Insulin receptor substrate influences female caste development in honeybees

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Insulin-like signalling (IIS), which can be coupled to TOR activation through downstream integration of Tsc-1 and 2 (tuberous sclerosis complex genes 1 and 2; e.g. [4]), is similarly crucial to nutrient-sensing and growth regulation in animals. IIS influences development and final body size, food-related behaviour, reproduction and longevity across many taxa ([5] and references therein). Thus, this pathway is also likely to influence honeybee caste development [6,7]. However, functional evidence for this hypothesis has been limited.

Most of what has been revealed about IIS in animal model systems relies on impaired insulin signalling caused by either knockout (disruptive mutation) or knockdown (downregulation via RNA interference, RNAi) of key insulin signalling proteins like the insulin receptor substrate (IRS) protein. Downregulation of IRS confers a substantial reduction of IIS [8]. Recently, we established RNAi-mediated irs gene knockdown in adult honeybee workers to show that the IRS product influences food-choice behaviour towards pollen (amino acids) and nectar (carbohydrate) [9].

Downregulation of IIS via disruptive mutation of irs reduces body size and fertility in Drosophila [10]. Thus, we reasoned that the course of larval development in response to rich queen diet could be blocked by decreasing IIS through irs repression. This should yield the small, essentially sterile worker phenotype, as previously shown, following downregulation of TOR gene transcript [3]. To test this hypothesis, we suppressed irs expression by RNAi in larvae reared on laboratory diet that elicits queen development.

This study provides functional evidence for IIS roles in honeybee caste development.

2. MATERIAL AND METHODS

(a) Irs dsRNA synthesis, bees, feeding treatments, sample collections

Synthesis of irs dsRNA was conducted as before [9]. Larvae were produced from two wild-type (and multiply mated) queens and genotype was a random factor in the experiment. In vitro feeding methods were essentially identical to those of [3]. We produced two treatment groups: larvae-fed queen diet mixed with irs dsRNA, and larvae-fed queen diet mixed with a standard control of gfp (green fluorescent protein) dsRNA.

Two replicate studies with 100 larvae per treatment group were performed. A random subset of larvae was collected into liquid nitrogen 72, 96 and 120 h after dsRNA feeding began (see the electronic supplementary material).

(b) RNAi validation, morphological phenotyping

Irs RNA abundance was tested by quantitative real-time PCR 72 h after dsRNA feeding began (see the electronic supplementary material). Developmental time (larva to adult) was assessed (n = 50), and a random subset (n = 20) measured at adult emergence for fresh weight. The first 12 individuals (only queens in the control group as intercastes typically emerge late) were dissected to determine ovary size by counting ovarian filaments (ovarioles) as before [3].

(c) Protein extraction, trypic digestion and proteomics analysis

These steps (see the electronic supplementary material) were essentially carried out as before [11]. Proteomics analysis was conducted using liquid chromatography coupled to tandem mass spectrometry (LC-MS²).

(d) Statistical analysis

Non-parametric Mann Whitney U-tests were used to individually compare irs expression, fresh weight, developmental time and ovary size between groups. Proteomic data were analysed by an established combination of Mann Whitney U-tests with correction for type I error inflation (see the electronic supplementary material; [12]).
3. RESULTS
(a) Verification of *irs* RNAi
Larvae treated with *irs* dsRNA in queen diet showed reduced whole-body *irs* expression compared with control larvae-fed queen diet with *gfp* dsRNA (p < 7.4E − 07, n = 12, figure 1a). RNA quantification to actin or tubulin housekeeper genes gave corresponding results (see the electronic supplementary material).

(b) Morphological phenotyping
Compared with controls, *irs* knockdowns took longer to develop (p < 2.2E − 16, n = 50, figure 1b), had lower fresh weight (p < 1.5E − 11, n = 20, figure 1c), fewer ovarioles (p < 7.4E − 07, n = 12, figure 1d), and were smaller in size throughout development (figure 1e–h). As adults (n = 50), more than 80 per cent *irs* knockdowns exhibited a worker-specific structure on their hind leg (corbica, used to collect pollen) and lacked the mandibular notch typical of queens. The residual individuals (less than 20%) had one intercaste character; either lack of corbica or presence of mandibular notch. As previously noted [3], more than 50 per cent of controls had queen morphology, while the remaining individuals (less than 50%) displayed one intercaste trait (presence of corbica or lack of mandibular notch, total n = 30). Queen versus worker caste frequencies were significantly different between groups (Chi-square = 55.0, d.f. = 1, p < 1.0E − 5).

(c) Peptidome database
LC-MS/MS-based peptidomics was conducted on larvae collected 72, 96 and 120 h after the first feeding of dsRNA. A conservative data analysis corrected for an over-abundance of royal jelly proteins in the sample material suggested diverse metabolic differences between knockdown larvae and the control group (Mann Whitney *U*-tests, p < 0.05, n = 4, figure 2) including hexamerin 110, a fatty-acid binding protein and the product of *vasa intronic gene* (VIG). All peptidomics data have been deposited in NCBI’s Peptidome database (http://www.ncbi.nlm.nih.gov/peptidome/repository/PSE129).

4. DISCUSSION
It was hypothesized that IIS plays a central role during honeybee caste development, but functional evidence for the idea was largely missing. We fill this void by establishing that honeybee queen development is...
blocked by RNAi-mediated repression of irs, encoding a central player in IIS. We observed longer developmental times, reduced fresh weights, smaller ovaries and presence of corbicula but absence of mandibular notch in irs knockdowns. These findings are in good agreement with characteristic differences between queen and worker bees reared in natural nests [1].

Our study complements that of Patel et al. [3], who reported the same developmental effect of reducing nutrient sensing by TOR RNAi. Taken together, these results show that honeybee queen development cannot proceed if IIS or TOR transduction is reduced.

We profiled the proteome of larvae to observe the molecular response to irs RNAi. As a conservative measure, we opted to exclude proteins with reduced abundance in controls because royal jelly proteins were more abundant in this group. Honeybee larvae are submerged in jelly protein, and differences in amounts of jelly carried over to the proteomic analysis (e.g. owing to different larval size or gut content of food), could lead to underestimation of some relative protein levels in controls. Our analysis excluded these (putative) false positives.

Hexamerin 110 was reduced in irs knockdown (figure 2). Hexamerin protein levels were previously reported to be lower in worker-destined than in queen-destined larvae of Apis mellifera and other social Hymenoptera, e.g. Polistes metricus [13,14]. Furthermore, a link between hexamerin and caste is found in termite, where hexamerin RNAi biases development toward soldiers and away from reproductives [15]. The hexamerin protein family, therefore, can be central to caste differentiation in social insects, perhaps by representing a caste-specific nutrient storage and supply [16].

Higher levels of a fatty acid binding protein (FABP-like) homologue in controls suggested that fatty acid metabolism was altered by irs RNAi. In vertebrates, FABPs may have indirect effects on IIS with lower abundance in controls because royal jelly proteins are in good agreement with characteristic differences between queen and worker bees reared in natural nests [1].

Huntington's disease is characterized by a loss of neurons in the brain, leading to symptoms such as tremors and difficulty with movement. The genetic mutation that causes Huntington's disease is a repeat expansion of a CAG triplet in the huntingtin gene, resulting in an abnormal protein that accumulates in neurons and leads to cell death. Researchers have investigated the role of Huntington's disease in social insects like honeybees, looking for potential links between the disease and caste differentiation.

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