Supplementary material for Peichel and Marques, 2017, The genetic and molecular architecture of phenotypic diversity in sticklebacks, *Phil. Trans. R. Soc. B.* doi: 10.1098/rstb.2015.0486

**Supplementary Table S1.** This file is provided as a separate Excel file, and it contains a list of published QTL in threespine (*G. aculeatus*, *G. nipponicus*) and ninespine (*P. pungitius*) stickleback. Physical positions for markers and confidence intervals are given for three threespine stickleback assembly versions [14,17,18]. QTL were loosely grouped into nine functional categories: feeding (teeth, gill rakers, branchial bones, jaw, epaxial muscle), body shape (univariate measures, landmark x- and y-coordinates), defence (lateral plate number and size, dorsal spines, pelvic spines and girdle), behaviour/sensory system (behaviours, lateral line), swimming (vertebrae number, pterygiophore position and number, fin ray position and number), pigmentation (reproductive coloration, melanisation, barring), respiration (opercle size and shape), body size (centroid size, standard length, body weight), and reproduction (testes size, sperm number).

**Supplementary Table S2.** Published QTL studies in threespine (*G. aculeatus*, *G. nipponicus*) and ninespine (*P. pungitius*) stickleback. The mapping crosses used in each study are indicated, including the geographic origin of the populations: Alaska, USA (AK), British Columbia, Canada (BC), California, USA (CA), Switzerland (CH), Finland (FI), Japan (JP), Northwest Territories, Canada (NWT), Scotland, UK (SC), Washington, USA (WA). The ecotype comparisons, trait categories, cross type (backcross (BCx), F2 intercross (F2), admixture mapping (admix)), and number of progeny in the crosses for each study are indicated. If a gene has been identified that underlies a QTL found in a particular study, the trait name, gene name, and reference is indicated. Reference numbers refer to those in the main text.

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| **Species** | **Crosses** | **Ecotypes** | **Trait categories** | **Cross type** | **Number of progeny** | **Gene identification** | **QTL refs** |
| *G. aculeatus* | BC (Priest benthic female x Priest limnetic male) x BC Priest benthic female | benthic-limnetic | defence, feeding | BCx | 92 |  | [10] |
| *G. aculeatus* | JP Pacific Ocean marine female x BC Paxton benthic male | marine-freshwater | defence | F2 | 360 | Plate morph: *Eda* [64]; Plate size: *Gdf6* [70] | [23] |
| *G. aculeatus* | AK Bear Paw, Boot, Whale lakes x AK Rabbit Slough marine | marine-freshwater | defence | F2 | 98, 116, 77 | Plate morph: *Eda* [64]; Pelvic reduction: *Pitx1* [68] | [24] |
| *G. aculeatus* | JP Pacific Ocean marine female x BC Paxton benthic male | marine-freshwater | defence | F2 | 375 | Pelvic reduction: *Pitx1* [25,68] | [25] |
| *G. aculeatus* | AK Bear Paw lake x AK Rabbit Slough marine | marine-freshwater | respiration | F2 | 98 |  | [26] |
| *G. aculeatus* | SC Loch Fada, North Uist female x SC River Kelvin, Glasgow male | lake-stream | defence | F2 | 177 | Pelvic reduction: *Pitx1* [68] | [27] |
| *G. aculeatus* | JP Pacific Ocean marine female x BC Paxton benthic male | marine-freshwater | pigmentation | F2 | 360 | Pigmentation: *Kitlg* [28] | [28] |
| *G. aculeatus* | JP Pacific Ocean marine female x BC Paxton benthic male | marine-freshwater | body shape | F2 | 372 |  | [29] |
| *G. aculeatus*; *G. nipponicus* | JP Pacific Ocean marine female x JP Japan Sea marine male; (Japan Sea female x Pacific Ocean male) x JP Pacific Ocean male | marine-marine | body size, behavior and sensory system; defence, reproduction | F2, BCx | 70, 76 |  | [30] |
| *G. aculeatus* | BC Hotel Lake female x BC Little Campbell marine male | marine-freshwater | body size, pigmentation | F2 | 176 |  | [31] |
| *G. aculeatus* | BC Enos Lake benthic-limnetic admixed population | benthic-limnetic | body shape, pigmentation | admix | 508 |  | [32] |
| *G. aculeatus* | BC Little Campbell marine female x BC Paq, Graham, Hoggan, Cranby lake males | marine-freshwater | body shape, defence, feeding | F2 | 374, 361, 290, 374 |  | [33] |
| *G. aculeatus* | BC Paxton benthic female x JP Pacific Ocean marine male | marine-freshwater | behavior and sensory system, defence | F2 | 234 | Lateral line: *Eda* [66] | [34] |
| *G. aculeatus* | BC Paxton benthic female x JP Pacific Ocean marine male | marine-freshwater | behavior and sensory system | F2 | 229 | Schooling: *Eda* [67] | [35] |
| *G. aculeatus* | BC Paxton limnetic x BC Paxton benthic | benthic-limnetic | body shape, defence, feeding | F2 | 530 |  | [36] |
| *G. aculeatus* | CH Lake Geneva stream female x CH Lake Constance lake male | lake-stream | body shape, defence, feeding, swimming | F2 | 377 |  | [37] |
| *G. aculeatus* | JP Pacific Ocean marine female x BC Paxton benthic male | marine-freshwater | feeding | F2 | 272 | Tooth number: *Bmp6* [38] | [38] |
| *G. aculeatus* | BC Little Campbell marine female x WA Fish Trap Creek male; BC Little Campbell marine female x BC Paxton benthic male | marine-freshwater | feeding | F2 | 279, 270 |  | [39] |
| *G. aculeatus* | WA Fish Trap Creek female x BC Little Campbell marine male; BC Little Campbell marine female x AK Bear Paw lake, BC Paxton benthic males | marine-freshwater | feeding | F2 | 273, 384, 418 |  | [40] |
| *G. aculeatus* | FI Baltic Sea marine female x FI Lake Pulmanki male | marine-freshwater | body shape, body size, defence | F2 | 190 |  | [41] |
| *G. aculeatus* | JP Pacific Ocean marine female x BC Paxton benthic male | marine-freshwater | body shape, defence, feeding, respiration, swimming | F2 | 370 |  | [42] |
| *G. aculeatus*; *G. nipponicus* | JP (Japan Sea female x Pacific Ocean male) x JP Pacific Ocean male | marine-marine | defence | BCx | 76 |  | [43] |
| *G. aculeatus* | BC Paxton limnetic female x BC Paxton benthic male; BC Priest limnetic female x BC Priest benthic male | benthic-limnetic | body shape, defence, feeding | F2 | 403, 323 |  | [44] |
| *G. aculeatus* | BC Little Campbell marine female x CA Cerrito Creek freshwater male | marine-freshwater | feeding | F2 | 171 |  | [45] |
| *G. aculeatus* | WA Fish Trap Creek female x BC Little Campbell marine male; BC Little Campbell marine female x AK Bear Paw lake male | marine-freshwater | defence, feeding | F2 | 360, 363 |  | [18] |
| *G. aculeatus* | BC Paxton benthic female x JP Pacific Ocean marine male | marine-freshwater | behavior and sensory system | F2, BCx | 376, 95 |  | [46] |
| *G. aculeatus* | BC Paxton, Priest, Enos benthic females x BC Little Campbell marine male | marine-freshwater | body shape, defence, feeding | F2 | 186, 180, 180 |  | [47] |
| *G. aculeatus* | (CA Matadero stream female x BC Paxton limnetic male) x CA Matadero female | stream-limnetic | pigmentation | BCx | 429 |  | [48] |
| *P. pungitius* | NWT Fox Holes Lake female x AK Pt McKenzie creek | lake-stream | body shape, defence | F1 | 120 |  | [49] |
| *P. pungitius* | FI Baltic Sea female marine x FI Rytilampi pond male | marine-freshwater | body size | F2 | 283 |  | [50] |
| *P. pungitius* | FI Baltic Sea female marine x FI Rytilampi pond male | marine-freshwater | defence | F2 | 283 |  | [51] |
| *P. pungitius* | FI Baltic Sea female marine x FI Rytilampi pond male | marine-freshwater | behavior and sensory system | F2 | 283 |  | [52] |

**Supplementary Table S3.** Identification of genes that underlie phenotypic diversity in threespine stickleback. A combination of ahigh resolution linkage mapping, bassociation mapping, ccomplementation crosses, and dgenome scans have been used to identify candidate genes; eallele specific expression and ftransgenic manipulation have been used to provide evidence that the gene does have an effect on the phenotype of interest. Reference numbers refer to those in the main text.

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| **Trait** | **Species** | **Chr** | **PVE** | **Gene** | **Gene ID method and evidence** | **Coding *vs* regulatory** | **Same *vs* different gene or mutation** | **Standing variation *vs* new mutation** | **References** |
| Plate morph | *G. aculeatus* | IV | 77.6 | *Eda* | a, b, e, f | regulatory | same gene | standing variation | [23,64,65] |
| Lateral line patterning | *G. aculeatus* | IV | 64.8 | *Eda* | a, f | regulatory? | not tested | unknown | [34,66] |
| Schooling body position | *G. aculeatus* | IV | 13.5 | *Eda* | a, f | regulatory? | not tested | unknown | [35,67] |
| Pelvic loss | *G. aculeatus* | VII | 100 | *Pitx1* | a, b, e, f | regulatory | same gene; different mutations | new mutation | [25,68] |
| Pelvic loss | *P. pungitius* | VII | ND | *Pitx1* | c, e | regulatory | same and different genes | unknown | [49,51,69] |
| Plate size | *G. aculeatus* | XX | 9.9 | *Gdf6* | a, d, e, f | regulatory | same gene? | standing variation? | [23,70] |
| Tooth number | *G. aculeatus* | XXI | 30 | *Bmp6* | a, e | regulatory | different gene | unknown | [38,42,45] |
| Pigmentation | *G. aculeatus* | XIX | 56.1 | *Kitlg* | a, e | regulatory | same gene | standing variation | [28] |

**Supplementary Table S4.** Distribution of QTL on stickleback chromosomes. For each chromosome (Chr), the chromosome length in megabases and number of genes are based on the assembly of Glazer *et al.* [18], and the number of QTL in each trait category are taken from electronic supplementary material table S1. Using a goodness-of-fit test (chisq.test in R), we found that the observed number of QTL per chromosome differs significantly from the expected number of QTL, given either the length of the chromosome in megabases or the number of genes on the chromosome, for all QTL (length: 220 = 446.19, *p* < 2.2e-16; genes: 220 = 611.33, *p* < 2.2e-16), feeding QTL (length: 220 = 217.18, *p* < 2.2e-16; genes: 220 = 275.49, *p* < 2.2e-16), body shape QTL (length: 220 = 234.38, *p* < 2.2e-16; genes: 220 = 282.70, *p* < 2.2e-16), and defence QTL (length: 220 = 180.15, *p* < 2.2e-16; genes: 220 = 224.96, *p* < 2.2e-16). The remaining trait categories had too few QTL for statistical analyses. Specific chromosomes with more or fewer QTL than expected were identified by examining the standardized residuals for each chromosome; following Agresti [1], chromosomes with a standardized residual of greater than 3 had more QTL than expected based on achromosome length or bnumber of genes, while chromosomes with a standardized residual of less than -3 had fewer QTL than expected based on cchromosome length or dnumber of genes.

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|  |  |  | **Number of QTL** | | | | | | | | | |
| **Chr** | **Length** | **Genes** | **Total** | **Feeding** | **Shape** | **Defence** | **Behaviour** | **Swimming** | **Pigmentation** | **Respiration** | **Body size** | **Reproduction** |
| I | 29.63 | 1,328 | 92 | 26 | 46a,b | 7 | 0 | 5 | 4 | 2 | 1 | 1 |
| II | 23.70 | 907 | 31c | 15 | 8c | 6 | 0 | 1 | 0 | 1 | 0 | 0 |
| III | 17.80 | 1,004 | 12c,d | 4c,d | 6d | 2 | 0 | 0 | 0 | 0 | 0 | 0 |
| IV | 34.14 | 1,410 | 205a,b | 89a,b | 58a,b | 43a,b | 4 | 8 | 3 | 0 | 0 | 0 |
| V | 15.56 | 861 | 25d | 12 | 6 | 2 | 4 | 1 | 0 | 0 | 0 | 0 |
| VI | 18.85 | 760 | 14c,d | 2c,d | 3c,d | 2 | 2 | 0 | 4 | 0 | 1 | 0 |
| VII | 30.84 | 1,481 | 119 a,b | 40 | 41 | 32a,b | 0 | 0 | 4 | 2 | 0 | 0 |
| VIII | 20.53 | 924 | 43 | 26 | 11 | 4 | 1 | 1 | 0 | 0 | 0 | 0 |
| IX | 20.58 | 1,016 | 26c,d | 9 | 4c,d | 8 | 4 | 0 | 1 | 0 | 0 | 0 |
| X | 18.03 | 931 | 28d | 14 | 4c,d | 8 | 1 | 1 | 0 | 0 | 0 | 0 |
| XI | 17.64 | 1,108 | 27d | 10 | 3c,d | 9 | 4 | 0 | 1 | 0 | 0 | 0 |
| XII | 20.76 | 1,138 | 57 | 11 | 40a,b | 1 | 2 | 0 | 1 | 2 | 0 | 0 |
| XIII | 20.74 | 1,014 | 31c,d | 6c,d | 19 | 5 | 1 | 0 | 0 | 0 | 0 | 0 |
| XIV | 16.17 | 792 | 30 | 17 | 13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| XV | 17.32 | 823 | 13c,d | 8 | 4c,d | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| XVI | 19.52 | 864 | 72a,b | 17 | 50a,b | 5 | 0 | 0 | 0 | 0 | 0 | 0 |
| XVII | 20.25 | 1,064 | 36 | 23 | 7d | 2 | 1 | 1 | 0 | 1 | 1 | 0 |
| XVIII | 15.99 | 739 | 24 | 6 | 14 | 2 | 0 | 0 | 0 | 1 | 1 | 0 |
| XIX | 20.61 | 1,086 | 35d | 9 | 9 | 4 | 0 | 0 | 2 | 2 | 5 | 4 |
| XX | 20.45 | 990 | 78a,b | 45a,b | 18 | 10 | 2 | 3 | 0 | 0 | 0 | 0 |
| XXI | 17.35 | 614 | 106a,b | 33a,b | 35a,b | 23a,b | 9 | 5 | 0 | 0 | 1 | 0 |
| Total | 436.46 | 20,854 | 1,104 | 422 | 399 | 175 | 35 | 27 | 20 | 11 | 10 | 5 |

**References**

1. Agresti A. 2007 *An introduction to categorical data analysis*. Hoboken, NJ: John Wiley & Sons.

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