKEWPGDFCLDCIKSEITRFDGMQDGRIVELKIWLLHITLCETLKYKLDVTSWYAAYKMCENNKENVIAKLLEFADINLLLDFIDLHTPNEGLLELVNEHYLAKIFEQSTPFDRVKVLLDLLPFKHSVRMCYNAIKMLRDLKYLNFIVEYLLNNVSDESLRNVQISLKMLSIFSPFEQDQLLCLLYEPLSIIEILIMNTKLDKLASVLNIVKLEISQSEFDTAVISIKEIDELLRTYGEKTLDFRIITQPNPRLLRTPEFKLMQSLDSLNLGPYNKNFVMPDEVPIKDDWIPNNEVLECMCCQKIVFSMFNRRHHCRRCGRVICYNCSLHRMLVPTYDDILVRVCLDCYRQTVGESETSELNDSLSLKSAVYDFWILTDDDAHNTIVREEFSYEHAPNVSLCLSLMKYHSKTTEYPK* **(1337)**	GAAAAAGAAGTTAGGCTTCTACTTTTTTTGGTAAAAGAAGTTCTAGATGAGGTTAAGTTAAATAATACACCAGCAAAAGAGTCTGTCGAATATGCGAAGCTATCTCAGTTGAATAAGGTTGTCGCTGATACGATATGGAGAATGGAGCTTATAGGCGACATAAAGGGCAGTTCCAAATGTGAGAAGAATCTTTTGAAATATATGCTTTCCTCACCTGAATCTCTTATACAGATGTGTTTAGCTAGAAGTGACTTTGAGAGGGCATTTCAAGTTATTAAGATATTCTCATTGGAAGAACCTTACTTAACAAGCGAGATCAAGTTCAGTGAAAACTTAATCTCCCTTAGAGACACATTGAAGAAAACTATCAAGATCAAGGCAATTCAGAAAGTAAATCCGAAGATATCGATAACAACATTAAACGTATGTGTAGATAAAACAATAGAAATCTTTTTCAAGAAAAACTCAATCGTAACCAATCCCAAAATCGATACTACCATCGATAAGCTCTCACAGAAGTACAAATTTTTCAATCACTTTCATTCAAAAAATGAAATGTTCATGAATATCTTAGATTTGGCGATTACAGTCTCGCAAGATAATGAAAATTCCGAAATTATCCTGCAGCTGGCGTGCGAAAACAATTCCTTAGACGCAAATATTTGTTCGAATTATTCTAAATTTTGTAAGAGGCTTGTAGATCTATACAAAGAAATTGGAAAAGAGAAAAACCTCAGCCTTGGAGAGGTTATAGTTTTACCTGAGTACCATCTAGATCTTAACGTTTATACCAAAGAAGAAGAGTTTTTTGCTACATTTGCTCAAGCCTTTAATGACGCTATGAGTGATTTGACGCTCTCTGAACCCGGATACTTGAACATGAGACACCTTAGTCATAGAACAGTCTTAAAACTAAATAGTTTGTGTGTGGATAACTCGTATTCTCGAGTAATGGAAAACAAGTATATTTTGAAGTTGTTCAACTACTTGAAAGCATTCTCTCGAGTACTGTACATCGAACAAAACACTTCTGATATAGTTTCAAGAGGAAAGAACAGCTCGTACTTCGATTTACTAGTGTTCAACAGATCTGAGTTAATGGGAAAGCTTTTGTTCGAAAGAAATTTGGATCCA

					AGTGAATTTGAAAAGTATTTCGAGAAATTAAAGCTAGATTATTTATACCACGTAGTAGGCAACTGTTTTCCAACCATCAATCTTCACATTGAAGAAAATGTTGCAAAAGACGAATTATATCCAGAAAACAATCTATATGTTCCCAATAAAAGTATAATAACTTATATTCAAAAAAGAAATTGGCTGCTAGCTTATATTTTAAATAAAATGTATATGGTAGAGGGAGTTAGTATCGACATTAGCGAAATTAGAGTTAGAGTGTTCATGAACTACCTTGGGCTCAGAAAAGTGCAAGTTCTACAGCGAGTTTATAACGAAAATACTATTATTACTGCTTTGCAAAACGAAATAAGTATCCAGAAGGTTTCTGATTATATCAACGATCGGATATTGTTACACGAAAGATCAAGTAATCTACATCTCAGTCACAATTCGAGCGATAGCTTAGAAGCTGCTGAAGAGCTCGGAGAAGATACCTTGGGATACATCAATTGGAAGAGCGTCTATGATCTGGTAGCTTGTATTCCTGAAGACCAATGCCGGAAGAACCGCGTCTGCTTAAGCATGACTGATATGGTGTTGGTCAGTCTTATTCAAGATGGTGTAGAACCAGACTATTACAGATATGTCCTCTTGATAGGCAATAGAGATATGCGGATAAGTATGATTTTGGACCATATAAAGGAATGGCCCGGTGATTTTTGCTTGGATTGTATTAAGTCTGAAATAACGAGATTTGATGGAATGCAAGATGGCAGGATCGTAGAACTTAAAATTTGGCTGCTACATATTACTTTATGTGAAACGCTTAAATATAAATTGGATGTTACCTCATGGTATGCTGCATATAAGATGTGTGAAAATAACAAAGAAAATGTAATTGCGAAGCTTCTAGAGTTTGCTGATATAAATCTTCTCTTAGATTTTATTGATTTACACACACCAAACGAAGGACTGTTGGAGCTAGTCAACGAACACTACCTTGCTAAAATCTTTGAACAGTCCACACCTTTTGATCGCGTAAAGGTCTTACTGGACCTACTACCATTCAAACACAGCGTAAGAATGTGTTATAATGCAATCAAAATGCTTAGAGACTTGAAATACCTGAACTTCATCGTAGAATATCTG

					CTGAATAACGTTAGCGATGAGAGTTTAAGAAATGTTCAAATTAGTCTAAAGATGCTGTCGATATTTTCTCCATTTGAACAAGATCAGTTGCTGTGTCTCCTCTACGAACCACTGAGTATTATAGAAATTTTGATTATGAATACCAAATTGGACAAATTAGCTTCAGTTTTGAACATAGTTAAGTTAGAAATATCTCAAAGCGAGTTTGACACAGCAGTTATATCTATCAAAGAAATAGACGAGTTATTACGAACTTATGGAGAAAAAACTCTTGACTTCCGAATAATTACTCAGCCAAACCCTCGACTGTTACGAACACCTGAATTTAAGCTCATGCAGTCGTTAGATTCGTTGAATTTGGGGCCCTACAATAAAAATTTCGTAATGCCCGATGAAGTTCCCATCAAAGATGATTGGATACCTAATAATGAAGTTCTGGAGTGTATGTGTTGTCAGAAGATCGTGTTTTCCATGTTCAATCGAAGACATCACTGTAGGAGATGTGGTAGAGTTATTTGCTATAACTGCTCGTTGCATAGAATGTTGGTTCCAACCTATGATGACATTTTAGTCCGCGTTTGTTTGGACTGTTACAGACAAACTGTAGGAGAGAGCGAAACATCAGAACTAAATGATTCACTTTCACTCAAATCGGCAGTATATGATTTTTGGATTTTAACAGATGACGATGCACATAACACAATAGTCAGAGAAGAATTTTCTTACGAACACGCTCCTAACGTGTCACTGTGCTTGTCCCTTATGAAATACCATTCGAAGACAACCGAATACCCTAAGTAAGTATT **(4,468)**
MSTRG.34302.1	(1) Endonuclease-reverse transcriptase [Lasius niger](57%;51%) (1) Asialoglycoprotein receptor 2 [Leptinotarsa decemlineata] (98%;93%)/C-type lectin	Lower	(1) No hit (2) C-type lectin-like/link domain superfamily (IPR016186)/C-type lectin fold superfamily (IPR016187)/C-	(1)788-1096 MDDIKRISKKWQQYAQDRGEVKNGRDLCPAVDRRGCMMMMMMMIEKARSVFIKMESLFSSHDLPLGAKMSIIRCYVFSTLLYGIQAWTLSEGYFRKLDSFEM* **(103)** (1)3526-3281 TTQRDQNDWSETGGIGKPQPDNREVIQQGGAQEN	TGGATTTATAAATAATTTAATAGCGTAAATTTAATAATAAATACTTAATCCTACAACGTAAATTTAATATTATTAATAATTATGTATATTATTGTTGCACAAAATATTTTGAACTTTCTTTTACATTGTACCAGCTTTATTTTACATTCCCAGTGAAAGCTTAAACAATTTTTTATATTTTGTACTTTTTAGCTATTTTTTGTTTGAATTTTTTTTCTTTGGCAATTTTTTTCTTTTGTGTGAGGACATGCTGTGAATTCATTCTTACAAGAGGAGTTAAATGACCAAAAAGAATCTATTACAATCAATGATTATAGATC

	precursor [Tribolium castaneum](98%;90%)		type lectin conserved site (IPR018378)	CLAILNQFYNDGVNWHDVACHHVKPWVCEENEDLLKYVRYTNPNLLI* **(82)**	TGCTTAATAGCAGATGCATAAAGTGGTTATAGGAGTGAGACAAGGATGCATTCTGTCCCCGGTGGTATTTAATATGTACTGTGAACATATCTTCCAGCAAGCACTGGAAGAACTACAGGAAGGAGTAGTCAATCGAGTGCGTCTAAACAACATTATGTATGCCGACGACGCAGTTGGTTTTGCAGTTGGCTTAGATGATTTGCAAAGAATATCATCGCTCATATCATAAGTAGAGAACATGGACTTGATCTCAATCCGAAAAAATAAAGTAGATGATAATCAGTAAGCGCGAAATATTAAATACAGAGCTTTTGATTAACCAACAACCAATTGACAGGGTAAACAGTTACATTTAATTACCTTTGTACCAGCCAATGGGACTACTCTACTGAAATAAAACAACGCATTGAAAAGGCTGGCGCTCAAGAGAAGACAAATGCAGCAGAGGACGACCACCAACACGCGGGATGGACGACATTAAACGGATATCCAAGAAATGGCAACAATACGCACAGGACCGTGGAGAGGTGAAAAATGGGAGAGACCTATGTCCAGCAGTCGACAGAAGAGGTTGCATGATGATGATGATGATGATGATCGAAAAGGCAAGATCAGTGTTCATAAAGATGGAGTCTCTTTTCAGTAGTCACGATTTACCACTAGGTGCCAAAATGTCTATCATCAGATGCTATGTATTTTCTACGTTATTATACGGAATACAGGCCTGGACACTTTCTGAAGGTTATTTCAGAAAGCTCGATTCCTTCGAAATGTGATGTTGCAGATGCAGATGTATCTTGAGAATTTCATGGATGGATCGGAAGACTAATTTTGAGGTCTTACGTAGAATAGGCAAAGAAAGAGAGATTATTAACACAATCAAAGAGCTTAAACATATCTTGAAGGCATATGAATAGACATATGGCTTGTTGCAACTGATTCTTCAGGGCTAGGATAGGCACCGTATGACAAAGACCAGGCATAATAATAATAAAAATGCTTGGTGTGTTTTGGAATGGTCGTAGAAGTAAATATCATATCTCCACCAGATACAGATAGATTTACAGTTTATGTGTATAGTGTATAATGACATTTATACCTACACGAAAGAAAAAATTTTAACC

					TATCTGCCGATTTTTAATAATTTTCAAGATTTTTTTCGATATGAGTACAAATTTTATGATTTTTTCGCTTTATACAGAACTATACTCTAATATCGAATAAATAAAACGTTAAAATTATATTTCTAAATAATACGAAGATAAAACTCCGACTGTGTTTCTTATAATAACTATCTGTACATATTTTTTTCAAATTAAGTCAGTTTTCTGACATAAAAATTTACAAAACAGACTGCATACTTCCATCACAGTATAATGCTAACAAATCAATAGGGTCACTCCGCGAAAATCCTTTGTTTTCTATATTCCATTTTGGTGACGGCGAATCAGAATTTTAATTTGCAAAGATTGCAAAATTGGAACCGTCAAAATTTGAGAGTGAACTAACTAATTCTGTAGCACTAAACTGTGTCCTGGGTCTACACAGGGTGTTTCATTAATAATTGTCTATGTAGTAACTGGAGAAACCTTAGCACAAAATACGAAGATTTAACCTAAAACACTTAAATAAAATGTGGTTCCTTACTGAGTTACAGGGTGTTTTTTCTAAAAATTTAAAAACTATTTTTGCTCAGCATTTTAAAACTATTCGACATATCCTTTTCATACTTGGCAGAAAGTGCGAGTACTAGACACCCTACTAAATTTTAATAAACAAACGTTTCTAGCTACTACCAGAGGCGTACGACAGGGGATGGTGATTGGTTGACTCTTCTCAAATTCTACGCCACTGGAGAAATTACTATTTTAGTGCCATTTTTAGATTCTCCAATACTTTCTACGTAAATTCATTTCTACGTAAAATTTCTACGTACTTCATTGGTAACGGTAAAATCATTATTTTTCGAGATATTTGAAGTTAAATATGAAACGGCACAGTTATTTTGATTAATTTATGATATGATTCATATTATGATTAAAATTTAAAAATTATTTGTACCCAGTACTTTAAAACTATTTGGCATATTCTTATCATACTTGGCAGAAAGTGTAGGTACTGTACACCCTACTAAATTAAGATAAATAAACGTTTCTAGCTACTACCAGAGGCGTACGACAGGGGATGGTGATTGGTTGACTCTTCTCAAATTCTACGCCACTGGAGAAATTACTATTTTAGTGCCATTTTTAGATTCTCCAATACTTTCTAC

					GTAAATTCATTTCTACGTAAAATTTCTACGTACTTCATTGGTAACGGGTCCCTCCGGTGAGTACCGATCCCACAAGGACAGAAACTATTTTTCATTTATTAATTTATAATAAATGAAAAATTTCTGCCCCTGGTAGGATTCGAACTCCCGACAAATTGCTATCTTGGTGTAATTTTTTTTTTTTTTTTTTTGATTTTGCAATATTTTTTATATAAATAATATACTGTTCATTCGTATCGATAAAATTATTAGTTTTCGAGATATTTGAAATTAAAAATGAAGCGACACAATACGTTAATCAAAATAACCGTGTCGTTTCATTTTTAACTTCAAAGATCTCGAAAACTAATGACTATCGTTACCAATGAACAGTATATAATTTTCATAGAAAGTATTGGAGAATCCGAAAATTGAACTAAAATAGTAATTTCGCCAGTGTCGTCGAATTTGGAAAGAGTCAACCATTCACTTCCCCCGTCGTACGCCTCTGGTAATAGCCAGAAACGTTTGTTTAACATAATTTAGTAGTTTGTACAGTACATATACTTCCTGCCAAGTACAAAAAGGATACGTCGAATAGTTTTAAAATACTGAGCAAAAAAAGGTTTCTCCAGTTATTATATGGACAATTATTAATTAAATACCCTGTATAGTATACGTCATTATTCAGTCACGAGCTATCTACAATTTTAAATTAACAAATTTGGGTTGGTGTACCTAACGTATTTAAGAAGATCTTCATTTTCCTCACACACCCAAGGCTTCACGTGGTGACATGCAACATCGTGCCAGTTAACTCCGTCGTTGTAAAATTGATTCAAGATGGCAAGACAGTTTTCTTGTGCTCCTCCTTGCTGGATGACTTCTCTGTTGTCTGGTTGTGGCTTGCCGATGCCTCCGGTTTCGGACCAATCATTCTGGTCTCTTTGAGTTGTT **(3,527)**
MSTRG.19533.2	(1) Glutamine-fructose-6-phosphate aminotransferase 2 [Anoplophora glabripennis](97%;90%)/ Glutamine-fructose-6-	Higher	(1) Nucleophile aminohydrolases N-terminal superfamily (IPR029055)/Glutamine	(1)96-1988 MCGIFGYLNYLTPKKREEILELLVNGIKRMEYRGYDSAGVAVDSPETKDIFIIKKTGKVALLAEEIKNKSDVLDMQKSMDIHCGIAHTRWATHGVPSEVNSHPQRSDVENG	AAAACGTAAACAGCGAAAATCTTGTTTAGTTTGACTTTTAAATAGGTTGAGGAGGTTTCTTTGATATTGTAACTAAGGTGTAAAGCGTGTTAACAATGTGCGGAATTTTCGGTTATTTAAACTACTTGACCCCCAAGAAGAGGGAAGAAATTTTAGAATTATTGGTAAATGGTATCAAACGAATGGAATACCGGGAT

	phosphate aminotransferase 2 [Leptinotarsa decemlineata](97%;89%)		amidotransferase type 2 domain (IPR017932)/Sugar isomerase (SIS) domain (IPR001347)/GlmS/AgaS SIS domain 1 (IPR035466)/GlmS/FrlB SIS domain 2 (IPR035490) GO:1901135 carbohydrate derivative metabolic process GO:0097367 carbohydrate derivative binding	FVVVHNGIITNYKEVKVFLEKKGHKFESDTDTEIIAKLIYHFYKLHPTYSFRELVENVVQQLEGAFALCFKSKFFPGECVATRRGSPLLVGIKTATRLATDHVPILYGKEDPSSPTQKEFRPHGRGEYPTLPRTGSTSEFEPLEDKQVEYFFASDASAIIEHTNRVIYFEDDDVAAVKNGSLSIHRIRRAGDDPQKREITTLKMELQQIMKGNYDFFMQKEIFEQPESVINTMRGRVNFENGTVTLGGIKDYIPEVKRCRRLMLIGCGTSYHSAIATRQLLEELTELPVMVELASDFLDRTTPVFRDDVCFFISQSGETADTLMALRYCKQRGALIVGITNTVGSSICRESHCGVHINAGPEIGVASTKAYTSQFISLVMFALVMSEDRLSLRQRREEIIDGLRNLQSQIREVLKLDDKVKRLAEDLYKKKSLLIMGRGFNFATCLEGALKVKELTYMHSEGIMAGELKHGPLALVDETMPVMMIMMRDHVYTKCMNALQQVRTMCTYGICIINYFAENS **(632)**	ATGACTCAGCTGGTGTAGCTGTCGACTCCCCCGAAACCAAGGATATCTTCATAATTAAAAAAACCGGCAAGGTCGCTCTGCTCGCCGAAGAAATAAAAAATAAAAGTGATGTCTTAGACATGCAAAAGTCGATGGACATCCATTGCGGTATTGCTCACACCCGTTGGGCCACTCATGGTGTCCCCAGTGAGGTAAACAGCCATCCACAAAGATCAGATGTCGAAAATGGGTTCGTAGTCGTCCACAATGGTATCATCACGAACTACAAAGAAGTCAAGGTTTTCCTTGAGAAGAAAGGACACAAATTCGAGAGTGACACTGATACCGAGATAATCGCAAAATTGATTTATCATTTTTACAAGCTGCATCCTACTTATTCGTTTAGAGAACTCGTGGAGAACGTTGTGCAGCAGTTGGAAGGCGCTTTCGCTCTTTGTTTCAAATCAAAGTTCTTTCCCGGAGAATGCGTGGCTACAAGAAGAGGTTCTCCTCTTCTAGTTGGCATCAAAACCGCCACTCGTTTAGCCACCGACCATGTACCTATTTTATACGGAAAAGAAGATCCATCGTCACCAACTCAGAAAGAATTCAGGCCTCATGGACGAGGAGAATACCCTACGTTACCAAGAACAGGGTCAACATCCGAATTCGAACCTCTTGAAGACAAACAAGTCGAATATTTCTTTGCTTCAGATGCTTCCGCAATTATTGAGCATACCAACAGGGTGATTTATTTTGAAGATGACGATGTGGCAGCTGTTAAAAACGGTTCCCTTAGCATCCACAGAATCCGAAGAGCGGGAGATGATCCACAAAAACGAGAAATTACCACTTTAAAGATGGAGTTGCAACAGATAATGAAAGGAAATTATGATTTCTTCATGCAGAAAGAAATTTTTGAACAACCCGAATCTGTCATCAACACTATGAGAGGACGTGTAAACTTTGAAAACGGGACTGTAACTCTGGGTGGAATAAAAGACTACATTCCAGAAGTAAAAAGATGTAGAAGACTAATGTTGATCGGTTGCGGAACCAGTTACCACAGTGCCATCGCCACAAGGCAGTTGCTGGAAGAATTGACTGAATTACCCGTCATGGTGGAATTGGCGAGTGAC

					TTTTTAGATCGTACCACACCTGTGTTCAGAGATGACGTTTGCTTCTTTATTTCACAATCTGGGGAAACGGCAGATACACTCATGGCCTTGAGATACTGTAAACAAAGAGGTGCCTTAATTGTCGGTATTACCAACACTGTCGGTAGTTCCATTTGCAGAGAATCACACTGCGGTGTCCACATTAATGCAGGACCCGAAATCGGTGTGGCTTCCACTAAAGCATACACAAGTCAGTTTATTTCATTGGTTATGTTCGCACTAGTCATGAGCGAAGATAGATTATCTCTTAGACAAAGAAGAGAAGAGATAATCGATGGCTTAAGAAATTTGCAGAGTCAAATCCGTGAAGTACTTAAATTGGACGACAAAGTGAAAAGACTCGCTGAAGACTTGTACAAAAAGAAATCTCTGCTTATTATGGGTCGTGGATTTAACTTCGCTACTTGTCTGGAGGGAGCTTTGAAAGTAAAAGAATTAACTTACATGCACAGTGAGGGTATTATGGCCGGCGAATTGAAGCATGGACCTCTGGCTCTTGTCGATGAAACCATGCCCGTAATGATGATCATGATGAGAGATCATGTTTATACTAAATGCATGAATGCTCTGCAACAGGTAAGAACAATGTGTACTTACGGTATATGTATAATAAATTATTTTGCGGAAAACTCTT **(1,989)**
MSTRG.20345.1	(1) Tetraspanin-2A [Anoplophora glabripennis] (99%;70%)/PREDICTED:CD9 antigen [Tribolium castaneum](99%;70%)	Higher	(1) Tetraspanin/Peripherin family (IPR018499)/Tetraspanin family (IPR000301) GO:0016021 integral component of membrane	(1)2-382 ALGAAIFALCLWLRFEEGIQEWLQKLDSEQFYIGVYVLIVASLIVMIVSFIGCISALQESTMALLVYIGTQVLSFIFGLSGSAVLLDNSARDSHFQPRIRESMRRLIMNAHHDQSRQTLAMIQENVS **(128)**	GGCTCTCGGTGCAGCAATCTTCGCTCTTTGCCTTTGGCTACGATTCGAGGAGGGCATTCAAGAATGGCTCCAGAAATTGGATTCAGAACAATTTTACATCGGAGTATATGTACTTATAGTCGCTTCACTGATCGTCATGATTGTGTCCTTTATAGGATGTATTAGTGCCCTGCAGGAGAGTACCATGGCCCTTTTAGTGTACATCGGCACCCAAGTGCTCAGTTTTATATTCGGTTTATCCGGTTCGGCGGTTCTTCTGGATAACAGCGCCAGAGATTCCCACTTCCAACCGAGGATCCGAGAGAGTATGCGACGTCTTATCATGAATGCTCATCACGACCAATCCAGACAAACACTAGCCATGATTCAGGAAAATGTAAGT **(382)**

MSTRG.26837.1	(1) Myrosinase 1-like [Leptinotarsa decemlineata](99%;60%)/glycoside hydrolase family 1 [Phyllotreta striolata] (99%;55%)	Higher	(1) Glycoside hydrolase superfamily (IPR017853)/Glycoside hydrolase family 1 (IPR001360)/Glycoside hydrolase family 1 active site (IPR018120) GO:0005975 carbohydrate metabolic process GO:0004553 hydrolase activity hydrolyzing O-glycosyl compounds	(1)288-1478 MGLTHYRFSISWSRLLPTGFISPVNLIAISYYQDLIRELEKYKIEPVVTIYHWDLPQMLQELGGWENSKIVDYFVDYADLVFASFPSVKHWITFNEPKQVCRSGYGKGNMAPGIARSGTADYMCSYHVIKAHAAAYHKYQDRYKSLGGKITMALDGVWSIPYWDNEEDRQAAERQLNFEFGLYAHPIFFGDWPQVVKDRVNYRSKMENYPESRLPEFTAEEMKYINRTADYVAFNFYNTKLIKDIDEASFDITSFDNDLRVKDDVDPRWTIAMDGNTIYPQGLRSYLKWISENYNSPEIIITENGIADNGTSLEDSERISYLSDYLNAVLDSIYEDKVNVTGYTMWSLLDNFEWTSGYSMRFGFYSVDFEDSNRTRAAKTSVDYYSQIIKNRKIPE* **(397)**	AATGGACGATGTACTGTGGACTAAGTATTTTCAACGAAGATTAAAATAATGTTTTTTTACATTCTAGCTTTGCTGACAATGACAGAACTTTTCCTGAAACATTTTCATTTGGAGCGGCAACAGCTGCGTTCCAAATAGAAGGAGCGTGGAACGAAAATGGGAAAGGAGAAAGCATCTGGGATCGTTTCATTCATACAAATCAATCAAGAGTCGTAGATGGTAGTAACGCAGATATTGCATGTGACTCGTATCATAAATATACAGAAGATGTGGCTTTGGCTGCGAAAATGGGTTTGACACATTACAGATTTTCCATTTCTTGGTCAAGATTATTGCCAACTGGTTTCATATCTCCAGTAAATCTCATAGCCATATCTTACTACCAAGATTTGATCCGTGAGCTCGAAAAGTATAAAATAGAACCTGTAGTGACGATTTACCACTGGGATTTGCCTCAAATGCTACAGGAACTAGGTGGTTGGGAAAATTCAAAAATCGTCGATTACTTCGTTGATTATGCAGATTTGGTATTTGCAAGTTTTCCATCTGTTAAACATTGGATTACATTTAATGAACCTAAACAGGTGTGTCGAAGTGGATATGGTAAAGGTAACATGGCTCCTGGTATAGCACGAAGTGGAACAGCTGACTACATGTGCAGCTATCACGTCATTAAAGCACATGCCGCTGCATATCACAAATATCAAGACCGCTATAAATCTCTTGGAGGAAAAATTACTATGGCTCTAGATGGCGTTTGGAGTATACCGTATTGGGATAATGAAGAAGATCGACAAGCCGCAGAGCGCCAGCTAAATTTTGAGTTTGGATTATATGCTCATCCAATCTTCTTTGGCGACTGGCCGCAAGTGGTAAAGGACAGAGTTAATTATCGTAGCAAAATGGAGAACTATCCTGAATCTCGTTTACCAGAGTTTACAGCCGAAGAAATGAAGTACATTAATAGAACTGCTGACTATGTTGCTTTTAATTTTTACAATACAAAGTTAATTAAAGATATAGATGAAGCTTCTTTTGATATTACCTCTTTTGATAACGACTTAAGAGTAAAAGATGATGTGGATCCTCGTTGGACTATTGCGATGGACGGTAATACAATATATCCCCAA

					GGGTTAAGATCATACCTGAAATGGATCTCAGAAAATTACAACAGTCCCGAAATTATAATTACTGAAAATGGCATAGCTGATAATGGTACTAGCCTAGAAGATAGTGAAAGAATATCATATTTATCGGACTACCTAAATGCTGTTTTGGATTCTATTTATGAAGATAAAGTTAATGTTACTGGTTACACAATGTGGAGTTTACTGGATAATTTTGAATGGACTTCAGGATACAGCATGCGTTTTGGATTTTACTCTGTAGATTTTGAAGACAGCAACCGCACAAGAGCAGCGAAAACATCTGTAGATTATTACAGTCAAATAATTAAAAATAGGAAAATTCCCGAATAGAAAAAATCAAATTTGAATCAGAGCTATTAATAGCTCTGTTAAGAGTACATGGCTTTTATTGTATGGTATTCTACAGTTCGTACAATATAGATACCGTTCCACGTCATCCGCGTAATGGCACGTGACGTCACATGATGCCAACACGAAATATTTAAGTCGTAGGTGTGTTCCTTTTTGGAATCGTTTAGGTGAGTACACTGGAATTACAGCCACAAGACATATTTCATTATATACGCATAGAAATAATATTGGAAGATTTCTATTAATGTAACTTGTAATTAGTTGTAATTTGTTTCATTTAATTTGTATAAGTGGAATACAAAGCGTTTTATAAAGCACACTTGTTCGGATTACACTCTAACTGCGATCGAACAGAGGTGACATGTTGGCACAAATTGGTAACATGTATTTTACAGTGGCGATATTGACACTTCAGATGTGTTTTTATTCTAGGCTATAAGTATTTGTTTTATTATATTTATTGTTTTTATTATTAACTTTAACGTAAGATTATAATTTAATTCTTGTTTTCTATTTTCAATGTTTTTATTTATTTACATTGAATATTAATTTGTTATGTTGTATAATCCACTTCGCAACAATTAGGAATGTGATATATTTTATTTAAAATGAATTCAAGAATTTTTTGTAATTGGGCAACAATGTTAATTTAGATCTCTGACCTAGATAATGACGTGCAACGGTATTTATATTGTACGGACTGTATTGATGTAAGTATTAATCTATTAGAAAACATTGTAACTTTTGTATTCTTTAATTAAAATTTATAGAGCACA

					CACTATTACACCAATTGTTGATTTTATATGTATTTTTTATTTCCTTGTTAGAAGGTCTTACATGTTTAACATTCTTACTACTTTCTGGCAGATCTTCTTTTACCAGAAGCTCATCTATTGCTTGTGCAATTGAATTTGCATCCAAAGCTTTCAGCTCAGCACATCCGAGGAATACTTCGTCGACTCCGTTAGATTTATTATCAAATTATCGCAACCCAACGGATAGTTGTTCAGTACAAACGATATATAGACCTGGATCCCGCGTATGAAAA **(2,547)**
MSTRG.79630.1	(1) Craniofacial development protein 2-like [Lasius niger] (97%;58%) (2) endonuclease-reverse transcriptase [Lasius niger](76%;49%) (3) Endonuclease-reverse transcriptase [Lasius niger] (97%;44%) (4) Voltage-dependent L-type calcium channel subunit alpha-1C-like [Centruroides sculpturatus](52%;68%)/endonuclease reverse transcriptase [Lasius niger] (52%;68%)	Higher	(1) Endonuclease/ exonuclease/phosphatase superfamily (IPR036691)/ SWR1-complex protein 5/Craniofacial development protein family (IPR027124) (2) Reverse transcriptase domain (IPR000477) (3) Reverse transcriptase domain (IPR000477) (4) No hit	(1)668-1042 MGDFNAKIGKGKCYPNVEPYGLGERNDRGDRLIEFCQEHNVIAANTFFKLPKRRLYTWKSPADKDNKIVRNQIDYILIKHRYRNPIQAVKAYPEADVSSDHSLSIARFQLQLKNTQKSRNDDKL* **(125)** (2)1571-1927 MKTNKFNNFRALVQLLLKIIHAKIHSKLELDNISDTQFGFRNVMGTREALIPFNVPRQRCLDVNRPLYICFIDYNKAFDKVKHERLMEILKTKNLDERDLRLKTPLLHSASNSKNYER* **(119)** (3)1917-2192 MKDETVGIRLNRVLVDNIRYADDTVIIADSLQDLQRLMSKKVKCSREYGLALNIQKTNFMKISKNNHKNNEILIIQDHQIERVKKYTYLGR* **(92)** (4)2315-2473 MLGIQCTLLWSGIMDVKCRDNETTKAFEMWTYRRIM	CCAGTCGTTAATATCCCAATCGACATGTTGTGGTGTAAAACTTAAACGTGCTATATGGTGTGCACTCGTCAACAGTACAGCAGTAGCAGGCATTCTGGCTCTGACTCAAATTTCCCTTAATCTGTTTCTAACCAAATTGGCACTCATTCGAACATTACGGGCTGTGGAAAGATCATTTCGCAGTTTTCTAGCTGTAAATGCCCTTCATCTGGGGTGTTCGTGCACCTAGGAAGTCCTGGAACTGGTCGTCTTGTGTATTCTCCACTTACTTTATACCTTCTTAAAGCACTTGAAGGGAAACTGAGGAATATACAGCAAGAGATGATGCGACTAGTTATCGATATATTAGGAATAAGCGATAAAAGATGGGTCAGCTATGGCAAACTCAATACAGGCAATGGACGAATCTATTACTCTGGAAGCAGCTACACCCAACACAGATATGGAGTTGCTATGATCCTCAGTGAAAAAAATAACAGTGTCCGAAAGACACTGTTACGATGTCCGAAAGAATTATAATGTTGCAGTTATTGACAACCCATGGAAAAATAAACCTAATCCAGATTTATGCGCCAAATGCTGACAAAAATTAAGAATAAATAGAAAACTTTTATAGCGAACTTCAAAAAACATAACACCTCACAGCATCTAGAGAAATAATAGTGATCATGGGTGATTTCAATGCAAAAATTGGCAAAGGAAAATGCTACCCTAATGTAGAACCATATGGGCTTGGCGAACGAAACGACAGAGGGGATCGACTAATAGAATTTTGCCAGGAGCATAATGTTATAGCCGCAAATACATTCTTTAAATTACCTAAGCGACGCCTTTATACATGGAAAT

				KVFWVDRVTNNEALRRI **(54)**	CGCCAGCTGACAAAGACAACAAAATCGTCAGAAATCAAATTGACTACATCCTAATAAAGCACAGATATCGAAACCCAATTCAAGCAGTAAAGGCATATCCAGAAGCAGACGTATCTTCTGATCACAGTCTCTCTATTGCTAGGTTTCAACTTCAACTAAAAAATACGCAAAAAAGCCGCAACGACGATAAACTTTAACATACAAAAACTAAAGTCAGAAGAAACGAAAGAAAATCTAAAACACGAAATCATCACAAATCTAGACAGAAACCCAGGAAATAATTGCAACGTAGAACAGCAGTGGCAATTCTTCAAAACCTCTATATTAGAGCCAAGTAAGAAAGTACTTATAACAGCCAAATGTAAGAAAGAAGAATGGATGACGGAGGAAATTCTAGAGTTGATGAATGAAAGAAGAAAAACCAAAACCATCAATAAGACCCGCTATAAACAGCTTTAAAACCAAATAAGAAGAAAAATTAGGGAGGCTAAAAAACCTACTTCTCAGAAAAATGTAAAGAAATAGAAGAACTGCAAAACAGATACGACAACTTCAACCTACATAAAAAAGTCAAAGAACTAGCCCGAATAGGAAATAGAAGAACCTTAAATATATTGCTCGACAAAAAATGGAAAGAGTACATCGAGGAACTATTTCATGACCAGAGAGAAGCTAATACATCCGTAGATAGCCAACAAATGAGAGGTTAGTCAGGCAATAGACTCTATGAAAACCAATAAATTCAATAATTTCAGAGCTCTTGTGCAATTACTACTAAAAATTATCCACGCCAAAATACACTCTAAACTGGAGCTAGATAATATTAGTGACACTCAATTTGGGTTCCGCAACGTTATGGGTACCAGAGAGGCATTAATCCCCTTCAACGTGCCGAGACAGAGATGTTTGGATGTTAACCGTCCTCTTTACATCTGTTTCATAGACTACAATAAAGCGTTTGATAAAGTAAAACATGAGCGACTCATGGAAATTCTGAAAACTAAAAACCTAGATGAAAGAGATTTAAGACTAAAAACACCTCTATTACATTCAGCAAGCAATAGTAAGAATTATGAAAGATGAAACAGTCGGCATAAGATTAAATAGAGTCTTAGTTGACAACATCAGATAT

					GCAGATGATACGGTAATAATAGCCGATAGTTTACAAGACCTGCAAAGACTCATGAGTAAAAAAGTAAAGTGTAGTAGGGAGTACGGACTCGCTCTCAATATCCAAAAGACGAATTTTATGAAAATTAGTAAAAACAACCATAAAAATAATGAAATTTTGATAATACAGGACCACCAGATCGAAAGAGTAAAAAAGTACACTTATCTAGGAAGATAAGATAATGACTACACTGCAGAAATCAAAGTCAGATTGGAAAAAGCACGTTCTAATTTTATGAAAATGAAAAAGGTTCTATGTAGCATAGATTTAACATTAGCTCTTAAAGTACGCCTAACAAAATGTTAGGTATACAGTGTACTCTACTATGGAGTGGAATCATGGACGTTAAATGTAGAGACAATGAGACGACTAAAGCCTTTGAAATGTGGACCTATAGAAGAATTATGAAGGTGTTCTGGGTAGATAGAGTTACGAACAACGAAGCACTGAGAAGAATA **(2,473)**
MSTRG.91250.2	(1) Protein Skeletor, isoform B/C [Anoplophora glabripennis] (95%;80%)	Higher	(1) DM13 domain (IPR019545)	(1)178-507 MRSVEVLAIIGLVSSIHSGLCAKPIEPYYGRKIGNLVEFAHGIKGTAYAVDESTIFIKGFYYDGTGPDAFFWIGNSPRPSPEGTIIPYPEDYNGRDPPVLRAYNNTDIIL **(111)**	TTCCAGAGCAGATAAGAGAGGATTCCCACCGGACGTTGGAAAAAGTCGAATCATAAACACACCTAAAATTTCATTCGTTGTTCGTGTGTGTTATAAGATTGACCAAAAACCAATATTGAAGTTGAAGACAAGTAACTAGTTGAGCTAAGTGATCGTCTACACCGTTTTAATGCCACGATGAGAAGTGTTGAGGTCCTTGCCATTATTGGATTGGTGTCTTCAATTCACTCTGGATTATGTGCCAAACCCATAGAACCTTACTACGGAAGAAAAATAGGAAACTTAGTCGAATTCGCCCACGGTATAAAAGGGACTGCATACGCGGTAGATGAGAGTACGATATTCATCAAAGGATTTTATTATGACGGTACTGGTCCAGACGCTTTCTTCTGGATCGGCAATTCTCCAAGGCCTAGTCCAGAGGGAACAATCATACCATATCCGGAAGACTACAATGGCAGGGATCCACCGGTATTACGGGCTTACAACAACACTGACATAATCCTC **(507)**
MSTRG.35370.1	(1) Zinc finger CCHC domain-containing protein 4	Lower	(1) Zinc finger, CTCHY-type	(1)109-1458 MTKGGVQVIEKDIRNHPCCPHGPTILFSRKIEDETRR	GTTATGTGTGTTTTGTTTTTAGGTTAGCTGCCATCATGTTCTGAAAGGAATATTTTAAATTTTAACAAATAATTGTAACTATCATTAT

	[Leptinotarsa decemlineata] (94%;63%)/ Zinc finger CCHC domain-containing protein 4 [Anoplophora glabripennis] (95%;60%)		superfamily (IPR037275)/Zinc finger GRF-type domain (IPR010666)/Zinc finger CTCHY-type domain (IPR017921)/Zinc finger CCHC-type domain (IPR001878)/DNA methylase, N-6 adenine-specific conserved site (IPR002052) GO:0032259 methylation GO:0003676 nucleic acid binding GO:0008168 methyltransferase activity GO:0008270 zinc ion binding	YFACSACRDRKQCNFLLWEDEKSKNKETFWATENQKFVKGINHRKMFLNLNEISSQDVSKRSFCSTCNMFCRDDEKHSTHKVVKGLTDLQLRHPSTILPALDDSKREAQYHFSETSVTVIMDIFKELGYRNVICIGTPRIHEYIQSNCDQMSSILLDIDKRFHNFFGPLQFCWYNMFNNHFFFKEAKDVFIDFLQSDGGKDMVIITDPPFGGRTELISATFKSINNQYQKLNQTQNTLPMFWIYPYYMEPQILNSLPDFSMLDFKVEYDNHQSFQNNSGGRKQGSPIRIFTNVKPSLIKLPSSDYKHCKICKRWVAKENKHCAACNSCTSKNGVTYVHCEECNRCVKPTWKHCKKCGRCAQVQHSCAKIEFVKECFNCKKSGHKKADCPLLTPTQGQKRKKSAEANRKKKKK* **(450)**	ATCTTATTAAAAACTTTAACATGACTAAAGGAGGTGTACAAGTTATCGAAAAAGATATAAGGAATCATCCCTGCTGTCCACATGGGCCTACAATACTGTTTTCAAGAAAAATTGAAGATGAAACCAGGAGATACTTTGCTTGTTCTGCTTGCAGAGATAGAAAACAGTGTAATTTTCTTCTTTGGGAGGACGAAAAGTCGAAAAATAAAGAAACCTTTTGGGCAACAGAAAACCAAAAATTTGTGAAAGGTATAAATCATCGAAAAATGTTTCTTAATCTGAATGAAATATCTTCGCAGGATGTTTCTAAAAGGTCGTTTTGTAGTACCTGTAACATGTTCTGTAGGGATGATGAAAAACACTCCACTCACAAAGTTGTTAAAGGTTTGACTGATTTACAACTGAGACATCCCTCTACCATTTTGCCAGCCTTGGATGATTCGAAACGAGAAGCACAGTATCATTTTTCAGAAACGTCAGTAACTGTTATTATGGATATATTTAAAGAACTTGGATATAGGAATGTTATATGTATTGGAACTCCTAGAATTCACGAGTACATTCAAAGTAATTGTGATCAAATGTCTAGTATTTTGCTAGATATAGATAAAAGGTTTCACAATTTTTTTGGTCCTCTTCAATTTTGTTGGTATAACATGTTCAACAACCATTTTTTCTTCAAAGAAGCCAAAGATGTGTTTATTGATTTTCTTCAGTCGGATGGTGGTAAAGATATGGTAATAATAACAGACCCACCATTTGGGGGAAGAACAGAGTTGATTTCAGCAACATTTAAAAGCATAAATAATCAATATCAGAAGCTTAACCAAACCCAAAATACTCTGCCGATGTTCTGGATATATCCGTACTATATGGAACCACAAATTTTAAATTCACTACCAGATTTTTCTATGCTGGATTTTAAGGTGGAATATGACAACCATCAATCTTTTCAAAATAATTCCGGAGGAAGAAAACAAGGGTCCCCGATCAGAATTTTTACTAATGTCAAACCCAGTTTGATAAAATTACCTTCTTCAGACTATAAACATTGTAAAATATGTAAAAGATGGGTGGCAAAAGAAAATAAACATTGTGCTGCATGCAACTCTTGTACTTCAAAAAATGGAGTTACATATGTT

					CACTGTGAGGAGTGTAATAGATGTGTGAAACCCACATGGAAACATTGTAAAAAATGTGGCAGATGTGCCCAAGTTCAACATAGCTGTGCAAAAATTGAGTTTGTTAAGGAATGTTTTAATTGTAAGAAATCAGGCCATAAGAAAGCTGATTGTCCACTGCTAACTCCAACACAAGGCCAGAAGAGGAAAAAATCAGCTGAAGCAAATCGCAAAAAGAAGAAAAAGTGATAATTATTTGTTATTTTAAATAATATACTTTATTATAAATTTTCAATAAGAA **(1,510)**
MSTRG.40734.1	(1) Beta ureidopropionase [Leptinotarsa decemlineata] (98%;75%)/ Beta ureidopropionase [Anoplophora glabripennis] (99%;76%)	Lower	(1) Carbon-nitrogen hydrolase superfamily (IPR036526)/Carbon-nitrogen hydrolase domain (IPR003010) GO:0006807 nitrogen compound metabolic process	(1)158-1312 MSAIELDSIESVLKTLSIEDYEKVCGLLYGKGVSKITLKEEVLHLAEKYDIEVAIEKFISQEEQLRSPRNTRVGLFQHKTPLPTWSRIKEMRDAMFKLASEALEIAYKGGVNVFCFQEAWNMPFAFCTREKSPWCEYAEEAEHGPTTEFLKGLAKRYNMVILSSILERDSVHGDTIWNTCVVIDNHGEYLGKHRKNHIPRVGDFNESTYYFEGNTGHPVFKTEFGKIAINICYGRHHPLNWLGFALNGAEIVFNPSATIGGLSEPLWGVEARNAAIANSYYTCAINRVGTEVFQNEFTSGNGQPAHKDFGHFYGSSYVTAPNGSRTHGLSRTRNGLLIAELDLNLCRQVRDVWGFQMTQRLDMYADLLKEAIKPDFKPQLIEKS* **(385)**	TAAATTGACGTTTTATTATCATTTAACACTGAACGCAAACAAGGTGAAGTTATTTATACATTATACGAGTACCACAGTATTAAAAACAAACGAGTACTATCTACTAGAACGCTAGAAAGTTATTGTAAACGTACATTTACATTTTTTATTGTTAAACATGTCAGCAATAGAATTAGATAGTATAGAGAGTGTGTTAAAAACGCTTTCCATTGAAGATTATGAAAAAGTGTGTGGTTTATTATATGGGAAAGGAGTAAGCAAAATTACTTTAAAAGAGGAGGTACTTCATCTTGCTGAGAAGTACGACATAGAAGTTGCAATTGAAAAATTCATTTCCCAAGAAGAACAACTCCGTTCTCCTAGAAATACCCGTGTTGGTCTTTTCCAGCACAAGACGCCTCTTCCAACATGGAGTCGTATCAAAGAAATGAGGGACGCTATGTTCAAACTAGCCTCAGAAGCTTTGGAGATTGCATACAAAGGAGGCGTTAACGTATTTTGTTTCCAGGAAGCATGGAATATGCCGTTTGCCTTTTGTACGAGGGAAAAATCACCATGGTGTGAATATGCAGAGGAAGCAGAACATGGACCAACTACAGAATTTTTGAAAGGGCTTGCCAAGCGGTATAATATGGTGATCCTTTCGTCAATCTTGGAAAGGGATTCTGTACATGGGGACACAATTTGGAATACCTGTGTTGTGATTGATAATCATGGTGAGTATCTTGGGAAACATAGGAAGAACCATATCCCAAGAGTAGGCGATTTCAACGAGTCGACATATTACTTTGAAGGAAATACCGGACATCCTGTGTT

					CAAGACTGAGTTTGGAAAAATTGCCATTAACATTTGTTATGGAAGACATCATCCACTGAATTGGCTAGGGTTTGCATTGAACGGTGCGGAAATTGTGTTTAATCCTTCAGCTACTATTGGTGGTTTAAGTGAACCTTTGTGGGGCGTAGAAGCAAGAAATGCAGCAATAGCAAATTCTTATTATACTTGTGCTATTAACAGAGTTGGGACAGAAGTTTTTCAAAATGAGTTCACGTCTGGAAATGGCCAACCAGCTCATAAGGATTTTGGACATTTTTATGGGTCCAGTTATGTAACCGCTCCAAATGGTTCTAGAACACATGGTTTATCACGAACAAGAAATGGTTTGCTTATTGCTGAACTAGACCTTAATCTATGTCGCCAAGTAAGAGACGTATGGGGATTCCAAATGACTCAAAGGCTGGATATGTATGCAGATCTACTGAAAGAAGCTATTAAGCCCGACTTTAAACCACAACTCATAGAGAAATCATAACTGCTCTAAAACTAAAGTATTTTTTGCACGAAAAATGTTTTTTTGTTTATTACATTTTATTTAATTTGATATTAAAAATGTGAGATCTTATTTTTTGATATTAATGTATTATTTTCAATATGATTTTAGATAGAGAAACAGAAAATTCACTATATAGGAACGCAGAATCCTTGGTGACCTATCTATTGCCTGAGCGTTTTACAAATTTATAAAGCATACAGGCCGATAAATAGTAGTGATGTTGATTATAGTTACTTTCGAGTATTCGTTACAAATCGTTACTTTTGTATAAAGTAATCATTTACAGTATTCGTTACTTTGATTACTATGATTACTTTTGTATTTGAGTACCGGTAATCATATCGAGAATCGTATTTCTCAGTAGGTAGGTATTTTGTATAAGTATTCCGATATTATTATAACAACGACCTTCACCGATATGTTTAAGGGATAAACATGATTTGATTACTATGATTACTTTTGTTACTTTTGCATTTGAGTACTGGTAATCATATCGA **(1,830)**
MSTRG.55035.1	(1) No hit	Lower	(1) No hit	(1)244-20 LLTHLPRVGVICCPRAVAIGILSILWILPCWHLYKTFSLFLKGFDLCIFWLAHHVLVT	TTAAAAAGCCCCTATAGGGCTACAAACATAGAAACAAAACGTTTTCGCTCTGTAACAAGAGCATCATCAGTGTTACAAGAACATGGTGAGCCAACCAAAAAATACAAAGGTC

				LMMLLLQSENVLFLCL* **(75)**	AAAGCCTTTCAAAAACAGACTAAAAGTCTTATATAGATGCCAACATGGCAAAATCCAAAGGATGGATAAAATTCCTATGGCTACGGCCCTAGGGCAACATATGACTCCCACACGTGGTAAGTGGGTCAATAGG **(245)**
MSTRG.55986.1	(1) No hit (2) No hit (3) No hit	Higher	(1) No hit (2) No hit (3) No hit	(1)1-186 RKWHICFVRQNRLKLSEQRLNSHAKIRLLFITCHNSCHLTYSTCSTHLNAHLVINSGLIFA* **(62)** (2)795-965 MNHFYCCTYLYVFKLHKYTLSLKYYLTYIYFYLIKLLNCLFVKFLSDENRSGLAGLP **(58)** (3)819-670 MYNSKNDSCTRRQAERPSQLIGKNRHLSVFLFRYLCQTVLALFKIDVTI* **(50)**	CGAAAATGGCACATTTGTTTTGTCCGACAGAACAGACTTAAACTCTCCGAACAGAGATTAAACTCTCATGCAAAAATCAGACTGCTATTTATCACCTGTCATAATTCCTGTCATTTGACATATTCTACATGTTCCACGCATTTAAACGCCCATTTGGTGATAAATAGCGGTCTGATTTTTGCATGAGAGTTTAATCTCTGTTCGGAGAGTTTATGTCTGTTCTGTCGGACAAAACAAATGTGCCATTTTCGTGTTCTGACCGTTCCAGATTTTTTACCTGTTCCACAATTAAAACTGCCCCTGTTCCAGTGTTCTCATATATCAAAGTTTATCCGACTAGACACCCTTAAGCTATTAACAAATTTTTAGCTTGCTATTAATCAACTTTTTTTTCATACGCGGGATCCAGATCTATGGTATCATAATATCATATTATGATGCTGCAATAAATTTATTTTAAAGATTCGCCTTTATCAATCCTACCTAATGTTTCTAGTTTCTTTTCCATTGTCACAACATTTTTACGTTTTGTTAACATTACAGTTTTGTTACCATTACGTAGACAAAAATCAGGCAAACACAATCTGAAGCACGATTACAGAACGGAAGTGATTAAAACAATGTTGTTATTTAAGAACAGACTAAGGCCATTGTTTTAAAAAAGAATTTTTAAATAGTCACGTCTATTTTAAACAATGCTAAGACAGTTTGACATAAATAACGGAAAAGGAATACAGACAGGTGCCTGTTCTTTCCGATAAGCTGAGACGGTCGCTCTGCCTGCCGCCGTGTGCATGAATCATTTTTACTGTTGTACATACTTATATGTGTTCAAATTACACAAATACACATTATCTCTCAAATATTATTTGACCTACATATATTTTTATTTGATAAAATTGTTAAATTGTTTATTTGTTAAATTTTTGTCTGATGAAAATCGGTCCGGGTTAGCCGGACTTCCGGG **(967)**

MSTRG.76395.1	(1) Uncharacterized protein LOC111032164 [Myzus persicae] (99%;58%)	Higher	(1) No hit	(1)2-1384 QELKELEVNGLEIQINEISNLRVHFVLGLVLGDNLGLNSFLDFSKSFSANFYCRICRVEKKDCQKFCIENTEMIRTISNYNSDLASSSENRGIICNSLLNDIPSFHVVHNYYVDIMHDIFEGVCHYCISHAIIYFIKMKYFDLKILNSRRENFEYGPKEIGNMPGKIELHHLNSKKLKMSAREMMTFISYFPLMVGDLIPDDDEVWIFLINLIEIIDILLCFEVANPDIILLQNKIKKLNSDYTVLFNDTLKPKFHNLTHYPNIIRQSGPLRKLWCFKYESNHIHSKIYCHCINSRKNICITLSKKYQLKFAYQILKNEEPTTTLSANSRHKRQSNFKNIIYEQLNIVDKSSVQFYSQLRYKGTQFKCGDYISVLNNDIHIYKIVEIILLNKDEILFFSQKLINTNYRSHFLAHEVDLSNLGQLSLISVNELIGPPVDLIRTAKGINMIKVKEHYSTIAF* **(461)**	ACAAGAATTAAAAGAGCTAGAGGTCAATGGGCTAGAGATTCAAATTAATGAAATTTCGAATTTACGTGTTCATTTTGTATTAGGTTTAGTATTGGGTGATAATTTGGGCCTAAACTCATTTTTAGATTTTTCCAAATCATTTTTCAGCAAATTTTTATTGTAGAATATGTAGAGTAGAAAAAAAAGACTGCCAAAAGTTTTGTATTGAAAATACCGAAATGATACGAACAATTTCTAACTACAATTCAGACTTAGCCAGTTCATCCGAGAATAGAGGAATAATTTGTAACTCTCTACTTAACGATATTCCATCTTTTCATGTTGTTCATAATTACTACGTTGATATAATGCATGATATATTCGAAGGTGTATGCCACTACTGTATTAGTCATGCAATTATTTACTTTATTAAAATGAAGTATTTTGATTTAAAAATTTTAAATTCAAGAAGAGAGAATTTTGAATATGGACCTAAAGAAATTGGTAATATGCCTGGAAAAATTGAATTACATCACCTTAATAGTAAAAAATTAAAAATGTCTGCTAGAGAGATGATGACATTTATAAGTTACTTTCCTCTTATGGTAGGAGATTTGATTCCAGATGATGATGAAGTTTGGATCTTTCTCATTAATTTAATAGAAATTATAGATATCTTACTATGTTTTGAAGTAGCAAATCCGGATATTATTTTATTACAAAATAAAATTAAAAAACTTAACAGCGATTATACTGTACTATTTAACGACACGCTTAAACCCAAATTTCATAATTTGACTCACTATCCAAATATTATTCGGCAATCTGGACCTCTTAGAAAATTATGGTGTTTTAAATACGAATCTAATCATATCCATTCTAAAATTTACTGTCACTGTATTAATTCTAGAAAAAATATATGTATTACCTTGTCCAAAAAATATCAGTTAAAATTTGCCTACCAAATTTTAAAAAACGAAGAACCCACCACTACATTGAGTGCGAATAGTAGACATAAAAGACAGAGTAATTTCAAAAATATTATTTATGAGCAACTAAATATCGTTGATAAAAGTTCTGTTCAATTTTATTCTCAATTAAGATACAAAGGAACCCAGTTTAAATGTGGTGATTATATATCTGTATTAAACAATGATATTCATATCTATAAAATT

					GTAGAAATTATTTTACTGAATAAAGATGAAATATTATTCTTTTCACAAAAATTAATAAATACAAACTATAGGTCCCATTTTCTTGCCCATGAAGTGGATTTAAGTAATTTGGGCCAATTATCACTGATTTCAGTTAATGAATTAATAGGACCACCAGTAGATTTAATAAGAACAGCGAAAGGCATTAACATGATAAAAGTAAAAGAACATTATTCTACAATAGCATTCTAATAAGGCTTTTCATTCCGAGTCATTAGTTTCGAGCTTCTGTCATGTGTCACATAATATTAATATATCTACGTCATACGTTATTGGCATATACCAATGATGCAAACCAAAGACGTGTGACGTAGATATATTAATATCATGTGACACATGACAGAAGCTCGAAACTAATGACTCGGAATGAAAAGCCTTATTAGAATGCCCACGAATATACGACCCTCTTGGATTATCGCGACAACGAATATTTTACTGTGCAAAATATGAAGAACGAAAGTAAATTGCAAATTATATTCTTGTTTATTGGAGTAATTATTAGAGCAAAGTACTTTCGTACTTCTTAAGTTGCACACTAAAATATTCGTTGTCGCGATAATCCAAAACAGTCGTATATTCGTGGAACCCACCATACATATTTTGCAACGAGCATTTAATGACGGTAATTACCATGCGATTGACGTATACGATCACGAGCTGCGATGCGATGAGTGTCGTATGAAAGACGAGCATCATAATAACAATTAAAACACTGAAAACATTTGTTTTCAATAGTTCCTCAAAATTTATTATTCAACTATGTCACTACAGCTGTTTCTGCAAAGTGCCTTTATATAAAATAAATCACTTGAGAAAGGCACTCAAAATAATAAATTTTGAGGAAGTATTGAAAACAAAAGTTTTTAGTGTTTAATTGTCAGATAAAATGAACTTCTACCAAGTAACCGTCGAACCCATTAATTAATTAAATGTAAGTTGTATACATGATTTTTTTATAATCATTCACAAAAAAAAATAAATCCAAATTTATTTATTTTGTAACACAAAATTAAGTACTTACATATAAGCTTAAGGCAGGTTTCACCAACAACATATAAATCGGTGGATAGTTATTGGTCGAATAAAATTTATTAGTCGAGTATATATTTA

					ATTTCGTGTCAACAACTATTTGTCATTTGTATTCCACAATTAGTTGTTCGTCGACGAATAAGTCCTATAAATATATAATGATTTTCCACCAGTACTCGTTGGTATAATAAAAACAAGCGCATTGCATTCCACTGTTGTAATCGTATGAGATATACATAACCTATATTTTGTTATTTGTTGATATTTATCACAATACATAATAGAAAATATTTGTTTGATTTGTTTATTGAAAATAGACAAAAAAACGTGAAAAGATAATTAATTTTTATGTTTATGTTTTATAGTCTGCATGTTATATACAATAATCATTATTGGAATAAATTTGAGGCGACGTAACTTTTCTTACGTTGTTTTTACAGACATTTTCTTAAAATTATTTAATTTTGGAACTGTTAGTTTATTTAAATATTAAATATTCTTTGTCTAAATTATAAACTGTCCAAATGAATGAATTTGACTTGGCATTGATCGTTGCGTATGTGCTACCGACACGACGTTACAGAACGTCATCTCGCGATTTTATTAGTTAAAATCTGTATCACCATGAATCTCATTATACATGACAGGTAGCCAAATCATAATTGATAATATATTAAAGTATGAGAGTAGAAAAAACAACCTAATAATATAATTTAACCAATATTTCAATAAAATCATAACATTTTTAAACGTTTTGAGCTAGCTAGAACATCATGTATCAAAATAATGACGGAGAAACAGATGCCACTTACCAAATCGGTCAGAATTTGGCGAATTTTCTTGGCAATGAATATATTATGCCTCCAGAGATGAAAAATAATATAGCGCAACAAAACGAAACTGTACAACAACTCGAGTCAATGCTGACAGATTTATCCAAATGCCATACAAATGATTCAAACCAAAATCTACATGACTACGAGATTGAACATCAAAGTGAATCTGAAGTAAGCGACATTGCTGGCACCAATAGTAACAAGAATTCCCAAGATGAAAATCTCGAATCAATTGAACTCAGAAATTTATTAAAATTATGGAATATGGAAAGTCTGACAGATCATTTAAT **(3,346)**
MSTRG.1810.1	(1) Uncharacterized protein LOC111055027	Higher	(1) No hit	(1)527-703 MLLVATNKLNYYYYYVSLWTSLTSNEEVLQRIGKER	CGCGAAGCAAAATAGCAAAGTAAACAAAACAGTGTAACATGTGTAAAAAATTTATGGGGAGGCTAAGCCTCCCTTGCCTCCTCT

	[Nilaparvata lugens](64%;55%)			ELSNTAKVRKILYLNRPQTDKQ* **(59)**	GACTAGCCGCCACTGCTCGATACTCTTTCCCCTCCTCCAATACAGCTGTTTGATTATAATAAAGTTCGGTAATATTTCTAAGAATAAATGTTTAAATTGTGAAAATTATTGTAAAAATGAATAAAACACCTTCAAAAAGTCATGATAATTTTCATAGAAAACGAAATCTGCCAGAAGAATCCCACTGGAAATGTGTCGAAAATAATTTCTTGAATTTTATGAGAGATTTTCTTAGGTCCATAAACAAAATTTAACAGTAACTGAATTAGTAAGAAGAATTGCCCAAATTTGAAGACAGATGATCAAAAAAGACTATATTTGATTCCTTTTTGTAAACTTTAAGATAAATTAATGTTATTTAATATAATCAAAATTTAACCCTCACGCACAAGTTGTAGTCTATGTGACAAACAACTTCAGTGAGAAATTGGGTTTATTTATTATGTTATTAGTTGCTACAAATAAACTCAATTATTATTATTATTATGTTTCTCTTTGGACATCGCTTACTTCAAACGAAGAAGTGCTGCAGAGAATAGGTAAAGAACGAGAACTTTCCAACACAGCGAAAGTTAGAAAAATATTATACCTAAATAGGCCACAAACTGATAAACAGTAAGTACCAATATGCTTAACTAATAGTGAAAGGAAAAATCGAGGGAAAAAGAGTACTAGGAAGGAAAAGACTATCGTGGATCAGAGACATCGGACAATGGACAGGGCAAAATTTTGAACAGATAATACGAACGGCTGAAGACAGACAATAATTTGCAATTGTAGTAGCCAACCTCCATTGAAGAGAGGGCACTTTAAGAAGAAAAAGAAGTAATTCTCATGCCCTTCGTATCTAAATTCTTTCGTTGGAGTAATTGTATGAGGTGACACAGATGTACAGTGGTTAATTTATATCCATGCACCTTTGAACCAACACCTTATGGCACATAAGGTTCTAACGAATAATTTTTAAGAATAAGCTTTAGACGATTATAAAAAGCTTAGTCAGTGATATATCTATGGTAAAATTTTTAAAGAAATATAATTAGCAATGTTGGAGTTTAACAACATATTATTAAATATCTACATATTCTCTGTTGAAGTACAACGGCCTC **(1,193)**

MSTRG.22922.1	(1) No hit	Lower	(1) No hit	(1)225-1 LMDWFAASLSNTLYRKSMMTFSVNIGTEEEDNCSSFTMRKSATALIQIKRWCHFALNDTLSMLIYTVSVKYGTNS **(76)**	AGAATTTGTTCCATACTTTACGGACACAGTGTATATTAGCATAGAGAGAGTGTCATTCAGAGCGAAGTGACACCATCTTTTTATTTGGATTAGTGCTGTTGCACTCTTACGCATAGTAAAGCTGCTACAGTTGTCCTCCTCTTCCGTGCCTATATTCACACTGAATGTCATCATAGATTTTCGATACAATGTGTTAGAAAGAGATGCAGCAAACCAGTCCATGAGAT **(227)**
MSTRG.36906.4	(1) MFS-type transporter SCLC18B1 [Anoplophora glabripennis] (96%;67%)	Higher	(1) GroES-like superfamily (IPR011032)/NAD(P)-binding domain superfamily (IPR036291)/Polyketide synthase enoylreductase domain (IPR020843)/Alcohol dehydrogenase N-terminal domain (IPR013154)/Alcohol dehydrogenase C-terminal domain (IPR013149)/Alcohol dehydrogenase, zinc-type, conserved site (IPR002328) GO:0055114 oxidation-	(1)155-1795 MDKETSDTFARNFTSDNIDLSLNTSNSYTFTGRIVLRTLQRSKSMSCVSPDSFSSGEVRRMRERLLRTNAHVTPSSIMSLSRYQKMTLLSLALVDFMSFCSMSIMAPFFPREAFEKGMSDTMTGFVFSFYALVMFISSPIFGKILPVFGAKFLFILGIFVAGLCNILFGLLEYISNYTLFTTFCILIRGFEALGASAFSTASYIFVVNSFPNNIGSVIGILETFVGLGMSTGPAVGGILYSLGGFSVPFYVLGVAMVFIGLINLLLLPNVEDCDSMTNKTTSMMKLIKIPAVIVTGLVVTVVSSIWAFLEPTLEPHLRDFNLSPEKIGLIFLLFSALYGISSPAWGWVADRINHPWLMMVAGLFMCTLGLLLLGPCPYIPVLSQNLWLDLVALSILGISVALTLMPTFLRILTSATKAGYSDSLVTYSVVAGVWSCMYSLGEVLGPALGGFLMGRYGFPMASTVMATVIFSLAIFTTIFFILNSTVCKEAERKSDSGISESWRSSNLSMSNEHTPLLLSTIDGGLQSSYKKQYYTQNARNCDAVSE* **(547)**	CGAGAGATAAACCATTAGAGATAACTTCTATTTACAAGGATTCTAGAATCATTAACCATATTATTAGTTTTTGACTTCATCCTGCCTGTAAGTGAATGTGTGCCGTAGTAATTAAATCTATATCGTCGATCTTGATGAAAAACTTTAAAGAACAATGGATAAAGAAACAAGTGACACGTTTGCCAGAAACTTTACATCTGATAATATAGATCTTAGTTTAAATACTTCTAATAGTTATACATTTACTGGCCGAATAGTATTGAGAACTTTGCAAAGGAGTAAGTCTATGTCATGTGTTTCGCCAGATTCATTTTCCTCTGGGGAAGTAAGAAGAATGAGAGAGCGGTTATTAAGGACAAATGCACACGTAACACCCTCAAGTATAATGAGTTTAAGTAGATACCAAAAGATGACATTGTTATCACTAGCTTTGGTCGATTTTATGAGTTTCTGTTCAATGTCGATTATGGCTCCCTTTTTCCCAAGGGAGGCGTTTGAGAAAGGAATGTCGGATACAATGACTGGTTTTGTATTCAGTTTCTATGCTCTAGTCATGTTTATATCATCTCCAATATTTGGAAAAATTCTACCAGTATTTGGAGCAAAGTTTTTATTTATACTTGGTATATTTGTGGCAGGATTATGTAATATTTTATTTGGGCTTTTGGAGTACATTAGCAACTATACGCTTTTTACGACATTTTGTATACTGATACGAGGATTTGAAGCGTTGGGTGCAAGCGCTTTTTCGACCGCTAGTTATATTTTCGTAGTTAATTCTTTTCCAAATAACATTGGATCTGTTATAGGCATTTTAGAAACTTTCGTAGGACTAGGAATGAGTACTGGTCCTGCAGTAGGCGGCATACTATATTCGCTTGGTG

			reduction process GO:0008270 zinc ion binding GO:0016491 oxireductase activity		GATTTAGTGTGCCATTTTACGTTTTGGGGGTAGCAATGGTTTTCATAGGTTTGATCAACCTATTGCTGTTACCAAACGTTGAAGACTGTGATAGTATGACAAATAAAACCACATCTATGATGAAACTAATTAAAATTCCAGCTGTGATTGTGACTGGTCTTGTTGTTACTGTTGTATCCAGCATTTGGGCGTTTTTGGAACCAACTTTAGAACCACATTTAAGAGATTTTAACCTGAGTCCAGAGAAAATCGGTCTCATATTTCTATTATTTTCTGCTTTATACGGAATTTCCAGTCCCGCATGGGGTTGGGTAGCTGATAGAATAAATCACCCTTGGCTTATGATGGTCGCTGGATTGTTTATGTGTACATTAGGATTATTGTTACTAGGGCCTTGTCCATATATTCCTGTCTTATCACAAAATTTGTGGTTGGATCTGGTTGCTTTATCCATCCTGGGAATATCTGTTGCCTTAACCTTGATGCCAACATTTTTAAGAATCTTAACCTCTGCCACAAAGGCAGGCTATTCAGACTCTCTGGTAACTTACAGCGTAGTAGCTGGTGTTTGGTCATGTATGTATTCACTAGGAGAAGTTCTAGGACCAGCCCTTGGTGGCTTTTTGATGGGTCGCTACGGATTTCCAATGGCGTCCACTGTAATGGCCACTGTTATATTTTCATTAGCAATATTCACCACCATATTTTTCATTTTAAATTCGACAGTATGTAAGGAAGCAGAAAGAAAGTCCGATAGTGGAATAAGCGAATCGTGGAGAAGTTCTAATTTATCTATGTCCAATGAGCATACACCACTTCTTTTGTCAACCATAGATGGAGGTCTTCAGTCATCTTATAAAAAACAGTATTATACTCAAAACGCAAGGAACTGTGATGCAGTAAGTGAATGAGTTCGACTACTACCATACTTTAATGGAACCGAAAACATCTGTCTCAGTTTCCAAAACTGGAAAGGGGTCCTCTGAAATTTAATGTTAAATTATTACCACCAGTTAAAAATAAATATAATCTTATTTTGTAGCTGACTAAA **(1,935)**
MSTRG.41888.1	(1)	Lower	(1)	(1)156-1232	GACAAGTTTTGCCTACCACCTTTAAAATTCTTATCGAAAATGAATAAACAATACTACG

	Sorbitol dehydrogenase [Anoplophora glabripennis] (98%;78%)		GroES-like superfamily (IPR011032)/NAD(P)-binding domain superfamily (IPR036291)/Polyketide synthase, enoylreductase domain (IPR020843)/Alcohol dehydrogenase, N-terminal domain (IPR013154)/Alcohol dehydrogenase, C-terminal domain (IPR013149)/Alcohol dehydrogenase, zinc-type conserved site (IPR002328) GO:0055114 oxidation-reduction process GO:0008270 zinc ion binding GO:0016491 oxidoreductase activity	MASTKDNLSAVLYGINDLRLEQRPIPVPKDNQVLLQMEVVGICGSDVHYLVSGRCGPFVVKDPMVIGHEASGTVVQVGKNVKNLKPGDRVAIEPGVPCRTCHHCKTGAYHLCPDIFFCATPPDDGNLSRYYVHDADFCWKLPDNMDLEEGALMEPLSVGVHACKRAEIKVGDVCLITGAGPIGLVTLLSAKAMGASKVVITDILDVKLEMAKQLGADYTIKIEKGMSEEDIVKRVIQLLGQEPNKSMDCTGVEQCVRVCVSATGVNGCVVLVGLGKIEMTLPLTNALIKEVDVRGTFRYVNDYPTSIELVRSGRVNVKPLVTHHYKLEDSVKAFHTAKTQEGNPVKILIHANPNWKPS* **(359)**	TCGTCGTATTTCATTCTATATAAGCTGAAACGACAGTCAAGAACAAACACATTGTCGTGGTTTGGTCTGTGAAACGGTCAGAAACGCAAAACAAAATATGGCGTCAACTAAGGACAACTTGAGTGCTGTTCTCTATGGGATCAATGACCTAAGATTGGAACAAAGACCAATTCCAGTTCCAAAAGATAACCAGGTCCTTCTTCAGATGGAAGTAGTTGGAATTTGCGGTTCTGACGTTCATTACCTAGTTAGTGGAAGATGTGGTCCATTTGTTGTCAAAGACCCCATGGTAATTGGTCATGAAGCTTCAGGAACAGTTGTGCAAGTTGGAAAAAATGTTAAGAATCTTAAACCAGGTGACAGAGTAGCCATCGAACCTGGTGTACCATGCCGTACCTGCCATCACTGTAAAACTGGTGCTTATCATCTCTGCCCCGATATCTTCTTCTGTGCGACTCCTCCTGATGATGGTAACCTCTCCAGATACTACGTACATGACGCTGATTTCTGTTGGAAACTTCCTGATAACATGGATCTCGAAGAAGGTGCTTTGATGGAACCCTTGTCTGTTGGTGTCCACGCTTGTAAACGAGCTGAAATTAAAGTAGGTGACGTTTGTCTTATTACCGGAGCTGGACCAATCGGTCTCGTTACTCTCTTATCGGCTAAAGCTATGGGAGCTTCAAAAGTTGTTATCACAGATATTTTAGACGTAAAATTAGAGATGGCTAAACAATTGGGAGCAGATTATACCATCAAAATCGAAAAGGGTATGTCTGAAGAAGACATCGTCAAAAGAGTAATCCAACTTTTGGGGCAAGAACCAAATAAGAGCATGGACTGTACTGGAGTCGAACAATGTGTCAGAGTTTGCGTATCTGCAACTGGAGTAAATGGATGCGTAGTACTTGTAGGATTAGGTAAAATTGAAATGACTCTCCCATTAACTAACGCCTTGATCAAAGAAGTTGATGTCAGAGGAACATTCAGATATGTTAACGATTACCCCACCTCTATTGAGCTAGTAAGATCTGGAAGAGTAAATGTCAAACCTTTGGTGACTCACCACTATAAACTAGAAGACTCAGTTAAGGCATTCCATACCGCTAAGACTCAAGAAGGCAA

					CCCAGTCAAGATCCTGATCCACGCCAATCCTAACTGGAAACCATCTTAATAATTTAATTGCCGCCATACGTATTAGTTTTTGTTGAAAAAAATTGTTGGAGTGTATGTTGTTTTTTTGTGTACGTTAATAAAGAAATTTTAATGTTTACTGTAA **(1,337)**
MSTRG.49163.1	(1) No hit	Higher	(1) No hit	(1)466-239 INRGCQLNIWIGDMNPQTLVKFRPGSSLTCQQSLEFFFGPISEWSDTFVPSYFSFGISCVVFFYFAKVVLENLES* **(76)**	ACAGTGTAGCGTGTGTAAAAAATTTATGGGGAGGCCAAGCCTCCCTTGCGTCCTCTGACGAGCAGCCACTGGTTTCCTAAACACAACTGCTTTCATACCTTTTCATTTTTTTTGCCACAGCATTGATTTTCTTATACTTTATTATTGTTATTTAAATAATAAAATGAAAGAATACAAGCTATTTTTCTTTCATTTTTAGGCTAAACATTCAAAGCAATATAAAATAACAGAAGATAAACTAAGATTCCAAATTTTCCAAGACAACCTTCGCGAAATAGAAGAACACAACGCAAGATATGCCAAAGGAGAAGTAGGATGGTACAAAGGTGTCACTCCATTCGCTGATTGGACCAAAGAAGAATTCAAGGCTCTGTTGACACGTCAAGCTGCTTCCAGGCCTAAACTTAACGAGAGTTTGGGGGTTCATGTCGCCGATCCAAATGTTAAGTTGGCATCCTCTGTTGATT **(467)**
MSTRG.15366.1	(1) NFX1-type zinc finger-containing protein 1-like [Leptinotarsa decemlineata](99%;60%)	Higher	(1) P-loop containing nucleoside triphosphate hydrolase superfamily (IPR027417)	(1)3-1025 YIKNPRDKQQDIKVYEGVKFLNAESINDQNCQRIQFDFSNKKTKFEYENSKRFMFGSLLCFTDDRFKTLLFGKIVDRKAELLGNGQLIVGFSSDMELPAGLYDKSFLLVESKVYFEPYYQVLTVLKNMPIEHFPMERYIIQVLTDTRPPQYLLKIDPVFYTIERTRFWPLNWGDRQFYGLNEAQNKAFQSALTREFAIIQGPPGTGKTFLGLKIARTMLKNSEAWYSDSPMLVICFTNHALDQFLEGLLPTTDEIVRVGGQSKSEKLNDYNLRNRKRVRASPNRAVSERHFVVRN	GGTACATCAAAAACCCACGAGATAAACAGCAGGATATTAAAGTGTACGAAGGTGTCAAGTTTCTCAATGCGGAATCTATAAACGACCAAAATTGTCAGAGAATCCAATTTGATTTCTCTAACAAGAAAACAAAGTTTGAATACGAGAATTCCAAAAGATTTATGTTTGGTTCTTTGCTGTGTTTTACAGATGATAGGTTTAAAACACTACTTTTCGGAAAAATTGTAGACCGAAAGGCAGAATTGCTAGGAAATGGTCAGCTCATCGTTGGGTTTAGTTCAGATATGGAGTTACCTGCAGGTCTCTATGACAAATCTTTTTTGTTGGTTGAGAGCAAAGTTTATTTTGAACCTTATTATCAAGTTCTTACTGTTTTAAAAAATATGCCAATTGAACATTTTCCAATGGAAAGATATATCATACAAGTGCTCACAGACACAAGACCTCCCCAGTATCTCTTGAAAATAGATCCAGTTTTTTATACC

				LMRDIGSINGYLNIIAKYDTVVDFGAFSGVVPEYATSWFAKAQKEH **(342)**	ATAGAGCGTACCAGATTTTGGCCTCTGAATTGGGGTGACCGACAATTTTATGGTTTGAATGAAGCCCAAAATAAAGCTTTTCAATCTGCGCTAACCAGGGAATTCGCAATCATACAAGGACCTCCAGGAACTGGCAAAACATTTCTGGGATTAAAAATTGCTAGAACAATGTTAAAAAATAGCGAAGCATGGTATAGCGACTCTCCCATGTTAGTAATTTGTTTTACAAATCACGCGTTGGACCAGTTCTTGGAAGGATTGCTGCCAACAACAGATGAGATCGTCCGTGTAGGTGGACAATCAAAAAGTGAAAAACTAAACGATTACAATCTTCGGAATAGAAAAAGAGTTCGAGCTTCTCCAAATCGAGCTGTCTCTGAAAGGCATTTCGTAGTAAGGAACCTAATGCGAGATATCGGATCAATAAATGGATATCTAAACATAATCGCAAAGTATGACACTGTCGTCGATTTTGGTGCATTTTCAGGTGTTGTACCAGAATATGCGACATCTTGGTTTGCAAAAGCCCAAAAAGAACATA **(1,026)**
MSTRG.16720.3	(1) Glycoside hydrolase family 31 [Phaedon cochleariae](97%;61%)/ Glycoside hydrolase family 31[Chrysomela tremula](93%;61%)	Higher	(1) Glycoside hydrolase superfamily (IPR017853)/Glycosyl hydrolase all-beta superfamily (IPR013780)/Glycoside hydrolase family 31 (IPR000322) GO:0005975 carbohydrate metabolic process	(1)1-1932 ATIDYLQLKMLSVRKGWRAILIAILLVGVNQVIVQCSTVNEIILKPSSNGLAIEVNQKEEKKLKGTIGVGIDFTNINCYGQESCQVGDADFSVKQSEDGFHIKWETNNLTSVFQDCFDFEEGVHWYGGPERKKQSWPIEKLEIESYQAYVLHQLDNFAVAERYWLNSKGLYIYLNSKVPLYVDQNISNKNRVCFMAKIEGPYINRHKNFLEYDIVIKDDPREAHVHAVKTFLGKPSGYPDERMITEPIWTTWAKYKTKISDEIVLDFAKDIRDNGYEKGQIEIDDYWEKCYGAQEFTPTTFPDITNTIKTLKSWSYRVTLWIHPFVNSDCQDNSKIGLEKGYFVLDQNSRAN	GCAACTATTGATTATCTACAATTAAAAATGTTATCAGTTAGAAAAGGTTGGAGAGCGATTTTAATTGCAATTCTACTGGTTGGAGTGAATCAAGTTATAGTTCAATGTTCTACAGTAAATGAAATAATTCTCAAACCAAGTTCAAATGGATTGGCCATTGAAGTAAATCAGAAGGAAGAAAAAAAACTGAAAGGAACAATCGGAGTTGGCATAGACTTCACCAATATTAACTGTTACGGACAAGAATCCTGTCAAGTTGGAGATGCTGATTTCTCAGTAAAACAATCTGAAGACGGATTTCACATCAAATGGGAAACAAATAATTTAACGAGTGTTTTTCAAGATTGCTTTGATTTTGAAGAGGGTGTCCACTGGTATGGAGGCCCGGAGAGAAAGAAACAAAGCTGGCCCATAGAGAAATTGGAAATTGAAAGTTATCAGGCGTATGTACTACATCAGTTGGATAATTTTGCTGTAGCTGAACGTTACTGGTTGAACTCAAAAGGATTGTATATCTATCTAAATTCTAAAGTACCTTTGTATGTTGACCAAAATATTTCGAATAA

			GO:0004553 hydrolase activity hydrolyzing O-glycosyl compounds	GSWWNGNDSYQIDFTNPEAAEWWSARLKKLQQNPGIDSFKFDAGETDYGPQPSVYHGVNQEDVPNILSERYVRTCAKFGPLVEVRSGSRTQDLPIFIRMIDKDSNWEDSNGLYTLITTLLQMNINGYTLVLPDMIGGNGYAGKLPDAELLVRWTQANTFMPAMQFSYLPWEITSTKFNVAKIVKKFVALHEKYADHIIRAMKNSVEKGSPVNPPIWWIAPKDVQALGCDDEYLVGEEILVAPVIKEGATSRDVYLPAGKWVDGNNGDIYLGPVTVDYDAGIDILPFFILSQ* **(644)**	AAATAGAGTTTGCTTCATGGCCAAAATAGAAGGCCCTTATATTAATAGACATAAGAATTTTTTGGAATATGATATTGTAATAAAAGATGATCCAAGAGAAGCGCACGTACACGCTGTCAAGACGTTTTTGGGAAAACCATCAGGATATCCAGATGAGCGAATGATAACTGAACCCATCTGGACAACATGGGCAAAATACAAAACGAAAATCAGCGACGAAATCGTACTTGACTTTGCGAAAGATATTAGAGATAACGGGTATGAAAAGGGACAAATAGAAATTGATGATTATTGGGAGAAATGCTACGGAGCTCAAGAATTTACACCAACAACTTTTCCAGACATAACCAATACTATAAAAACTCTAAAAAGTTGGAGCTATAGGGTCACTTTATGGATACATCCCTTCGTGAATAGTGACTGTCAAGACAATTCCAAGATTGGTTTAGAAAAAGGATATTTCGTCCTAGATCAAAATAGCAGAGCAAATGGCAGTTGGTGGAACGGTAATGACTCATACCAAATTGATTTTACTAATCCAGAAGCAGCGGAATGGTGGTCTGCTAGGCTAAAGAAACTTCAACAGAATCCTGGGATAGACAGTTTTAAATTTGATGCAGGAGAAACTGATTACGGTCCTCAACCTTCAGTTTATCATGGTGTGAACCAAGAAGATGTCCCCAACATTCTAAGCGAAAGATATGTGAGAACCTGTGCTAAATTTGGCCCTCTTGTAGAAGTTAGATCGGGTTCCAGAACACAAGACCTACCAATATTCATTCGAATGATCGACAAAGACTCGAATTGGGAAGACAGCAACGGATTGTACACTTTAATTACCACTCTTTTACAAATGAATATAAATGGATACACGTTAGTTTTGCCTGATATGATTGGTGGAAATGGTTACGCTGGAAAATTGCCCGACGCTGAACTTCTAGTGCGATGGACACAGGCTAACACTTTTATGCCCGCAATGCAATTTAGTTATTTGCCATGGGAAATAACATCAACAAAGTTTAACGTTGCCAAAATTGTAAAGAAGTTTGTGGCCCTTCATGAAAAATATGCTGATCACATTATTAGAGCCATGAAAAACAGCGTTGAGAAAGGTTCACCGGTCAA

					TCCTCCAATTTGGTGGATTGCGCCTAAAGACGTACAAGCCTTGGGATGTGATGATGAGTACTTGGTTGGAGAAGAAATCTTAGTGGCACCAGTAATAAAAGAAGGAGCAACTAGCAGGGACGTATATTTGCCAGCAGGAAAATGGGTAGATGGAAATAATGGTGATATCTACCTAGGGCCCGTAACAGTTGATTATGATGCTGGAATAGACATATTGCCTTTTTTTATCCTTAGTCAATAGGACACAAAAATAAATTTATATAAAGCTAATGAATAAATGTATTTTTGATATTATTGTAATAACTTAAAATGGAAAATAATAAATAACCCCATAAAATAAGGGTGTTTGTTTG **(2,044)**
MSTRG.45573.1	(1) Galectin-4 [Anoplophora glabripennis] (99%;52%)/Galectin-8-like [Leptinotarsa decemlineata](90%;41%)	Higher	(1) Concanavalin A-like lectin/glucanase domain superfamily (IPR013320)/Galectin carbohydrate recognition domain (IPR001079) GO:0030246 carbohydrate binding	(1)310-1347 MMDEVAVDALDFIIVEQDTFPHYVDDLPDPLVPGTIIKVTGFVRPDCSRFAVNLCCNRSPSSDIALHLNPRISQRYVVRNSRIKDHWGSEEVTSITKFELARNKQIHIDIVVADTEFLISINGKHVCAFVYRIPIETVKAIVVEGPVDVSGVEYGKTNVYPVVNSPIENIEEIVKEDGESHGTSQNYEVPLTLSFPTGFDKGWQLDIQGRVKILPANFFVNLQDGPQLWPHPNIYLHLSPRFAYLNTRHVFVRNSWLDGDWGPEERVDKCPFTPSSTFSIAIRSYVDHFSIWVNGQLAGEFKYRGDPRKANTLYIQGDVIITGVVMRHNISDKYFTKSRQSIDSM* **(346)**	CCGCAGTATAATCTCAAAATCAATTATATAACGTTAAAAGTCAGTCTTGTCTGCAGCTAGTTCAATGCAATGCGTGTTTTCTAAGAGCCAAACTACATTACAAATGAAGCCAACCATATCAGAGATTACAGTTTAATGTTTTACACATACCAGTCAGTTGATTTGCTTTGTTGTTGTCATCCAAACGAAAATAATGCGCCCAAGTAATACTCGTATAGACAACACACATGAGTCATAATCCTGCTAATTAGTATTCAAAATTCACATGTTTTGATATGTCGGAATCTGCGGTTTAATCTTTGTTAAATAATGATGGATGAAGTCGCTGTAGATGCTTTAGATTTTATTATTGTTGAACAGGACACTTTTCCACACTACGTGGATGATCTTCCCGACCCACTGGTACCTGGAACAATAATAAAAGTCACTGGATTTGTTCGGCCCGACTGTTCAAGATTTGCTGTTAATCTATGCTGCAATAGGTCTCCATCTAGTGATATAGCCTTGCATTTAAATCCTAGAATATCACAAAGGTATGTTGTGAGAAATTCCCGTATAAAAGACCATTGGGGTTCAGAAGAAGTAACGTCAATAACCAAGTTCGAACTTGCTCGAAACAAACAAATTCACATCGACATAGTTGTAGCTGATACTGAGTTCTTGATCTCCATAAATGGTAAACACGTATGTGCCTTTGTGTACAGAATTCCTATAGAGACTGTTAAGGCGATAGTAGTTGAAGGCCCAGTAGATGTTAGCGGGGTG

					GAATATGGAAAAACGAATGTCTATCCGGTGGTAAATAGTCCAATTGAAAATATCGAGGAAATTGTGAAAGAGGATGGGGAGTCACATGGTACTAGTCAAAATTATGAGGTTCCTTTAACTTTGTCATTTCCAACAGGTTTCGACAAAGGATGGCAGTTGGATATCCAAGGAAGAGTGAAAATTCTGCCAGCGAATTTCTTTGTCAATTTACAAGATGGGCCTCAATTGTGGCCTCATCCCAACATATATCTTCATTTAAGTCCTCGATTTGCTTACTTAAACACCAGGCATGTATTTGTACGGAATTCTTGGTTAGATGGCGACTGGGGTCCAGAGGAAAGAGTTGACAAATGTCCATTTACTCCATCTTCTACATTTAGTATCGCCATCCGAAGTTACGTCGATCACTTTTCCATCTGGGTGAATGGACAATTAGCAGGGGAATTTAAATATCGCGGGGATCCAAGAAAGGCGAATACGTTGTACATTCAAGGAGATGTTATTATAACTGGGGTTGTTATGAGACATAATATAAGCGACAAATATTTTACGAAAAGTAGGCAGAGTATAGATTCTATGTAAATTATTATTTAGGGCATCTGCTGAGTGATAAACAACGTGAAAACTTACATAATATTATTTTAATATACACTCACAGACAAAATATTGCTTATTTTATTTTGAGTTTACTTTTTTCTTTTGAAAAGTTTTGTACATTGTATTTGCTAAATAAGTTATGCTGGACTATTATAAGTATAACCATTATGAAGTAACTTAAATATTGAGGAGCTACAACAATTTCTTAGAGAAATTAATGAAATAGTCTTATTTTGCTTATAACATTTAATTAGAAACAGAACCAATAATGACAATAGAACACTTTTTACGGAAACTTTGTAACAATTTGGTACTTAGTATTTCTTCCTCTATATCTAGTGATAGCCTGCTTCCTTCTAGGTAAGCTTCACAGAAGGTCTTGGATTGTCATGGAATTGCATCATCCTCAAGATATTGAATGACTGTGTTCCGATAGTAGGTTACGGAATCAATTAAAAATAAGTGTAAACAATGAACAGTAATATATTTATTTATTTTGGGTAAACAAGCGTGCTTCGTTTATTATCTTGTAAGGGTTTGT

					TAGCGAGGGTGTGTCTGAATCGGTCGCCTGCTGTGTCGATACTGCCAGACCACAATACTCTATTATGCCATCATGCTTGCGGTTTATAATATAGCTAGAAAGGCAATAAATTACTAACATCTGCGTTTTAAAAGATGAGAAACTTTCAGTATCTTAAGCACATGACATAAAGAGCGTGGCAATCTGGCCTCGGAATCTATTAGGGTTTCCTTGAAAAAAACATTAATTTTATACAATCTGCTTAGGGATACATTTCGTTTCTTAAACTTAACGGCCCTTGTTAGCATATGGTTTGTATATTAAATGTTATTTCGTTTTGAGAAAAGTTATTAAAAATTTAGCAAAAATAGTAATTACAGCGTATCGCTATAATCGTACCGCTTATCTGGATCTTGGCCCCCTCTTAATTATTTCTTCTGCATGTACACCGGCATTAGCACAAGTCATGATGAATGAAGCCAGAATAAGGAAAATATGCTCTTCGTGGATGTGTGTTGCGTATATATCAGTCAGCATTCATTCAAATGTTTACTTTAATAAGCTACGTACGACTCTTCGTAGTAATACTTCGTACGTTTACCCCATAGCATAATGGAACTGCCACCAAAGCTAACATTTTGTACAATATTATATTCTGCGAAACGTTCCCCAGACCTTCACTAGACCACGTCTATCTTGCTTCCACAATTGTTGTCCTTGTTTCAGCTGTGAAAACATCTTTTGTCCATTTAAGTTGGTTCCAGTTAACTTGGGCTCTTGCAAAATGCAACCGTTGTGTTTTGTGGAACTCTTGTAGGCCGTGTTGAATTTAAACCAATCTCTTTTTCAGCCAAGTCTTCTATTCACTGTTTTGATACTTGCAGTAACTTGTCTTTTAATCAGTAATTATTTTTTGAGGTTAGGAGCTGTGAGTAATGTCTCAAAGATTGAAGGCTCAAATGTTGGTCATCTCTTGGCGTTGTACATCTTTTTCGTTCTTGACTAGGTTGCCGTTTATATTCTGCAGTTTCATTGTATCACTTTATTACATGAGAAATAGGCGATTGATGGATACGTAATCTCCGCGCAACATCTTGAGGTCTGTATATCTTACTGGCTAAAGTAAAAATTTAGCACACACAAGTTCGCTTAAATCT

					GGCATATCAGCAAGAGAAGTGCATAATCAAAAAATAAAACTCTCCAACTGACATTTTATTATCAAGAAATAAAAACAATTTTAAGTCGCCAAAGCACACATTTAATATAAAGCAATGTTTTTTAGTGTGTAATATTATTGCAATTAAAACTCACAATTAGGTCAAGATAAGGATATAAAGATCAGAATAGACATAGCTGGAAAAGGATTTATAAAATACAGGTCAATATTTACAAATAAGAAATTGAGTATGCCATTAGATTGAGGTTCGTCGAATGTTATGTTTGGTCTCAACTACTATATGGGGTAAAAGCTTGGATTCTAAAAGCCCAATCCATAAAAAACTTGGAGACATTCGAAATGTGGCTACATAGGCGTATTCTGAAAATTCCTTGGACTGCGACAGTCTCAAACGAAGAAGTGTTAAGAAGAATGGGACATGGCAGGAAGCTTATGAACAATGAACATAATTAAAATAAGAAAAACATCGTATTTGGGCCCCATACTTCGAAACGATAAATAATACTCTCTGCTACACGTCATCATGCAAGGAAAAGTAGAGGGGAAAAAAGGCTTGGGAAGAAAGAAGAAATCTTGGCTGAGGAATACCAGAGATTGGACTAACCTCAGTTTTGAACATATATTTTGTTGTGAAAACAACAGTTATTTACATTAATTTGCTTTTATAAAAATATCGCTCTGTAAATCTGTTGGGACAATCTGTATTGTGTTTAAAATATTTAATTCTCTGAAAAACTTGAGTGTAGCGTTGTGTGTTTCATAAAATATACATCTGCATTTTTTATAGTTTCGGGGTAAAAGCAGGTCATTTTGCCAAAGAAGTGTAACATGTGTTTGGCCCTTTTCAGGGCGAATGGTGTAAACTAAACTATCAAAGATAATAGTGCAGAGATTTGAATAGAATTTCAGTAGTCTCTTTCTGNN **(3,983)**
MSTRG.67375.10	(1) Mucin-4 [Pan troglodytes](83%;49%)	Higher	(1) No hit	(1)339-1 LASARTISNKWESGNNQDDLPTSIVTNPPDAATDSSSVSPSDSPPEPVTDSSSTAPTNSPPEPVTDSSSTAPTDSPPEPVTDSASTAPTDS	TGTTACTGGCTCAGGTGGAGAATCTGTAGGTGCAGTAGATGATGGATCTGTTACTGGCTCAGGTGGAGAATCTGTAGGTGCAGTAGATGCGGAATCTGTTACTGGCTCAGGTGGAGAATCTGTAGGTGCAGTAGATGATGAATCTGTTACTGGCTCAGGTGGAGAAT

				PPEPVTDPSSTAPTDSPPEPVT **(114)**	TTGTAGGTGCAGTAGATGATGAATCTGTTACTGGCTCAGGTGGAGAATCCGAAGGTGAAACAGATGAAGAATCAGTCGCTGCATCAGGTGGATTAGTTACTATAGAAGTTGGTAGATCATCTTGATTATTCCCGGACTCCCATTTATTGCTGATCGTTCTCGCTGATGCTAA **(339)**

Table 3. Abundance of transcripts significantly differentially expressed in pyrethroid-resistant (R-Lab; R-Field) and pyrethroid-susceptible (S-Lab; S-Field) WCR populations.

Transcript ID	Mean transcript abundance (TPM±SE)			
	S-Field	R-Field	S-Lab	R-Lab
MSTRG.24908.1	264.6±114.35	2425.56±335.25		
MSTRG.75696.1	36.54±20.35	429.97±63.84		
MSTRG.24907.1	6.73±4.88	176.18±35.19		
MSTRG.23988.2	0.17±0.12	1.46±0.58		
MSTRG.96000.1	0.32±0.04	2.89±0.48		
MSTRG.84401.1	0.34±0.06	8.10±1.11		
MSTRG.75321.1	1.27±0.62	13.53±2.17		
MSTRG.12727.1			1.22±0.09	2.03±0.10
MSTRG.12896.1			1.70±0.55	11.52±3.41
MSTRG.13177.1			222.86±26.74	553.82±36.83
MSTRG.15366.1			3.25±0.32	5.94±0.45
MSTRG.16720.3			13.36±2.63	27.92±2.56
MSTRG.17015.1			65.02±7.21	137.12±11.60
MSTRG.1766.1			7.49±1.89	1.37±0.33
MSTRG.1810.1			0.08±0.02	0.45±0.10
MSTRG.18102.1			12.06±0.67	18.84±0.93
MSTRG.19112.1			51.31±10.12	2004.09±293.83
MSTRG.19533.2			9.66±1.86	23.45±2.30
MSTRG.19832.1			15.18±0.60	9.32±0.61
MSTRG.20345.1			24.71±2.05	41.71±2.10
MSTRG.20829.1			8.46±0.74	4.45±0.35

MSTRG.22086.2			31.08±1.99	20.05±0.52
MSTRG.22143.1			41.32±3.73	922.35±146.40
MSTRG.22917.1			0.33±0.21	2.98±0.30
MSTRG.22922.1			5.49±1.07	0.63±0.37
MSTRG.23764.1			5.80±0.44	0.97±0.43
MSTRG.24781.1			0.01±0.01	1.61±0.10
MSTRG.24813.1			0.14±0.08	1.05±0.26
MSTRG.25208.2			7.29±0.56	3.37±0.34
MSTRG.25260.1			1.42±0.11	3.93±0.49
MSTRG.25345.1			0.33±0.05	0.72±0.08
MSTRG.25915.1			19.31±1.23	10.55±0.79
MSTRG.26270.1			0.44±0.10	0.01±0.01
MSTRG.2650.1			0.32±0.15	2.95±0.96
MSTRG.26837.1			16.74±1.38	27.67±1.66
MSTRG.27946.1			6.79±0.88	13.63±0.71
MSTRG.2797.2			5.72±0.64	11.53±0.94
MSTRG.29667.1			2.60±0.36	5.77±0.40
MSTRG.29792.1			11.76±1.26	23.58±1.90
MSTRG.29796.1			28.06±2.30	47.82±3.27
MSTRG.3101.1			0.14±0.03	1.25±0.46
MSTRG.31399.1			8.86±0.63	5.41±0.31
MSTRG.34302.1			0.96±0.24	0.06±0.04
MSTRG.35370.1			4.86±0.45	2.79±0.16
MSTRG.36287.1			1.39±0.20	3.76±0.34
MSTRG.36906.4			0.15±0.07	0.90±0.17
MSTRG.38519.1			3.46±0.56	0.72±0.44
MSTRG.3860.1			33.30±3.89	65.53±4.10

MSTRG.38739.1			6.15±0.94	18.05±2.31
MSTRG.39053.1			13.01±1.42	24.44±1.47
MSTRG.39495.1			0.43±0.43	5.70±0.72
MSTRG.39954.2			3.08±0.28	1.80±0.10
MSTRG.40228.1			12.05±1.40	23.08±1.47
MSTRG.40734.1			13.00±0.78	8.40±0.55
MSTRG.40933.1			1.82±0.17	0.71±0.14
MSTRG.41828.1			0.11±0.05	5.98±1.02
MSTRG.41888.1			244.59±16.68	167.60±6.85
MSTRG.42718.1			1.01±0.09	0.24±0.04
MSTRG.43013.1			10.25±0.97	19.60±1.72
MSTRG.43015.1			11.34±1.29	22.66±1.82
MSTRG.45015.1			4.88±1.26	21.59±3.10
MSTRG.45573.1			1.00±0.11	2.24±0.27
MSTRG.48033.1			1.01±0.18	10.65±3.63
MSTRG.48586.1			9.60±0.68	5.45±0.29
MSTRG.49163.1			153.26±23.97	343.22±31.15
MSTRG.50645.3			2.73±0.20	7.19±1.23
MSTRG.53652.2			6.96±0.81	16.92±1.69
MSTRG.5480.2			8.55±0.66	17.54±1.48
MSTRG.55035.1			23.28±2.17	4.88±2.03
MSTRG.55986.1			3.74±1.31	11.44±1.43
MSTRG.56151.1			3.94±0.61	0.17±0.17
MSTRG.58405.1			0.11±0.03	5.18±0.32
MSTRG.58993.1			1.71±0.71	9.41±1.45
MSTRG.59366.1			9.48±1.91	377.56±58.73
MSTRG.60092.1			2.55±1.62	15.51±2.34

MSTRG.63174.1			35.38±3.67	995.59±148.87
MSTRG.65003.2			17.84±0.89	31.80±2.13
MSTRG.65069.1			0.12±0.05	4.97±0.87
MSTRG.65512.1			17.06±2.00	38.78±2.60
MSTRG.66987.1			1.19±0.18	0.12±0.09
MSTRG.67375.10			0.57±0.12	9.36±3.03
MSTRG.71693.1			8.61±1.89	406.17±57.47
MSTRG.75310.1			0.30±0.19	3.70±0.71
MSTRG.76395.1			0.19±0.10	0.76±0.08
MSTRG.77164.1			42.51±4.04	6.00±3.12
MSTRG.78210.1			3.87±0.42	11.38±1.24
MSTRG.78713.1			448.39±51.86	955.15±72.60
MSTRG.7894.1			4.83±2.44	31.45±7.57
MSTRG.79626.1			0.07±0.01	0.25±0.03
MSTRG.79630.1			0.10±0.02	0.36±0.06
MSTRG.80801.1			4.64±1.15	25.06±5.97
MSTRG.81903.1			2.48±0.23	4.43±0.39
MSTRG.84058.1			0.19±0.13	1.96±0.32
MSTRG.84584.1			3.72±0.72	10.68±1.04
MSTRG.87517.1			57.72±4.06	33.36±1.83
MSTRG.87888.1			3.20±0.35	7.21±0.75
MSTRG.88057.1			0.25±0.19	4.63±1.14
MSTRG.89601.1			7.09±0.58	4.41±0.28
MSTRG.90901.1			1.43±0.14	0.26±0.10
MSTRG.90902.1			3.08±0.15	6.67±0.39
MSTRG.91250.2			10.11±0.85	23.72±3.63
MSTRG.94228.1			0.01±0.01	1.19±0.12

MSTRG.94228.2			1.92±0.15	0.02±0.02
MSTRG.95019.2			6.42±0.93	0.96±0.68
MSTRG.97619.1			0.12±0.01	0.42±0.07
MSTRG.9784.1			0.21±0.12	15.56±1.99

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Vssc1 MTEDSDSISE EERSLFRPFT RESLLQIEQR IA-EHEKQKE LERKRAAEGE ----------
ALB   MSVASDSFSE EEVSLFRPFT RESLAAIEAR IAEEHAKQKE LEKKR-AEGE TGFGRRKKKK
CPB   MSVASDSFSE EERSLFRPFT RESLSAIEAR IAEEHEKQKE LEKKR-AEGE ----------
WCR   MSVASDSFSE EERSLFRPFT RESLAVIETR IAEEYAKQKE LEKKR-AEGE ----------

Vssc1 QIRYDDEDED EGPQPDPTLE QGVPIPVRMQ GSFPPELAST PLEDIDPFYS NVLTFVVISK
ALB   EIRYEDEDED EGPQPDATLE QGLPIPVRLQ GSFPPELAST PLEDIDPFYH NQMTFVVVSK
CPB   -IRYEDEDED EGPQPDATLE QGLPLPVRLQ GSFPPELAST PLEDIDPFYH NQMTFVVISK
WCR   QIRYEDEDED EGPQPDPTLE QGLPIPVRLQ GSFPPELAST PLEDIDPFYH NFQTFVVVSK

Vssc1 GKDIFRFSAS KAMWLLDPFN PIRRVAIYIL VHPLFSLFII TTILTNCILM IMPTTPTVES
ALB   GKDIFRFSAT NALWILDPFN PIRRVAIYIL VHPLFSLFII TTILVNCILM TMPTTPTVES
CPB   GKDIFRFSAT NALWILDPFN PIRRVAIYIL VHPLFSLFII TTILVNCILM IMPTTPTVES
WCR   GKDIFRFSAI NALWILDPFN PIRRVAIYIL VHPLFSLFII TTILVNCILM IMPTTPTVES
                                             I-S1

Vssc1 TEVIFTGIYT FESAVKVMAR GFILCPFTYL RDAWNWLDFV VIALAYVTMG IDLGNLAALR
ALB   TEVIFTGIYT FESAVKVMAR GFILQPFTYL RDAWNWLDFV VIALAYVTMG IDLGNLAALR
CPB   TEVIFTGIYT FESAVKVMAR GYILQPFTYL RDAWNWLDFV VIALAYVTMG ----------
WCR   TEVIFTGIYT FESAVKVMAR GFILQPFTYL RDAWNWLDFV VIALAYVTMG IDLGNLAALR
                 I-S2                                I-S3

Vssc1 TFRVLRALKT VAIVPGLKTI VGAVIESVKN LRDVIILTMF SLSVFALMGL QIYMGVLTQK
ALB   TFRVLRALKT VAIVPGLKTI VGAVIESVKN LRDVIILTMF SLSVFALMGL QIYMGVLTQK
CPB   ---------- ---------- ---------- ---------- ---------- ----------
WCR   TFRVLRALKT VAIVPGLKTI VGAVIESVKN LRDVIILTMF SLSVFALMGL QIYMGVLTQK
                  I-S4                             I-S5

Vssc1 CIKRFPLDGS WGNLTDENWF LHNSNSSNWF TENDGESYPV CGNVSGAGQC GEDYVCLQGF
ALB   CIKNFPNDGS WGNLTDENWE RFVSNETNWF FDPDKGEIPL CGNSSGAGQC KPGYTCLQGY
CPB   ---------- ---------- ---------- ---------- ---------- ----------
WCR   CVKNFPHDGS WGNLSHENWE RFMDNEANWY VD-ESGDYPL CGNSSGAGQC KPGYTCLQGY

Vssc1 GPNPNYDYTS FDSFGWAFLS AFRLMTQDFW EDLYQHVLQA AGPWHMLFFI VIIFLGSFYL
ALB   GENPNYGYTS FDTFGWAFLS AFRLMTQDYW ENLYQLVLRS AGPWHMLFFI VIIFLGSFYL
CPB   ---------- ---------- ---------- ---------- ---------- ----------
WCR   GDNPNYGYTS FDTFGWAFLS AFRLMTQDYW ENLYQLVLRS AGPWHMLFFI VIIFLGSFYL
                                                                  I-S6

Vssc1 VNLILAIVAM SYDELQKKAE EEEAAEEEAI REAEEEAAAK AAKLEERANV AAQAAQDAAD
ALB   VNLILAIVAM SYDELQKKAE EEEAAEEEAI REAERAAQAK QDRAEARAAA AEESRQAALQ
CPB   ---------- ---------- ---------- ---------- ---------- ----------
WCR   VNLILAIVAM SYDELQKKAE EEEAAEEEAI REAEKAAQAK QDRADARAAA AEEAREAAA-

Vssc1 AA-AAALHPE MAKSPT-YSC ISYELFVGGE KGNDDNNKEK MSIRSVEVES ESVSVIQRQP
ALB   ASLAAEAGPD IVKSPSDFSC ASYELFVGA- KGHDDNNKEK MSIRSEGLDS VS------EQ
CPB   ---------- ---------- ---------- ---------- ---------- ----------
WCR   AALAAENCPD IVKSPSDFSC HSYELFVGQA KGHDDNNKEK MSIRSEGLDS VS------EQ

Vssc1 APTTAPATKV RKVSTTSLSL PGSPFNLRRG SRSSHKYTIR NGRGRFGIPG SDRKPLVLQT
ALB   RRIPTNPTKM RKVSAASLSL PGSPFNLRRG SRGSHQFTLR NNR-RMVAPP GDRKPLVLST
CPB   ---------- ---------- ---------- ---------- ---------- SDRKPLVLST
WCR   RRIPTNPTKM RKVSAVSVSL PGSPFNPRRG SRGSHQFTMR SNR-RMIPPP GDRKPLVLST
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Vssc1 YQDAQQHLPY ADDSNAVTPM SEENGAIIVP AYYCNLGSRH SSYTSHQSRI SYTSHGDLLG
ALB   YLDAQEHLPY ADDSNAVTPM SEENGAMVVP IYYANLGSRH SSYTSHASRM SYTSHGDLLG
CPB   YLDAQEHLPY ADDSNAVTPM SEENGAMVVP MYYANLGSRH SSYTSHASRM SYTSHGDLLG
WCR   YLDAQEHLPY ADDSNAVTPM SEENGAMVVP IYYANLGKYH ASYTSHASRI SYTSHGDLLC

Vssc1 GMAAMGASTM TKESKLRSRN TRNQSIGAAT NGGSSTAGGG YPDANHKE-Q RDYEMGQDYT
ALB   GNG----KGM TKESQLRCRS MRN------- --GPAAA-NN FTEFTHRPHR GDYD-GPTGQ
CPB   GLGGNG-KVM TKESQLRSRS MRN------- --GPATAPNN FREYTPRAYQ GDYE-GPTGQ
WCR   GLGGTA-KVM TKESQLRNRS LRT---GPPP AATATTTPNN YTEYNHRAHR GDYD-GPTSQ

Vssc1 DEAGKIKHHD NPFIEPVQTQ TVVDMKDVMV LNDIIEQAAG RHSRASERG- --------ED
ALB   ISEGKLKHLD NPFIDCNQRQ TVVDMKDVMV LNDIIEQAAG RQSGASDHGV SVYLFSAQND
CPB   TCEGKLKHLD NPFIDSNQRQ TVVDMQDVMV LNDIIEQAAG RQSGASEHGV STYYFSAQND
WCR   -MEGKIKHLD NPFIDNNQRQ TVVDMKDVMV LNDIIEQAAG RQSGASDHGV SVYYFSAQND

Vssc1 DDEDGPTFKD IALEYILKGI EIFCVWDCCW VWLKFQEWVS FIVFDPFVEL FITLCIVVNT
ALB   DEEDEPTAKE RLLEFTMRMI DIFCVWDCCS PWLAFQKFVA LIVFDPFVEL FITLCIVVNT
CPB   GEQEEPTMKE RVLAFIMKVI DIFCVWDCCE PWLVFQKFIA LIVFDPFVEL FITLCIVVNT
WCR   DEEDEPTVKE RLLAFSMRVI DIFCVWDCCG PWLVFQKFVA LIVFDPFVEL FITLCIVVNT
                                                               II-S1

Vssc1 MFMAMDHHDM NPELEKVLKS GNYFFTATFA IEASMKLMAM SPKYYFQEGW NIFDFIIVAL
ALB   LFMALDHHKM DHDLEKALKS GNYFFTATFM IEATMKLVAM SPKYYFQEGW NIFDFIIVTL
CPB   LFMALDHHNM DKDLDKALKS GNYFFTATFM IEATMKLIAM SPKYYFQEGW NIFDFIIVAL
WCR   LFMALDHHDM DRNLEKALKS GNYFFTATFM IEATMKLIAM SPKYYFQEGW NIFDFIIVAL
                                    II-S2

Vssc1 SLLELGLEGV QGLSVLRSFR LLRVFKLAKS WPTLNLLISI MGRTMGALGN LTFVLCIIIF
ALB   SLVELGLEGV QGLSVLRSLR LLRVFKLAKS WPTLNLLISI MGRTMGALGN LTFVLCIIIF
CPB   SLLELGLEGV QGLSVLRSFR LLRVFKLAKS WPTLNLLISI MGRTMGALGN LTFVLCIIIF
WCR   SLLELGLEGV QGLSVLRSFR LLRVFKLAKS WPTLNLLISI MGRTMGALGN LTFVLCIIIF
             II-S3                                                  II-S4

Vssc1 IFAVMGMQLF GKNYIDHKDR FKDHELPRWN FTDFMHSFMI VFRVLCGEWI ESMWDCMYVG
ALB   IFAVMGMQLF GKNYTDNVDR FPDHDLPRWN FTDVMHSFMI VFRVLCGEWI ESMWDCMLVG
CPB   IFAVMGMQLF GKNYTDNVDR FLDHELPRWN FTDFMHSFMI VFRVLCGEWI ESMWDCMLVG
WCR   IFAVMGMQLF GKNFSDNVDR FPDHELPRWN FTDFMHSFMI VFRVLCGEWI ESMWDCMLVG
                                     II-S5

Vssc1 DVSCIPFFLA TVVIGNLVVL NLFLALLLSN FGSSSLSAPT ADNDTNKIAE AFNRIARFKN
ALB   DVSCIPFFLA TVVIGNLVVL NLFLALLLSN FGSSSLSAPT ADNDTNKIAE AFDRIGRFIK
CPB   DVSCIPFFLA TVVIGNFVVL NLFLALLLSN FGSSSLSAPT ADNDTNKIAE AFDRIGRFIK
WCR   DVSCIPFFLA TVVIGNLVVL NLFLALLLSN FGSSSLSAPT ADNDTNKIAE AFVRIGRFSR
                     II-S6

Vssc1 WVKRNIADCF KLIRNKLTNQ ISDQPSEHG- ---------D NELELGHDEI MGDGLIKKGM
ALB   WIKASVSHIA KLIRFKLTNQ ISDQPS---- ------DTRD GGLDIPGDEI LADGIIFKDK
CPB   WIKASVADIA KLIRFKLTNQ ISDQPSGEGP SNSWNQDPRD GGLDIPGDEI LADGMIFKDK
WCR   WIKAGVADIA KLIRFKLTNQ ISDQPSGEGP SNLWNQDPRD GGLDIPGDEI LADGTIFKDK

Vssc1 KG-ETQLEVA IGDGMEFTIH GDMKNN--KP KKSKFMNNTT MIGNSINHQD NRLEHELNHR
ALB   KSPKDRLEVT IGDGMEFTIH GDSKTNLKRG KNINNINKSK TIGNSILDHG EFLGH-----
CPB   KSPKDRLEVT IGDGMEFTIH GDSKTNLKRG KNISNINKSK TIGNSILDHS DFLGH-----
WCR   KSPKDRLEVT IGDGMEFTIH GDSKTNIKRA KN--AISK-K TLGNSILEHG DFLGH-----

Vssc1 GLSIQDDDTA SINSYGSHKN RPFKDESHKG SAETIEG-EE KRDVSKEDLG LDEELDEEAE
ALB   ----LEDDEI SNKSYGSHKH R-FKDESHKG SADVLDEHEE KRDASKEELG IDEELDEDEC
CPB   ----LDDDEI SNKSYGSHKH R-FRDESHKG SAVVLDDQEE KRDASKEELG IDEEMEEDEY
WCR   ----LDDDEI SNKSYGSHKH R-FKDESHKG SADVLDDQEE KRDASKEELG IDEEL-EDEC

Vssc1 GDEGQLDGDI IIHAQNDDEI IDDYPADCFP DSYYKKFPIL AGDEDSPFWQ GWGNLRLKTF
ALB   DCQGPLDEDL ILDAATDDVI IDEYSADCFP EKCYKKFPFL AGDDDSPFWQ GWANLRYKTF
CPB   DCQGALEDD- IIDAVTDDII IDEYSADCFP EKCYKKFPFL AGDDDSPFWQ GWANLRFKTY
WCR   DCQGPLDEDL IIDAATEDII IDEYSADCFP EKCYKKFPFL AGDEDSPFWQ GWGNLRYKTF


Vssc1 QLIENKYFET AVITMILMSS LALALEDVHL PDRPVMQDIL YYMDRIFTVI FFLEMLIKWL
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ALB    RLIENKYFET AVITMILLSS LALALEDVHL SQRPILQDIL YYMDRIFTVI FFFEMLIKWL
CPB    KLIENKYFET AVITMILLSS LALALEDVHL SSRPILQDIL YYMDRIFTVI FFFEMLIKWL
WCR    QLIENKYFET AVITMILLSS LALALEDVHL SARPILQDIL YYMDRIFTVI FFFEMLIKWL
                     III-S1                                      III-S2

Vssc1  ALGFKVYFTN AWCWLDFVIV MLSLINLVAV WSGLNDIAVF RSMRTLRALR PLRAVSRWEG
ALB    ALGFQKYFTN AWCWLDFIIV MVSLINFVAS LCGAGGIQAF KTMRTLRALR PLRAMSRMQG
CPB    ALGFQKYFTN AWCWLDFVIV MVSLINFVAS LCGAGGIQAF KTMRTLRALR PLRAMSRMQG
WCR    AMGFQKYFTN AWCWLDFLIV MVSLINFVAS LAGAGGIQAF KTMRTLRALR PLRAMSRMQG
                                       III-S3
                          *(L1422)
Vssc1  MKVVVNALVQ AIPSIFNVLL VCLIFWLIFA IMGVQLFAGK YFKCKDGNDT VLSHEIIPNR
ALB    MRVVVNALVQ AIPSIFNVLL VCLIFWLIFA IMGVQLFAGK YYKCVDNNKT TLSYEIIPDY
CPB    MRVVVNALVQ AIPSIFNVLL VCLIFWLIFA IMGVQLFAGK YYKCVDNNKS VLSFEIIPDY
WCR    MRVVVNALVQ AIPSIFNVLL VCLIFWLIFA IMGVQLFAGK YYKCVDSNKT TLSYEIIPDV
                       III-S4

Vssc1  NACKSENYTW ENSAMNFDHV GNAYLCLFQV ATFKGWIQIM NDAIDSREVD KQPIRETNIY
ALB    NACKAENYTW DNSRMNFDHV GKAYLCLFQV ATFKGWIQIM NDAIDSRETN KQPIRETNIY
CPB    NACKAENYSW DNSPMNFDHV GKAYLCLFQV ATFKGWIQIM NDAIDSRELN KQPIRETNIY
WCR    NACKAENYTW DNSPMNFDHV GKAYLCLFQV ATFKGWIQIM NDAIDSREVR KQPIRETNIY
                                    III-S5
                                            *(I1558)
Vssc1  MYLYFVFFII FGSFFTLNLF IGVIIDNFNE QKKKAGGSLE MFMTEDQKKY YNAMKKMGSK
ALB    MYLYFVFFII FGSFFTLNLF IGVIIDNFNE QKKKAGGSLE MFMTEDQKKY YNAMKKMGSK
CPB    MYLYFVFFII FGSFFTLNLF IGVIIDNFNE QKKKAGGSLE MFMTEDQKKY YNAMKKMGSK
WCR    MYLYFVFFII FGSFFTLNLF IGVIIDNFNE QKKKISIQLE MFMTEDQKKY YNAMKKMGSK
                     III-S6

Vssc1  KPLKAIPRPR -WRPQAIVFE IVTDKKFDII IMLFIGLNMF TMTLDRYDAS EAYNNVLDKL
ALB    KPMKAIPRPR -WRPQAIVFE IVTNKKFDMI IMLFIGLNML TMTMDHYQQK ETFTKVLDYL
CPB    KPMKAIPRPR -WRPQAIVFE IVTNKKFDMF IMLFIGLNML TMTMDHYQQK ETFTKVLDYL
WCR    KPMKAIPRPR QWRPQAIVFE IVTNKKFDMI IMLFIGLNML TMTMDHYKQK ETFTKVLDYL
                                            IV-S1

Vssc1  NGIFVVIFSG ECLLKIFALR YHYFKEPWNL FDVVVVILSI LGLVLSDIIE KYFVSPTLLR
ALB    NMIFIVIFST ECLMKVFALR YHYFTEPWNL FDLVVVILSI LGLVLSDIIE KYFVSPTLLR
CPB    NMIFIVIFST ECLMKVFALR YHYFTEPWNL FDLVVVILSI LGLVLSDIIE KYFVSPTLLR
WCR    NMIFIVIFST ECLMKVFALR YHYFTEPWNL FDLVVVILSI LGLVLSDIIE KYFVSPTLLR
                 IV-S2                           IV-S3

Vssc1  VVRVAKVGRV LRLVKGAKGI RTLLFALAMS LPALFNICLL LFLVMFIFAI FGMSFFMHVK
ALB    VVRVAKVGRV LRLVKGAKGI RTLLFALAMS LPALFNICLL LFLVMFIFAI FGMSFFMHVK
CPB    VVRVAKVGRV LRLVKGAKGI RTLLFALAMS LPALFNICLL LFLVMFIFAI FGMSFFMHVK
WCR    VVRVAKVGRV LRLVKGAKGI RTLLFALAMS LPALFNICLL LFLVMFIFAI FGMSFFMHVK
                                                     IV-S4

Vssc1  EKSGINAVYN FKTFGQSMIL LFQMSTSAGW DGVLDAIINE EDCDPPDNDK GYPGNCGSAT
ALB    DKSGLDDVYN FKTFGQSMIL LFQMSTSAGW DGVLDGIINE EDCKQPDNEI GETGNCGNST
CPB    DKSGLDDVYN FKTFGQSMIL LFQMSTSAGW DGVLDGIINE EECKQPDNEI GETGNCGNST
WCR    NKSGLDDVYN FKTFGQSMIL LFQMSTSAGW DGVLDGIINE EDCKQPDNEI GETGNCGNST
                                  IV-S5

Vssc1  VGITFLLSYL VISFLIVINM YIAVILENYS QATEDVQEGL TDDDYDMYYE IWQQFDPEGT
ALB    IGIAFLLSYL VISFLIVINM YIAVILENYS QATEDVQEGL TDDDYDMYYE IWQQFDPDGT
CPB    IGIIFLLSYL VISFLIVINM YIAVILENYS QATEDVQEGL TDDDYDMYYE IWQQFDPDGT
WCR    IGIAFLLSYL VISFLIVINM YIAVILENYS QATEDVQEGL TDDDYDMYYE IWQQFDPDGT
                     IV-S6

Vssc1  QYIRYDQLSE FLDVLEPPLQ IHKPNKYKII SMDMPICRGD MMYCVDILDA LTKDFFARKG
ALB    QYIRYDQLSD FLDVLEPPLQ IHKPNKYKIV SMDIPICKGD LMFCVDILDA LTKDFFARKG
CPB    QYIRYDQLSD FLDVLEPPLQ IHKPNKYKIV SMDIPICKGD LMFCVDILDA LTKDFFARKG
WCR    QYIRYDQLSD FLDVLESPLQ IHKPNKYKIV SMDIPICKGD LMFCVDILDA LTKDFFARKG

Vssc1  NPIEETGEIG EIAARPDTEG YDPVSSTLWR QREEYCAKLI QNAWRRYKNG PPQEGDEGEA
ALB    NAIEETAELA EVQGRPNEAG YEPVSSTLWR QREEYCARLI QNAWRKHKRN R---------
CPB    NAIEETAELA EVQGRPNEAG YEPVSSTLWR QREEYCARLI QNAWRKHKRN R---------
WCR    NAIEETAELA EVQGRPNEVG YEPVSSTLWR QREEYCARLI QNAWRKHKRN R---------
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Vssc1 AGGEDGAEGG EGEGGSGGGG GDDGGSATGA TAAAGATSPS DP-DAGEADG ASVGGPLSPG
ALB   ---------- --------GG ATD------- ---------- QS-DEGEVDG ----------
CPB   ---------- --------GG ATD------- ---------- QS-DEGEADV ----------
WCR   ---------- --------GG ATD------- ---------- QSGDEGDIDG ----------

Vssc1 CVSGGSNGRQ TAVLVESDGF VTKNGHKVVI HSRSPSITSR TADV
ALB   --EGEPEARQ TAVLVE---- --RNGHKVVI HSRTPSISSR SADV
CPB   --EGELEARQ TAVLVE---- --RNGHKVVI HSRTPSISSR TADV
WCR   --EGELEARQ TAVLVE---- --RNGHKVVI HSRTPSISSR TADV
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Figure 1. Multiple alignment of the voltage-gated sodium channel amino acid sequences of housefly (*Vssc1*), Asian longhorned beetle (ALB), Colorado potato beetle (CPB) and western corn rootworm (WCR). Shadowed sequences represent predicted sodium channel domains structures (I-IV) and transmembrane segments (S1-S6). Amino acids marked with * and a box represent the locations L1422 and I1558 in *Vssc1* where non-synonymous substitutions were investigated in WCR.

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MSVASDSFSE EERSLFRPFT RESLAVIETR IAEEYAKQKE LEKKRAEGEQ 50
IRYEDEDEDE GPQPDPTLEQ GLPIPVRLQG SFPPELASTP LEDIDPFYHN 100
FQTFVVVSKG KDIFRFSAIN ALWILDPFNP IRRVAIYILV HPLFSLFIIT 150
TILVNCILMI MPTTPTVEST EVIFTGIYTF ESAVKVMARG FILQPFTYLR 200
DAWNWLDFVV IALAYVTMGI DLGNLAALRT FRVLRALKTV AIVPGLKTIV 250
GAVIESVKNL RDVIILTMFS LSVFALMGLQ IYMGVLTQKC VKNFPHDGSW 300
GNLSHENWER FMDNEANWYV DESGDYPLCG NSSGAGQCKP GYTCLQGYGD 350
NPNYGYTSFD TFGWAFLSAF RLMTQDYWEN LYQLVLRSAG PWHMLFFIVI 400
IFLGSFYLVN LILAIVAMSY DELQKKAEEE EAAEEEAIRE AEKAAQAKQD 450
RADARAAAAE EAREAAAAAL AAENCPDIVK SPSDFSCHSY ELFVGQAKGH 500
DDNNKEKMSI RSEGLDSVSE QRRIPTNPTK MRKVSAVSVS LPGSPFNPRR 550
GSRGSHQFTM RSNRRMIPPP GDRKPLVLST YLDAQEHLPY ADDSNAVTPM 600
SEENGAMVVP IYYANLGKYH ASYTSHASRI SYTSHGDLLC GLGGTAKVMT 650
KESQLRNRSL RTGPPPAATA TTTPNNYTEY NHRAHRGDYD GPTSQMEGKI 700
KHLDNPFIDN NQRQTVVDMK DVMVLNDIIE QAAGRQSGAS DHGVSVYYFS 750
AQNDDEEDEP TVKERLLAFS MRVIDIFCVW DCCGPWLVFQ KFVALIVFDP 800
FVELFITLCI VVNTLFMALD HHDMDRNLEK ALKSGNYFFT ATFMIEATMK 850
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LIAMSPKYYF QEGWNIFDFI IVALSLLELG LEGVQGLSVL RSFRLLRVFK 900
LAKSWPTLNL LISIMGRTMG ALGNLTFVLC IIIFIFAVMG MQLFGKNFSD 950
NVDRFPDHEL PRWNFTDFMH SFMIVFRVLC GEWIESMWDC MLVGDVSCIP 1000
FFLATVVIGN LVVLNLFLAL LLSNFGSSSL SAPTADNDTN KIAEAFVRIG 1050
RFSRWIKAGV ADIAKLIRFK LTNQISDQPS GEGPSNLWNQ DPRDGGLDIP 1100
GDEILADGTI FKDKKSPKDR LEVTIGDGME FTIHGDSKTN IKRAKNAISK 1150
KTLGNSILEH GDFLGHLDDD EISNKSYGSH KHRFKDESHK GSADVLDDQE 1200
EKRDASKEEL GIDEELEDEC DCQGPLDEDL IIDAATEDII IDEYSADCFP 1250
EKCYKKFPFL AGDEDSPFWQ GWGNLRYKTF QLIENKYFET AVITMILLSS 1300
LALALEDVHL SARPILQDIL YYMDRIFTVI FFFEMLIKWL AMGFQKYFTN 1350
AWCWLDFLIV MVSLINFVAS LAGAGGIQAF KTMRTLRALR PLRAMSRMQG 1400
MRVVVNALVQ AIPSIFNVLL VCLIFWLIFA IMGVQLFAGK YYKCVDSNKT 1450
TLSYEIIPDV NACKAENYTW DNSPMNFDHV GKAYLCLFQV ATFKGWIQIM 1500
NDAIDSREVR KQPIRETNIY MYLYFVFFII FGSFFTLNLF IGVIIDNFNE 1550
QKKKISISLE MFMTEDQKKY YNAMKKMGSK KPMKAIPRPR QWRPQAIVFE 1600
IVTNKKFDMI IMLFIGLNML TMTMDHYKQK ETFTKVLDYL NMIFIVIFST 1650
ECLMKVFALR YHYFTEPWNL FDLVVVILSI LGLVLSDIIE KYFVSPTLLR 1700
VVRVAKVGRV LRLVKGAKGI RTLLFALAMS LPALFNICLL LFLVMFIFAI 1750
FGMSFFMHVK NKSGLDDVYN FKTFGQSMIL LFQMSTSAGW DGVLDGIINE 1800
EDCKQPDNEI GETGNCGNST IGIAFLLSYL VISFLIVINM YIAVILENYS 1850
QATEDVQEGL TDDDYDMYYE IWQQFDPDGT QYIRYDQLSD FLDVLESPLQ 1900
IHKPNKYKIV SMDIPICKGD LMFCVDILDA LTKDFFARKG NAIEETAELA 1950
EVQGRPNEVG YEPVSSTLWR QREEYCARLI QNAWRKHKRN RGGATDQSGD 2000
EGDIDGEGEL EARQTAVLVE RNGHKVVIHS RTPSISSRTA DV         2042
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Figure 2. Amino acid sequence of WCR voltage-gated sodium channel.