

Temporal variation in brain transcriptome is associated with the expression of female mimicry as a sequential male alternative reproductive tactic in fish

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Abstract

Distinct patterns of gene expression often underlie intra- and intersexual differences, and the study of this set of coreregulated genes is essential to understand the emergence of complex behavioural phenotypes. Here, we describe the development of a de novo transcriptome and brain gene expression profiles of wild-caught peacock blenny, *Salaria pavo*, an intertidal fish with sex-role reversal in courtship behaviour (i.e., females are the courting sex) and sequential alternative reproductive tactics in males (i.e., larger and older nest-holder males and smaller and younger sneaker males occur). Sneakers mimic both female's courtship behaviour and nuptial coloration to get access to nests and sneak fertilizations, and later in life transition into nest-holder males. Thus, this species offers the unique opportunity to study how the regulation of gene expression can contribute to intersex phenotypes and to the sequential expression of male and female behavioural phenotypes by the same individual. We found that at the whole brain level, expression of the sneaker tactic was paralleled by broader and divergent gene expression when compared to either females or nest-holder males, which were more similar between themselves. When looking at sex-biased transcripts, sneaker males are intersex rather than being either nest-holder or female-like, and their transcriptome is simultaneously demasculinized for nest-holder-biased transcripts and feminized for female-biased transcripts. These results indicate that evolutionary changes in reproductive plasticity can be achieved through regulation of gene expression, and in particular by varying the magnitude of expression of sex-biased genes, throughout the lifetime of the same individual.

KEYWORDS

alternative reproductive tactics, behavioural plasticity, neurogenomic state, RNA-seq, *Salaria pavo*, sex-biased gene expression

1 | INTRODUCTION

Sexual dimorphisms in morphological and behavioural traits are ubiquitous in sexually reproducing organisms, and in most studied cases are paralleled by differential gene expression between the sexes for loci that are present in both males and females (Ellegren & Parsch,

2007; Mank, 2009, 2017). Thus, it has been hypothesized that sex biases in gene expression may play a central role in resolving sexual conflict and that sex-specific transcription regulatory mechanisms may be key in sexual selection (Pointer, Harrison, Wright, & Mank, 2013). This rationale can be extended to species with alternative reproductive tactics (ARTs) where multiple phenotypes may occur

within one of the sexes, typically males, with varying degrees of sexual dimorphism. In ARTs, at least two sexually mature (i.e., with functional testes) male morphs occur: (i) bourgeois males that fully express male secondary sexual characters and compete for the monopolization of access to mates (e.g. by defending breeding territories), expressing male-typical behaviour (e.g., aggression, courtship); (ii) parasitic males (aka sneakers) that do not express male secondary sexual characters and behaviour, and exploit the investment of bourgeois males to get access to mates (e.g., sneaking fertilizations) (Taborsky, Oliveira, & Brockmann, 2008). Hence, species with ARTs offer the possibility to test the hypothesis that differential expression of sex-biased genes is also a major genetic mechanism for the evolution of intrasexual variation in reproductive tactics by providing interindividual variation in the expression of behavioural and morphological sex-related traits. Moreover, in some species, female-mimicking sneaker males occur. These sneaker males are morphologically and behaviourally similar to females but have functional male gonads, and use their female resemblance to approach mating pairs in order to try to get parasitic fertilizations (Taborsky, 1994; Taborsky et al., 2008). Thus, these males have male and female traits expressed in the same phenotype. This raises the question of how regional differential regulation of gene expression may accommodate different sex phenotypes across different tissues and the role it may play in the evolution of ARTs. Interestingly, in some cases, female-mimicking ARTs are expressed by the same individual at different life-history stages, which raises the additional hypothesis that temporal differential regulation of gene expression may allow for the evolution of sequential ARTs within the same individual.

In recent years, the possibility of analysing gene expression profiles without a reference genome (e.g., RNA-seq; Wang, Gerstein, & Snyder, 2009) allowed us to test the above-mentioned hypotheses in nonmodel organisms (Zuk & Balenger, 2014). For example, in two horned beetle species with ARTs (*Onthophagus taurus* and *O. nigriventris*), gene expression in different tissues was as divergent between alternative male morphs as it was between sexes (Snell-Rood et al., 2011). However, in the bulb mite, *Rhizoglyphus robini*, the number of

sex-biased genes in whole-body expression analysis was much higher than the number of genes differentially expressed between male morphs (Stuglik, Babik, Prokop, & Radwan, 2014). Within teleosts, the variability of reproductive systems is vast, and most studies have focused on the characterization of whole-brain gene expression patterns associated with discrete reproductive phenotypes. In all studies, gene expression differences between members of the same species that differ in plasticity of mating tactics reflect how they differ in behaviour and life history (Aubin-Horth, Landry, Letcher, & Hofmann, 2005; Fraser, Janowitz, Thairu, Travis, & Hughes, 2014), and these differences are more pronounced among male tactics than between sexes (Nugent, Stiver, Alonzo, & Hofmann, 2016; Partridge, MacManes, Knapp, & Neff, 2016; Schunter, Vollmer, Macpherson, & Pascual, 2014; Stiver, Harris, Townsend, Hofmann, & Alonzo, 2015).

In this study, we investigate the role of gene expression in the expression of female-mimicking male ARTs in the peacock blenny *Salarias pavo* (Blenniidae; Figure 1) a littoral fish where female-mimicking males occur (Gonçalves, Almada, Oliveira, & Santos, 1996). In this species, nest-holder (bourgeois) males are larger than females, have well-developed secondary sexual characters (SSCs; viz. a head crest and a sex-pheromone-producing anal gland), which are used to attract females to their nests for spawning (Barata et al., 2008; Gonçalves, Barata, Oliveira, & Canário, 2002), and provide sole parental care to eggs until hatching (Fishelson, 1963; Patzner, Seiwald, Adlgasser, & Kaurin, 1986). In a population where nest sites are scarce, and the operational sex ratio is female-biased, females become the courting sex (Almada, Gonçalves, Santos, & Baptista, 1994; Saraiva, Barata, Canário, & Oliveira, 2009). Female courtship consists of the expression of a transient nuptial coloration and in stereotypic movements directed towards nest-holder males (Almada et al., 1994). In this population, an alternative male mating tactic is also present, consisting of smaller and younger males behaving as female mimics to get access to nests guarded by nest-holder males and sneak fertilizations (Gonçalves et al., 1996). Sneaker males switch to nest-holders at a later age (Fagundes et al., 2015), and hence, the same male expresses both male and female reproductive

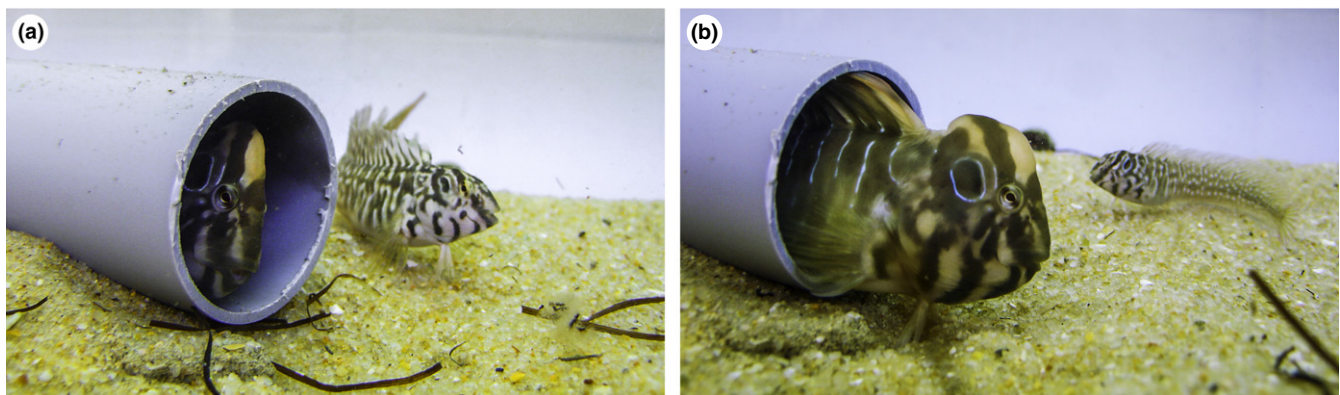


FIGURE 1 The peacock blenny (*Salarias pavo*) has two reproductive male morphs and sex-role reversal in courtship behaviour. Larger and older nest-holder males (inside the nest) with well-developed secondary sexual characters (e.g., head crest) are courted by (a) females and (b) smaller and younger sneaker males behaving as female mimics. Both females and sneaker males while courting the nest-holder male display a conspicuous nuptial coloration that consists on a pattern of dark and light band across the anterior portion of the body

behaviour during his lifetime. Here, we specifically tested: (i) whether differences in sexual dimorphism in reproductive behaviour between sneaker and nest-holder males are paralleled by gene expression differences in the brain; and (ii) whether the sneakers' brain transcriptome is closer to that of nest-holder males, as both are sexually mature males and hence are expected to have masculinized brains, or to that of females, because both express female courtship and nuptial coloration. We have also studied males that are in transition from the sneaker to the nest-holder male phenotype. These transitional males are no longer reproductively active as sneakers (i.e., they no longer express female-mimicking behaviour typical of sneakers), but they also have not become nest-holders yet, as they lack the male secondary sexual characters and do not defend a nest. Moreover, transitional males possess reduced testes which may result from their investment in somatic growth to become nest-holders, as nest-holders' reproductive success depends on body size (Oliveira, Almada, Forsgren, & Gonçalves, 1999). Thus, transitional males offer the opportunity to have an extra sampling point in the intrasex dimorphism continuum. As this is the first study reporting whole transcriptome sequencing for this species, we have also provided a brief characterization of the peacock blenny's transcriptome.

2 | MATERIALS AND METHODS

2.1 | Ethics statement

All procedures were performed in accordance with accepted veterinary practice under a "Group-1" licence issued by the Direção-Geral de Veterinária, Ministério da Agricultura, do Desenvolvimento Rural e das Pescas, Portugal (permit number 0421/000/000/2013).

2.2 | Sample collection

Individuals were collected during the breeding season at Culatra Island (Ria Formosa Natural Park, 36°59'N, 7°51'W, Portugal; for a detailed description of the sampling area, see Almada et al., 1994). During the breeding season, both females and sneaker males actively express courtship behaviour towards the nest-holder males, while nest-holder males defend nests and provide sole parental care to eggs (Almada, Gonçalves, Oliveira, & Santos, 1995; Gonçalves et al., 1996). The peacock blenny is an intertidal species, and hence, individuals were captured with hand nets during low tide; nest-holder males were collected from their nests, whereas females, sneaker males and transitional males were collected from surrounding areas, where they seek shelter in small pools under tiles and other debris. As sneaker males are female mimics, we used sperm release upon gentle abdominal pressure as an identification criterion. Transitional males, which represent the shift from sneaker to nest-holder males, were identified by having poorly developed secondary sexual characters (SSCs) and a larger body size than sneakers, while not releasing sperm upon abdominal pressure. Fish were euthanized using a lethal dosage of the anaesthetic MS-222 (tricaine methanesulphonate; Sigma-Aldrich) followed by rapid severance of the spinal cord with a scalpel. Brain

dissection occurred within 5 min after capture, and brains were immediately immersed in RNAlater (Sigma-Aldrich), kept at 4°C for 24 hr and stored at -80°C until further processing. Fish were then dissected to assess gonadal sex by direct inspection of the gonads.

Thirty-seven individuals (nine females, nine nest-holder males, nine sneaker males and 10 transitional males) were sampled for gene expression analysis, establishing two replicates of pools of 4 to 5 individuals for each phenotype. Among males, sneakers had the largest gonads relative to their body size (gonadosomatic index (GSI)), followed by nest-holders and then by transitional males (Welch's one-way ANOVA, $F_{2,11,0} = 47.708$, $p < .001$). This variation in GSI followed previously reported patterns (Gonçalves, Teles, Alpedrinha, & Oliveira, 2008; Gonçalves et al., 1996) confirming the reproductive state of examined male individuals (i.e., only nest-holder and sneaker males are sexually mature). All females used in this study were expected to be actively courting, as their GSI values indicate they were sexually mature (mean \pm SEM = 10.65 ± 3.54 ; see (Patzner, 1983) for a description of the ovarian cycle of this species), and in this species, all sexually mature females are known to exhibit courtship behaviour (Almada et al., 1995).

2.3 | RNA extraction and sequencing

Total RNA was extracted from whole brain tissue for each individual of the four phenotypes. Samples were transferred to 1 ml of QIAzol lysis reagent (Qiagen) and the tissue was homogenized (on ice) with a sonicator. RNA was then extracted using the RNeasy Lipid Tissue Mini Kit (Qiagen) following the manufacturer's protocol. RNA quality and concentration for each sample were determined using a NanoDrop 1000 spectrophotometer (Thermo Scientific). Equal amounts of RNA from each individual were used to prepare the RNA pools corresponding to the replicated libraries for each phenotype (two libraries per phenotype).

Preparation and sequencing of the eight pooled RNA libraries were performed by The Genome Analysis Centre (TGAC, Norwich, United Kingdom). Upon arrival, samples' RNA integrity was verified on the Agilent 2100 Bioanalyzer. Libraries were prepared from polyA+ RNA and sequenced in two lanes on the Illumina HiSeq 2000 as paired-end 100-bp reads with an approximate insert size of 341 bp. Each library was sequenced at a high depth (Table S1) to detect transcripts that can become underrepresented when analysing whole brain tissue expression. To improve the de novo assembly, four additional pooled libraries, one for each phenotype, were also prepared using RNA from the previous collection, and sequenced using Roche's 454 technology. Library preparation and single-end sequencing on a GS-FLX System were performed at Max Planck Institute (Berlin, Germany) using the manufacturer's protocol.

2.4 | De novo assembly

Quality filtering and trimming of Illumina reads were carried using implemented plugins in CONVEYOR software (Linke, Giegerich, & Goesmann, 2011), keeping only pairs of reads that had an overall Phred

quality score superior to 20 and a minimum read length of 50 bp (Table S1). In addition to the 454 data, a multitissue data set previously sequenced and used for microsatellite mining (Cardoso et al., 2013) was also included in the analysis. All 454 reads were quality-trimmed to have an overall Phred quality score of 15 and a minimum read length of 100 bp. Read quality was assessed using FastQC v0.7.2 (Andrews, 2010).

The de novo transcriptome assembly was carried out in two phases (Fig. S1). First, all 454 reads, which represent the long reads in this work, were assembled with Newbler (454 SEQUENCING SYSTEM SOFTWARE v2.6; Roche) using the *-urt* option to recover more complete representations of transcripts as well as low coverage transcripts. The resultant 63,521 Newbler isotigs (N50 = 464 bp) were then given as input together with the Illumina reads to Trinity assembler v20110820 (Grabherr et al., 2011) with default parameters. After redundancy and exogenous contig removal (see Supporting information for more details), 577,532 putative transcripts with an N50 of 1,165 bp (Table S2) were functionally annotated against UniProtKB (taxonomic division vertebrate databases, release April 2014) using BLASTX with an E-value cut-off of 10^{-5} , allowing a maximum of 10 hits per contig.

2.5 | Differential expression analysis

For differential expression (DE) analysis of transcripts, pairs of reads from each of the eight sequenced libraries (two pools from each male morph and female) were mapped separately against the filtered Trinity assembly using BOWTIE v1.0.0 (Langmead, Trapnell, Pop, & Salzberg, 2009) within RSEM v1.2.8 (Li & Dewey, 2011) with default settings. On average, 77.8% of the pairs of reads from each library mapped back onto the reference assembly (Table S2). Due to the high read depth of our data set and the use of pooled individuals for sequencing, we expected that some of the 577,532 contigs present in the assembly would represent assembly mistakes and rare variants (e.g., genetic polymorphisms, introns, chimeras, sequencing errors). To remove this low-level expression noise from the analysis we employed a filter similar to the one used by Harrison, Mank, and Wedell (2012), and discarded all contigs that did not have at least two fragments per million mappable reads (FPKM = 2, corresponding to 179,202 contigs retained; Fig. S2; Table S2 for more details).

Pairwise comparisons were made using the two libraries per phenotype as biological replicates in the R package DESEQ v1.14.0 (Anders & Huber, 2010) by applying the default parameters. DESeq has a more data-driven parameter estimation, allowing a better performance in controlling the false-positive rate while also maintaining the power to detect differentially expressed transcripts when analysing experimental designs with a low number of replicates per condition (Soneson & Delorenzi, 2013; Zhang et al., 2014). Transcripts were considered to be differentially expressed with a fold change >2 and a $p < .05$ after Benjamini–Hochberg adjustment for multiple testing (Benjamini & Hochberg, 1995). For visualization of the global expression patterns of differentially expressed transcripts among phenotypes, variance-stabilized transformed expression values were

retrieved and Trinity scripts for heatmap generation using the *hclust* function in R adapted to produce a hierarchical clustering of Z-transformed expression values using Euclidean distance with complete linkage. The reliability of the inferred tree was assessed by 1,000 bootstrap resampling of the expression values using the R package PVCLUST v1.2.2 (Suzuki & Shimodaira, 2006). A principal component analysis was also performed using the R package PLOT3D v1.1. Differences in transcript regulation bias towards up- or downregulation among phenotypes were analysed using a two-way contingency table simulation statistics (ACTUS2, Estabrook, Almada, Almada, & Robalo, 2002), based on 1,000 simulations. Other statistical analyses and graphing presented in this work were obtained using R (R Development Core Team 2014).

2.6 | Transcriptional co-expression network analysis

To investigate the network of co-expressed genes (i.e., gene modules) across phenotypes, a weighted co-expression network analysis (WGCNA) was conducted (R package WGCNA v1.51; Langfelder & Horvath, 2008). This analysis clusters together genes with highly correlated expression values across all samples into modules (Langfelder & Horvath, 2008). Variance-stabilized transformed expression values from all transcripts that underwent differential expression analysis in DESeq were used. A block-wise weighted signed network approach was followed, using a maximum of 36,000 transcripts in each block, due to constraints in R memory allocation when working with large data sets. In brief, this method preclusters nodes into large blocks in an unsupervised way, where hierarchical clustering is applied independently defining the dendrogram of gene modules (Langfelder & Horvath, 2008). Afterwards, the module detection results are combined across blocks by merging modules whose eigengenes (i.e., module-weighted average expression profiles) are highly correlated (Langfelder & Horvath, 2008). The soft-thresholding power (β) was set to 17, corresponding to an *R*-squared of >0.80 (Zhang & Horvath, 2005) (mean connectivity of 3,406.6; Fig. S3), with a minimum module size of 30 transcripts. Modules were merged when eigengene dissimilarity between modules was <0.20. Default settings were used for all other WGCNA parameters. Statistical significance of module correlation with each phenotype was determined when $p < .05$ after a Benjamini–Hochberg adjustment for multiple testing. These modules were subsequently validated in silico by assessing the relationship between transcript significance for each phenotype and module membership (i.e., correlation of the module eigengene with the transcript expression profile).

2.7 | Functional annotation

Sequences and BLAST results for the selected level of differential expression analysis (FPKM = 2) were imported into BLAST2GO v2.7 (Conesa et al., 2005), and mapping of Gene Ontology (GO) terms (Ashburner et al., 2000) proceeded against a local database (release April 2014). For the detected differentially expressed contigs, samples' mapping results were manually checked in IGV v2.3.37 (Robinson

et al., 2011) and annotations were further refined based on the characteristics of contig hit alignments by cross-checking BLASTX results from UniProtKB and NCBI's nr database (E-value cut-off of 10^{-5} , release April 2014). After this step of manual curation, detected chimeras, contigs whose BLAST hits belonged to different genes that showed no significant overlap, were not considered for further analyses ($N = 18$). GO terms were annotated using an annotation cut-off of 65 and a GO weight of 10, which resulted in 111,325 GO terms annotated to 30,367 contigs and exported in tabular form. GO term enrichment for modules and contigs detected as differentially expressed were evaluated by GOSTATS v2.32 R package (Falcon & Gentleman, 2007) using a "conditional" hypergeometric test with a $p < .01$. This method accounts for the hierarchical relationships of GO terms by removing genes from ancestor terms if they are significantly enriched in a child term. We did not apply any formal correction for multiple testing due to the implicit dependence between neighbouring GO terms, which do not comply with the independence of tests needed for correction of the p -values. Semantic similarity among phenotypes for enriched GO terms was computed using the Wang graph-based method available in the R package GOSEMSIM v1.30.3 (Yu et al., 2010) independently for each GO ontology, and the respective scores used to cluster samples according to their GO similarity using heatmap clustering. The relative contribution of GO enrichment data in terms of GO classes they represent was visualized using the GO slim vocabulary and the web tool CateGORizer (Hu, Bao, & Reecy, 2008).

3 | RESULTS

A total of 1.3 million single-end reads with an average size of 375 bp and 210 million paired-end reads with an average size of 93 bp remained after trimming and were used for de novo transcriptome assembly. After filtering lowly expressed transcripts, the reference assembly featured 179,202 transcripts with an N50 length of 1,646 bp (Table S2). The annotation of the peacock blenny transcriptome assembly against the vertebrate division of UniProtKB revealed that only 45,994 contigs (ca. 25.7%) had a BLAST hit and that more than half of these contigs had its top hit from one of three species of fish, *Oreochromis niloticus* ($N = 18,139$), *Xiphophorus maculatus* ($N = 5,190$) and *Gasterosteus aculeatus* ($N = 4,423$).

3.1 | Differential transcript expression across phenotypes

Six pairwise comparisons were performed using DESeq's negative binomial model with a false discovery cut-off of 5%, resulting in a total of 814 transcripts (corresponding to 0.45% of the transcriptome and 704 Trinity predicted genes) detected as being differentially expressed among the four phenotypes. Normalized expression profiles represented by hierarchical clustering were obtained considering all phenotypes (Figure 2a). All biological replicates were clustered according to their respective phenotype. The profile of DE

transcripts was more similar between nest-holder males and females than with transitional males or with sneaker males. Sneakers formed their own cluster apart from all other phenotypes. All clusters had high confidence, as illustrated by the bootstrap probability values (Figure 2a). Principal components analysis of DE transcripts also showed a clear separation among male morphs, with the first three components accounting for 85.2% of the observed variance in transcript expression (Figure 2b; Table S3).

Regarding the pairwise comparisons (Table 1; Tables S4–S9), the comparison between nest-holder males and females had the lowest number of differentially expressed transcripts ($N = 155$), whereas the comparison between sneakers and transitional males had the highest number of differentially expressed transcripts ($N = 348$). Overall, sneaker males differed from the other phenotypes in the expression of 644 transcripts (78.38% annotated), followed by transitional males (600 transcripts; 75.71% annotated), females (564 transcripts; 76.51% annotated) and finally nest-holder males (518 transcripts; 78.92% annotated). A bias in the direction of expression of these transcripts was also detected for each phenotype. Looking into the total number of transcripts that were either up- or downregulated in a phenotype, nest-holder males and females had more transcripts upregulated and fewer transcripts downregulated than expected by chance, whereas sneaker and transitional males had the opposite pattern with fewer transcripts upregulated and more transcripts downregulated than expected by chance (one-tailed p -value $< .05$; Figure 2c). These results point to different mechanisms of gene regulation acting across phenotypes. However, when the number of transcripts that were only found to be either up- or downregulated on a specific phenotype was examined, all phenotypes showed a bias towards downregulation (Z-tests with $p < .05$: nest-holder, $z = -12.69$; transitional, $z = -13.64$; sneaker, $z = -10.63$; female, $z = -12.01$; Figure 2c), indicating that negative regulation of gene expression was more specific within each phenotype than positive regulation.

3.2 | Gene Ontology (GO) enrichment analysis

GO analysis for upregulated transcripts within each phenotype revealed distinct classes of enriched terms in male morphs (Figure 3; Table S10). Nest-holder males had a predominant enrichment for processes related to lipid metabolism and transmembrane transport of ions at the cell level. Females showed a predominant enrichment for protein metabolism and, similarly to nest-holder males, transmembrane transport of ions. Sneaker males had a specific enrichment for processes related to morphogenesis, development, cell cycle and DNA metabolism. Finally, transitional males showed an enrichment primarily for regulation of cellular transport, cellular organization and biogenesis processes. Noteworthy, all phenotypes, with the exception of nest-holder males, had an enrichment for terms related to cell, cytoskeleton and organelle organization and biogenesis, whereas sneaker males were the only phenotype with enrichment for extracellular processes (Figure 3). These enrichment results were further used to obtain measures of GO semantic similarity among phenotypes separately for each ontology (Figure 3). For both

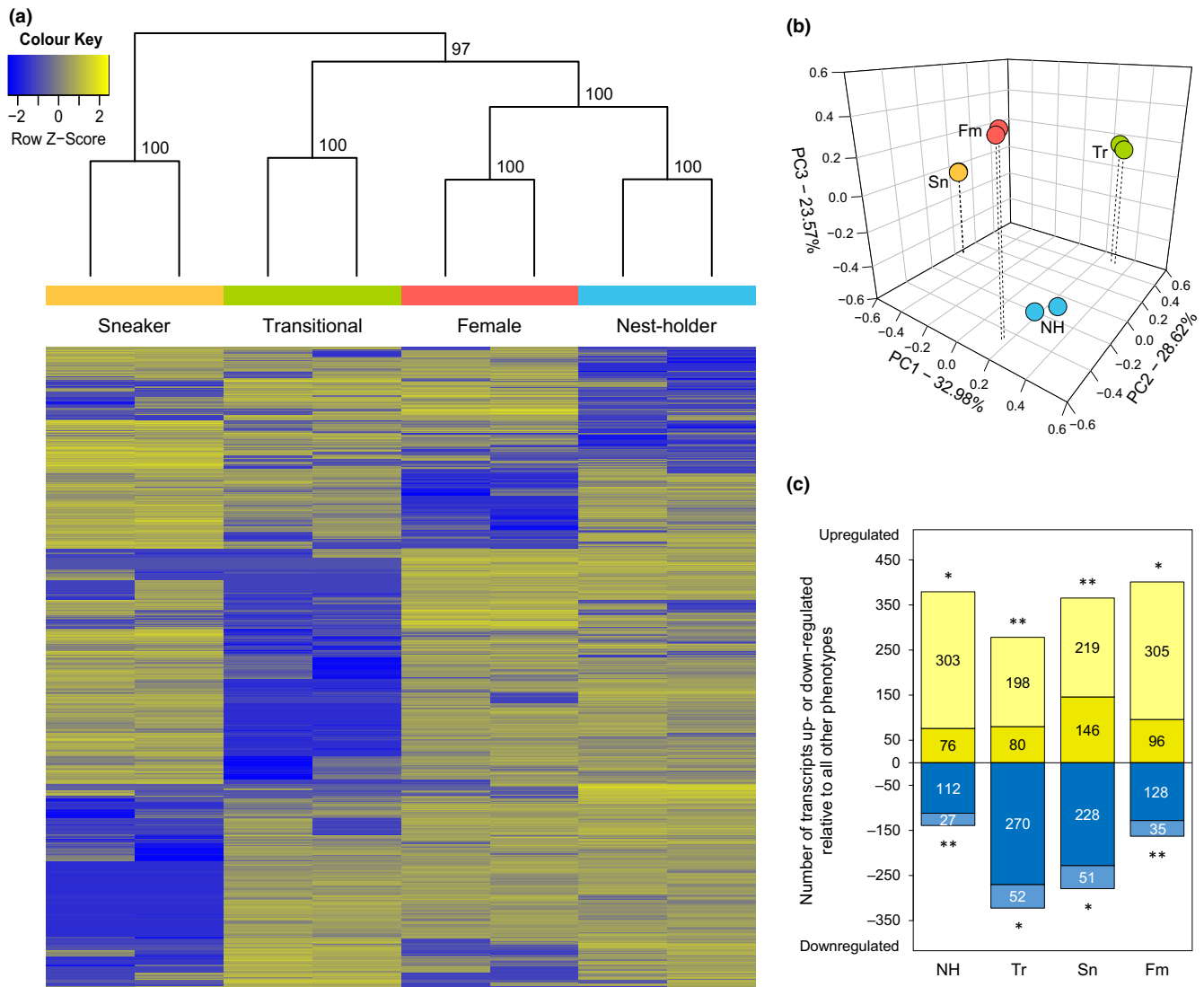


FIGURE 2 Differences in brain expression patterns across *Salaria pavo* phenotypes. (a) Heatmap of all transcripts differentially expressed ($N = 814$) between 2 or more phenotypes, either with or without functional annotation. Intensity of colour indicates relative expression levels of each transcript (rows) in each phenotype sample (columns), with blue representing downregulated transcripts and yellow upregulated transcripts. Similarity between phenotypes with hierarchical clustering can be seen above the heatmap with respective bootstrap values. (b) Principle components analysis (PCA) shows a clear separation between male morphs across the first three components, which account for 85.2% of the observed variance in transcript expression. (c) Total number of transcripts for which each phenotype showed significantly different expression from all other phenotypes. Differences in the degree of bias in expression for each phenotype towards up- or downregulation were tested using a two-way contingency table simulation statistics (* cases detected as significantly big, ** cases detected as significantly small based on 1,000 simulated tables in ACTUS2, one-tailed p -value < 0.05). Dark yellow and dark blue bars indicate the number of transcripts expressed exclusively by the phenotype. Light yellow and light blue bars indicate the number of transcripts expressed in two or more phenotypes regardless of the pairwise comparison. Each phenotype is colour-coded in agreement with blue for nest-holder males (NH), green for transitional males (Tr), orange for sneaker males (Sn) and red for females (Fm)

“Biological Process” and “Molecular Function,” nest-holder males and females had a GO enrichment more similar between themselves than with sneakers and transitional males. In contrast, for “Cellular Component” enrichment, transitional males were closer to nest-holders. Taken together, these results are in accordance with the gene expression level clustering.

Additionally, GO analysis for downregulated transcripts within each phenotype also presented distinct classes of enriched terms in male morphs (Figure 4; Table S11). Transcripts downregulated in nest-

holder males had a predominant GO enrichment for processes related to cell and organelle organization and biogenesis, cell differentiation and protein metabolism and modification at the cell and intracellular level. Downregulated transcripts in females showed a predominant enrichment for processes related to transporter activity, metabolism and biosynthesis. Finally, both sneaker and transitional males had transcripts downregulated with an enrichment for ion transport activity. Additionally, only transitional males presented an enrichment for processes related to lipid metabolism and development. GO semantic

TABLE 1 Number of significantly expressed transcripts and percentage of annotated transcripts in each pairwise comparison between phenotypes of *Salaria pavo*

	Total	Annotated (%)
Nest-holder > Female	84	76.19
Female > Nest-holder	71	74.65
Nest-holder > Sneaker	155	76.77
Sneaker > Nest-holder	92	84.78
Nest-holder > Transitional	174	81.03
Transitional > Nest-holder	59	79.66
Sneaker > Female	106	75.47
Female > Sneaker	173	76.88
Transitional > Female	72	69.44
Female > Transitional	195	78.97
Sneaker > Transitional	187	85.56
Transitional > Sneaker	161	64.60

> indicates higher expression in the phenotype on the left. FDR adjusted significance value of .05.

similarity analysis (Figure 4), showed that overall sneaker and transitional males had a GO enrichment more similar between themselves than with females or nest-holder males, with the exception for “Biological Process” where nest-holder males had the most dissimilar enrichment when compared with the remaining phenotypes.

3.3 | Demasculinization vs. feminization of the brain transcriptome of sneakers and transitional males

To further test how the brain transcriptomes of sneakers and transitional males are related to the ones of either nest-holder males or females, we analysed sex-biased transcripts (i.e., transcripts that were upregulated in either nest-holder males or females; Figure 5). Both sneaker males and transitional males expressed nest-holder-biased transcripts ($N = 84$) at significantly lower levels than nest-holders (Figure 5a), suggesting that the brains of these male morphs are transcriptionally demasculinized. Conversely, both sneaker and transitional males expressed female-biased transcripts ($N = 71$) at higher levels than nest-holder males (Figure 5a), suggesting that their brains are transcriptionally feminized. Interestingly, there were no significant differences between sneaker and transitional males in the expression of either nest-holder- or female-biased transcripts (Figure 5a).

Hierarchical clustering of expression levels showed that both sneaker and transitional males clustered together with high confidence with nest-holder males for nest-holder-biased transcripts, and with females for female-biased transcripts (Figure 5b). This clustering pattern suggests that the brain transcriptome of these two male morphs can be interpreted as intersex rather than either typically male or female. Hierarchical clustering of expression levels also showed that among the three male morphs, transitional and nest-holder males clustered together for nest-holder-biased genes, suggesting a higher degree of demasculinization of the sneakers' brain transcriptome than of the transitional males. In contrast, transitional and sneaker males

clustered together for female-biased genes, suggesting that their brain transcriptomes are equally feminized.

From the 71 female-biased transcripts, 37 were upregulated in sneaker males of which 25 were also upregulated in transitional males relative to nest-holder males (Tables S12 and S13). Thus, the 12 female-biased transcripts, which were exclusively upregulated in females and sneaker males, are potential candidate genes to control the expression of female-like courtship behaviour. These candidate genes had an enrichment in GO terms for biological processes mainly involved in histone modifications and in the regulation of Ral protein signal transduction, which is involved in neural plasticity among other processes (Table S13c).

From the 84 nest-holder-biased transcripts, 48 were also upregulated in sneakers of which 25 were also upregulated in transitional males (Tables S14 and S15). Thus, the 23 transcripts that were exclusively upregulated in nest-holder and sneaker males represent candidate genes for the control of male reproduction as both nest-holders and sneakers, but not transitional males, are sexually mature. These transcripts had an enrichment in GO terms mainly related to cell cycle regulation (Table S15b). From the 84 male nest-holder transcripts, 19 were exclusively upregulated in nest-holder males (but not in either sneakers or transitional males) (Table S14). Hence, these transcripts represent potential candidate genes for the control of male reproductive behaviour (i.e., nesting, breeding territoriality). From these transcripts, only two had GO terms enriched to cell–cell contact and actin cytoskeleton (Table S15d).

3.4 | Patterns of gene co-expression modules among phenotypes

The WGCNA showed that the transcriptome could be clustered in 171 modules, with modules ranging in size from 30 to 41,342 transcripts (Fig. S4 and Table S16). From these, only three modules could be significantly associated with one of the phenotypes after Benjamini–Hochberg correction: the plum3 module (Pearson's $r = .99$ with $p = .001$) with nest-holder males and the sienna3 and salmon modules ($r_{sienna3} = .99$, $r_{salmon} = -.96$, with $p_{sienna3} = .001$, $p_{salmon} = .04$) with sneaker males. All three modules showed a significant positive correlation between transcript significance between the phenotype and module membership, corroborating the importance of these modules for each of the male's phenotypes (Fig. S5). Plum3 module included 296 transcripts, of which seven transcripts were also found upregulated for nest-holder males. This module was mainly enriched for GO terms associated with energy production through the oxidative phosphorylation metabolic pathway (Table S17a). Sienna3 module included 1,031 transcripts, of which 17 were also found as upregulated in sneaker males. This module represented an enrichment for processes involved in the canonical *Wnt* signalling pathway, cytokinesis, glucose metabolism and carbohydrate transport (Table S17b). The only module with a negative correlation was the salmon module containing 7,951 transcripts, of which 142 transcripts were also found downregulated in sneaker males. This module was mainly enriched for processes involved in the regulation of G-protein-coupled receptor signalling pathway (Table S17c).

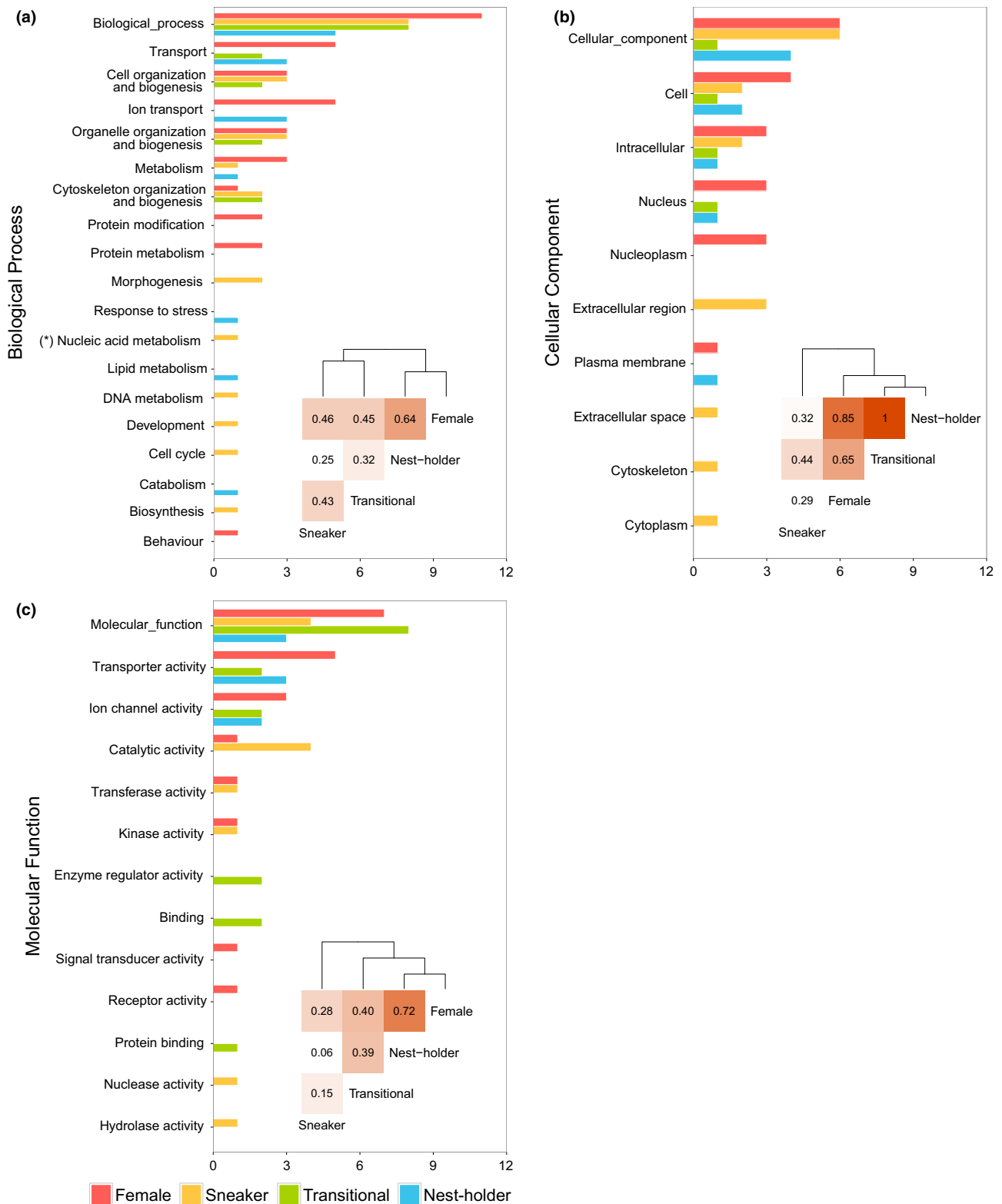


FIGURE 3 Representation of the relative contribution of enriched GO data in terms of GO classes for each ontology, (a) Biological Process, (b) Cellular Component and (c) Molecular Function. Enriched GO terms were obtained for upregulated transcripts in each phenotype and mapped to a total of 127 GO slim ancestor terms with CateGORizer. For each GO class, coloured bars represent the number of enriched terms for each phenotype, with blue for nest-holder males, green for transitional males, orange for sneaker males and red for females. Within each ontology, the heatmap clustering represents the semantic similarity scores for enriched GO terms among phenotypes computed using GOSemSim. Values range between 0 and 1, with higher values indicating greater similarity between groups of GO terms. (*) Complete term for GO class is “nucleobase, nucleoside, nucleotide and nucleic acid metabolism”

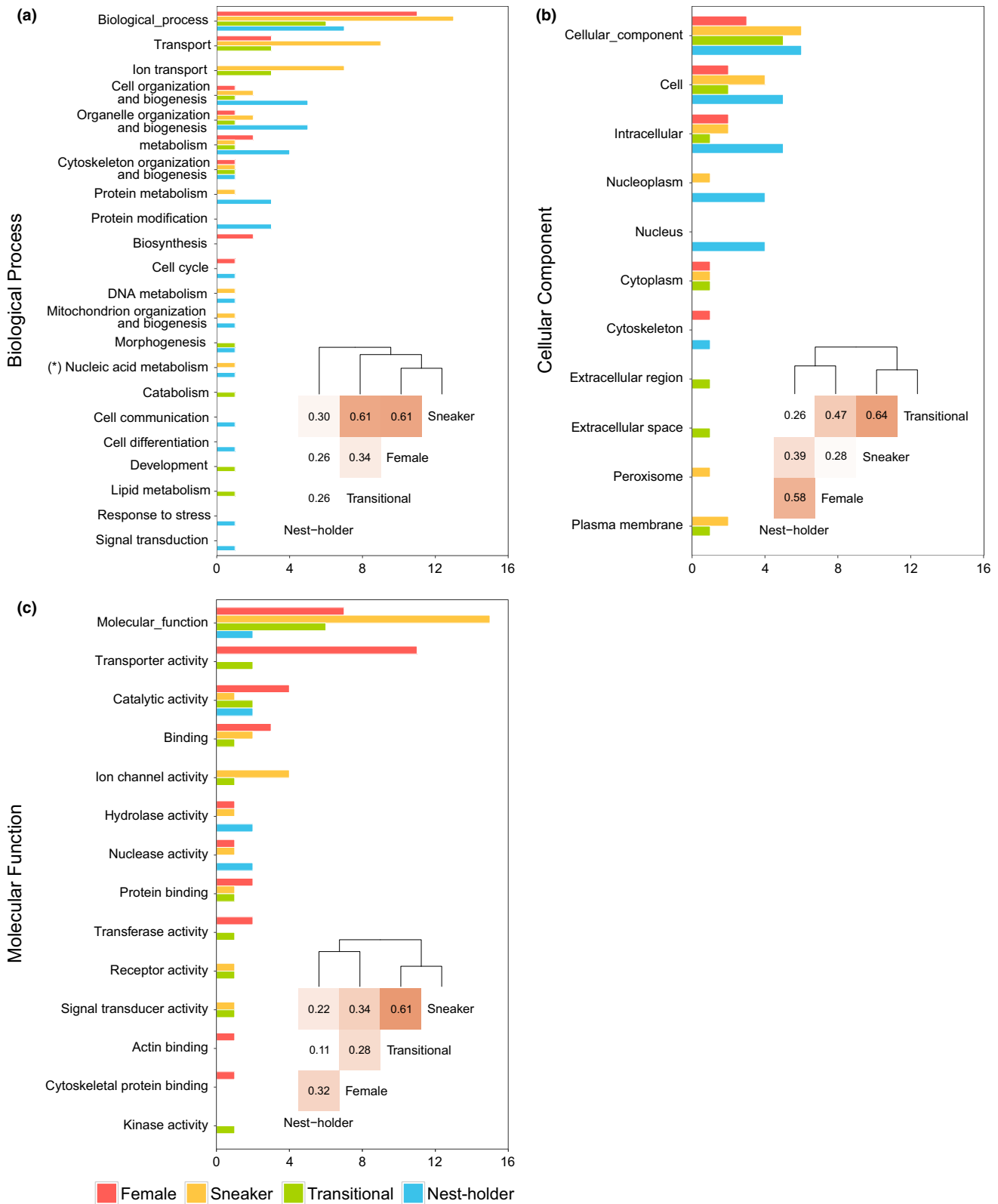


FIGURE 4 Representation of the relative contribution of enriched GO data in terms of GO classes for each ontology, (a) Biological Process, (b) Cellular Component and (c) Molecular Function. Enriched GO terms were obtained for downregulated transcripts in each phenotype and mapped to a total of 127 GO slim ancestor terms with CateGOrizer. For each GO class, coloured bars represent the number of enriched terms for each phenotype, with blue for nest-holder males, green for transitional males, orange for sneaker males and red for females. Within each ontology, the heatmap clustering represents the semantic similarity scores for enriched GO terms among phenotypes computed using GOSemSim. Values range between 0 and 1, with higher values indicating greater similarity between groups of GO terms. (*) Complete term for GO class is “nucleobase, nucleoside, nucleotide and nucleic acid metabolism”

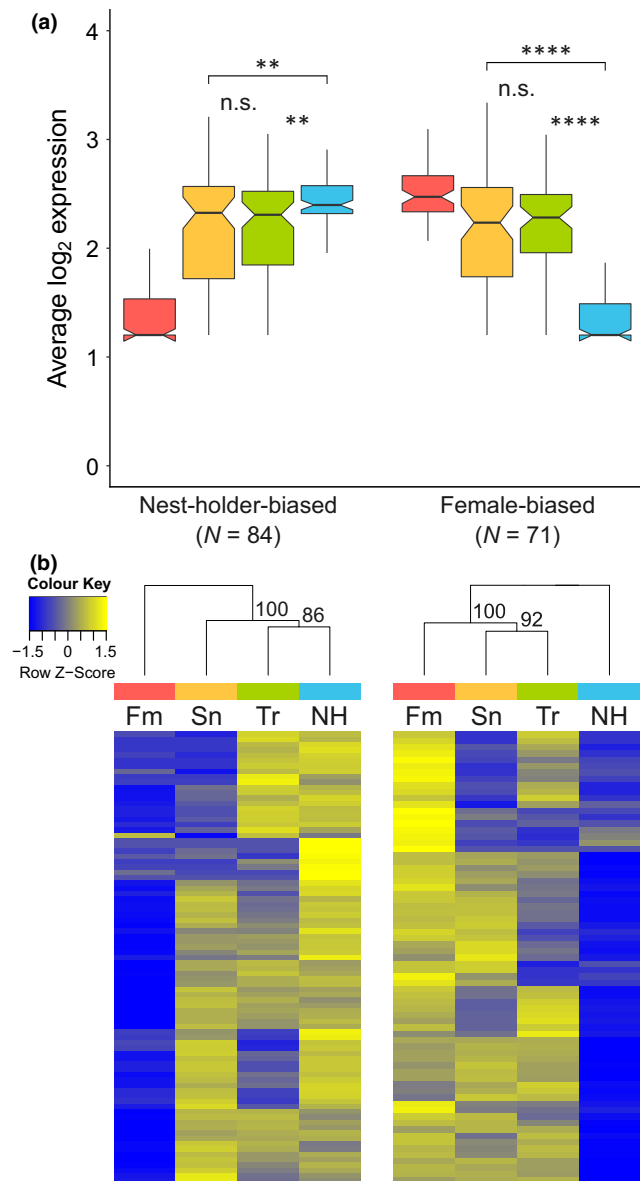


FIGURE 5 Expression patterns for sex-biased transcripts. Nest-holder-biased ($N = 84$) and female-biased ($N = 71$) transcripts in females (Fm, coloured in red), sneaker males (Sn, coloured in orange), transitional males (Tr, coloured in green) and nest-holder males (NH, coloured in blue) represented as average \log_2 variance-stabilized transformed expression values, (a) notched boxplot, excluding outliers, with asterisks indicating significant p -values calculated by the Kruskal–Wallis test, followed by Nemenyi post hoc test to perform multiple comparisons among male morphs (** $p < .01$, **** $p < .0001$), and (b) hierarchical clustering of the four phenotypes with respective bootstrap values

4 | DISCUSSION

Here, we describe the development of a de novo transcriptome and brain gene expression profiles of wild-caught peacock blenny, *Salarias pavo*, an intertidal fish with sex-role reversal in courtship behaviour (i.e., females are the courting sex) and presence of alternative

reproductive male morphs (Fagundes et al., 2015; Gonçalves et al., 1996).

4.1 | Brain transcriptomic architecture of alternative reproductive tactics

We found that each peacock blenny phenotype has a distinct transcriptomic profile (Figure 2a), indicating that distinct behavioural repertoires are associated with distinct neurogenomic states, which differentiate not only sex but also male morphs. These results are consistent with previous studies that have already described this parallel between specific behavioural states and neurogenomic states at different timescales (reviewed in Zayed & Robinson, 2012; Harris & Hofmann, 2014; Cardoso, Teles, & Oliveira, 2015), and with previous reports of specific brain transcriptomic profiles among species with ARTs for alternative male morphs, particularly in teleost fishes (Aubin-Horth et al., 2005; Fraser et al., 2014; Nugent et al., 2016; Partridge et al., 2016; Schunter et al., 2014; Stiver et al., 2015). For example, in bluegill sunfish (*Lepomis macrochirus*), the three male ARTs, encompassing two distinct life histories, presented distinct neurogenomic profiles, with sneaker males having the most divergent expression profile, while parental males were further discriminated in the analysis relatively to their reproductive state (i.e., spawning vs. nonspawning; Partridge et al., 2016). In sailfin mollies (*Poecilia latipinna*), differentially expressed transcripts were also associated with each ART: in which small males and large males have fixed alternative tactics, always displaying sneaking and courtship behaviour, respectively, whereas intermediate males display courtship or sneaking behaviour depending on the male composition of their social environment (Fraser et al., 2014). Interestingly, in sailfin mollies, the differentially expressed transcripts in the brain associated with the plastic male tactic tended to exhibit larger and more robust genetically regulated changes than socially regulated changes (Fraser et al., 2014). Thus, in both fixed and plastic ARTs, the expression of alternative morphs with specific behavioural phenotypes within the same sex seems to be achieved through differential gene expression in the brain. However, when one compares the available brain RNA-seq transcriptome data for teleost species with ARTs, no clear pattern emerges. Whereas in some species sneaker males exhibit the most distinctive transcriptome (e.g., *L. macrochirus* (Partridge et al., 2016); *Tripterygion delaisi* (Schunter et al., 2014; present study)), in other species nest-holder males are the most differentiated phenotype (e.g., *Symphodus ocellatus* Nugent et al., 2016). Similarly, the lists of differentially expressed genes for functionally equivalent phenotypes (e.g., sneakers) across species do not share significant numbers of transcripts, suggesting that ARTS may have evolved in different species through species-specific genetic architectures.

In contrast to the morph-specific profiles of differentially expressed genes, the patterns of gene co-expression modules were only specific for nest-holder and sneaker males. Indeed, the nest-holder phenotype was associated with a gene co-expression module enriched for GO terms associated with energy production,

which may reflect the metabolic demand of reproduction in nest-holder males, who have to defend breeding territories for extended periods of time, in which they do not exit the nest for feeding, hence presenting a sharp decline in their body condition over the breeding season (Gonçalves & Almada, 1997). On the other hand, the sneaker phenotype was associated with (i) the upregulation of a gene co-expression module involved in the canonical *Wnt* signalling pathway and metabolism, which may reflect their developmental stage; and (ii) with a downregulation of a gene co-expression module enriched for processes involved in the regulation of G-protein-coupled receptor (GPCR) signalling pathway, which may reflect a mechanism to make the brain of sneakers less responsive to male gonadal signals (e.g., sex steroids), given that sneakers have mature gonads. In fact, despite the fact that steroid hormones exert their actions by binding to intracellular nuclear receptors, which then bind to DNA to initiate gene transcription (i.e., steroid-inducible transcription factors), steroids can also activate GPCRs in the cell membrane, or even located intracellularly (e.g., G-protein-coupled oestrogen receptor), to initiate rapid nongenomic effects (Gaudet, Cheng, Christensen, & Filardo, 2015; Losel et al., 2003; Maggiolini & Picard, 2010). The lack of specific gene modules for transitional males and females can be due to the complex data set that generated a large number of gene co-expression modules. Nonetheless, the analysis revealed the same pattern as the DE analysis among females and male morphs and, for the three significant modules discussed above, a partial overlap was present between transcripts belonging to the morph-specific gene modules and the direction of expression of differentially expressed genes in those morphs.

Overall, these results suggest that the brain transcriptome reflects better reproductive plasticity rather than sex dimorphism. However, other factors present in the experimental design may have affected the observed patterns as well, namely age differences between phenotypes; analysis of whole brain gene expression data; use of pooled samples; and the low number of biological replicates. For example, the use of whole brain samples may have masked regional differences in gene expression between phenotypes. Nevertheless, whole brain transcriptome analyses have been very informative as a first approach to characterize behavioural phenotypes namely in the ART literature (Aubin-Horth et al., 2005; Fraser et al., 2014; Nugent et al., 2016; Partridge et al., 2016; Schunter et al., 2014; Stiver et al., 2015). Similarly, the use of sample pooled replicates offers the advantage of incorporating information from more individuals into DE analysis while still allowing for the estimation of biological variability (Todd, Black, & Gemmill, 2016), although greater power in the statistical analysis would have been gained using more biological replicates (Robles et al., 2012). Finally, differences among male morphs may be influenced by differences in age, as sneaker males are younger than nest-holder males and transitional males lay between the two. Hence, in this study it is not possible to disentangle the effect of age from that of reproductive tactic. However, it should be noted that the expression of a specific tactic is one of the most prominent phenotypic characteristics

of each age class and that in other studies, where it was possible to assess the effect of age and age-dependent behavioural tactic to the transcriptome, the latter was the most relevant (e.g., differences in gene expression associated with the transition from nurse to forager in honey bees are largely independent of natural age-related changes Whitfield et al., 2006). In summary, despite the possibility of more detailed studies in the future, the present results already reveal ART-specific brain gene expression profiles in the peacock blenny.

4.2 | Potential role of epigenetic mechanisms in alternative reproductive tactics

Although we do not aim to discuss in detail the list of genes differentially expressed between the different morphs of the peacock blenny, it is important to note the presence of enzymes responsible for post-translational modification of histones (i.e., chromatin rearrangements) and for repression of DNA transcription (i.e., DNA methylation), among the differentially expressed transcripts, hence providing some of the first evidence of the relevance of epigenetic marks in this species and more broadly in the context of ARTs. The role of epigenetic mechanisms in the expression of within-species differential behavioural phenotypes has already been highlighted in other contexts, namely in caste differentiation among social insects (e.g., Yan et al., 2014), and recently in relation to social status-dependent behaviours of fish (Lenkov, Lee, Lenkov, Swafford, & Fernald, 2015). In particular in our study, *dnmt3a*, encoding an enzyme responsible for de novo methylation of DNA (Okano, Bell, Haber, & Li, 1999), was upregulated in females, transitional and sneaker males, suggesting a common role for this enzyme in the modulation of behaviour among these phenotypes (e.g., decreased aggression in all three and/or display of female courtship in females and sneakers) when compared with nest-holders. This enzyme has been recently found to be required for brain feminization in female rat pups within the hormonally sensitive period of sexual differentiation (Nugent et al., 2015). During this period, aromatization of testosterone (T), synthesized by male testes, to oestradiol (E2) within the developing neurons, leads to a suppression of *dnmt3a* activity, which in turn enables male-specific neuronal organizational effects to take place and a consequent expression of male sexual behaviours in the adult (Nugent et al., 2015). A similar mechanism of brain feminization may be present in the peacock blenny. In this species, gonadal steroids regulate different aspects of reproductive behaviour in the different morphs (Gonçalves, Alpedrinha, Teles, & Oliveira, 2007; Gonçalves et al., 2014; Oliveira, Carneiro, Gonçalves, Canario, & Grober, 2001), and sneaker males have lower levels of brain aromatase mRNA (Gonçalves et al., 2010) and of brain aromatase activity (Gonçalves et al., 2008) than nest-holder males. Thus, neuronal intracellular levels of E2 are expected to be low in sneakers in comparison with nest-holder males, consistent with the observed upregulation of *dnmt3a* in sneakers. Further experiments are necessary to test this hypothesis further.

4.3 | Genetic architecture of female mimicry in sneaker males

Despite marked sex differences in sexual behaviour between nest-holders and females, in our study, relatively few genes were expressed differentially between the sexes, differences being more pronounced among morphs within the same sex (i.e., nest-holder vs. sneaker vs. transitional males). Thus, it is possible that the observed sex differences in reproductive behaviour are due to these few male- or female-biased genes. Therefore, in order to test the hypothesis that the lack of male reproductive behaviour (i.e., nesting and territorial defence) in sneakers was due to a demasculinization of their brain transcriptome, whereas their expression of female-like behaviour was linked to a feminization of their brain transcriptome, we looked into the expression of male- and female-biased genes across morphs. The fact that both sneaker and transitional males have a lower expression of male-biased brain transcripts than nest-holder males reflects a demasculinization of the brains of these morphs, which may reflect their lack of expression of male reproductive behaviour. On the other hand, the fact that both sneaker and transitional males have a higher expression of female-biased brain transcripts than nest-holder males suggests a feminization of these male morphs. Thus, the brain transcriptome of both sneaker and transitional males is intersex, rather than typically male (or female). However, as from these two male morphs only sneaker males are sexually active and express female-like reproductive behaviour (i.e., courtship and nuptial coloration), the feminization of the sneaker's brain transcriptome (that also occurs in transitional males) cannot be associated with the expression of female-like behaviour by these males. Therefore, female courtship expressed by females and by sneaker males seems to be associated with different brain transcriptomic architectures. This result is further supported by the lack of shared gene modules between sneakers and females in our WGCNA analysis. However, it has been recently shown that individual dimorphically expressed genes in specific regions of the brain may control one or a few components of a sex-typical behaviour in mice (Xu et al., 2012; Yang & Shah, 2014). Therefore, two alternative hypotheses may explain the genetic basis of female mimicry in the peacock blenny sneaker males: (i) despite their kinematic and structural similarities, the courtship behaviour expressed by females and sneaker males is controlled by different genetic programmes; or (ii) despite the lack of differences in the average expression of female-biased genes between sneakers and transitional males, there are specific female-biased genes, which are also biased in sneakers but not in transitional males, that regulate female courtship in both sneakers and females. In support of the latter hypothesis, we found 12 transcripts that were exclusively upregulated in sneakers and females, which have a functional annotation that suggests an involvement on neural plasticity, in some cases with interactions with oestrogen-responsive elements. Interestingly, the mate search component of female courtship in this species has been shown to be oestrogen-dependent (Gonçalves et al., 2014). Thus, the hypothesis of a shared genetic factor underlying the expression of female courtship in both females and sneakers is the most parsimonious of the two presented above. Newly available techniques of

genome editing (e.g., CRISPR/Cas9, Heidenreich & Zhang, 2016; Lee, Sundberg, Sigafos, & Clark, 2016) open the door to testing the role of specific candidate genes in the control of female courtship behaviour in both females and sneakers.

5 | CONCLUSIONS

In summary, our results are consistent with previous studies in species with ARTs and show that at the brain level, intrasexual behavioural plasticity is accompanied by broader changes in gene expression than intersexual differences in sex dimorphism, which is in clear contrast to what has been found in gonad (Dean et al., 2017; Harrison et al., 2015; Pointer et al., 2013) and whole body (Stuglik et al., 2014) transcriptional variation. However, the lack of reference genomes for most teleosts limits much of the work on ARTs possibly leaving other major regulatory and structural mechanisms unexplored (e.g., supergene in the ruff *Philomachus pugnax*; Küpper et al., 2015; Lamichhaney et al., 2015). Furthermore, our results for the peacock blenny also indicate that at the brain level, reproductive plasticity can be explained by varying the magnitude of sex-biased gene expression. A shift in expression of sex-biased genes has been found in response to sexual selection in mating behaviour (Hollis, Houle, Yan, Kawecki, & Keller, 2014; Immonen, Snook, & Ritchie, 2014) and has been considered one of the evolutionary processes for differential male and female adaptation. Our results suggest that a similar process may mediate the evolution of alternative reproductive morphs within one of the sexes, in our case males, that explore new areas of the sex-biased transcriptional landscape.

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DATA ACCESSIBILITY

Both raw data and transcriptome assembly were deposited in BioProject portal at NCBI (PRJNA329073).

AUTHOR CONTRIBUTION

S.D.C., D.G., A.V.M.C. and R.F.O. were responsible for the design and implementation of the study. Assembly of the sequence data was performed by S.D.C. and A.G. and subsequent analyses by S.D.C. S.D.C. and R.F.O. wrote the manuscript with contributions from all authors.

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