***Supplementary materials***

1. ***Genetic analysis methods***

***Microsatellite genotyping***

Genomic DNA was extracted from blood samples using a commercial kit following the manufacturer’s protocol (Quick-gDNATM MiniPrep, cat. no. D3050, Zymo Research, Orange, U.S.A.). Each individual was successfully genotyped at 27 microsatellite loci (sequences from Verkuil et al., 2009) and a bar-tailed godwit genome sequence, GenBank Acc. No. LXVZ00000000}. PCR-amplified sequences were fluorescently labelled (Schuelke, 2000) with a fluorescently labelled M13(-21) universal sequence (18 bp) primer (5’- TGTAAAACGACGGCCAGT -3’) included in the reaction mix along with the locus specific primer pair, one of which also included the generic primer sequence. The M13(-21) universal primers were 5’ labelled with 6-FAMTM (blue), VIC® (green), NEDTM (yellow), PETTM (red) allowing discriminating colour labelling of microsatellite amplicons and pooling of up to four different microsatellite loci amplicons for fragment length estimation. Template genomic DNA (2.0 µl) aliquots were dried on the base of 0.2 ml PCR tubes (70˚C, 10 min.). PCR reaction cocktails (10.0 µl) were added consisting of 1x MyTaqTM HS Mix (cat. no. BIO25045, Bioline, London, U.K.), locus-specific forward primer (0.2 µM), locus-specific reverse primer (0.6 µM), and one of the four alternative florescent dye-labelled M13 universal primers (0.6 µM). Thermocycling conditions for all primer pairs were: 95˚C/2 min., 1 cycle; 95˚C/30 sec., 52˚C/20 sec., ramping at 0.2˚C/sec to 72˚C, 72˚C/30 sec., 20 cycles; 95˚C/30 sec., 54˚C/30sec., ramping at 0.2 ˚C/sec to 72˚C, 72˚C/30 sec., 22 cycles; 72˚C/5 min., 1 cycle; 60˚C/30 min. 1 cycle; 15˚C/hold. Amplicon lengths were estimated on an *ABI3730* DNA Analyzer with the GeneScan™-500 LIZ™ Size Standard (Massey Genome Service, Massey University, N.Z.). PEAK SCANNER™ v.2.0 (Life Technologies, Carlsbad, U.S.A.) was used to estimate amplicon fragment sizes with the software TANDEM used to round the fragment sizes to valid integer values (Matschiner and Salzburger, 2009).

***Microsatellite analyses***

GENALEX v.6.5was used to check for samples having identical genotypes and for calculating a range of standard population genetic parameters (i.e. allele frequency, alleles/marker, expected (He) and observed (Ho) heterozygosities) (Peakall and Smouse, 2006). MICRO-CHECKER v.2.2.3 (van Oosterhout et al., 2006) was used to detect possible genotype scoring errors and to detect possible null alleles, as indicated by an apparent excess of homozygotes. Linkage disequilibrium (LD) analysis was performed using ARLEQUIN v.3.5.1.3 (Excoffier and Lischer, 2010) using 10,000 permutations, 10 initial conditions and an interval of confidence (IC) of 0.05. ARLEQUIN v.3.5.1.3 was used to detect possible deviations from Hardy-Weinberg equilibrium (HWE). Each HWE analysis consisted of 1,000,000 iterations of the Markov chain Monte Carlo (MCMC) and 1,000,000 dememorization steps. Sequential Bonferroni corrections (*P* < 0.05) for multiple comparisons were applied to both HWE and LD results to minimize type I statistical errors (Rice, 1989). Summary statistics for the 27 microsatellite loci are listed in Supplementary Table 1, with details of the primers used to amplify the loci provided in Supplementary Table 2.

**Supplementary Table 1** Summary statistics for the 27 microsatellite loci used in this study. GenBank accession numbers for sequences of one allele of each locus are listed. *Abbreviations*: n, number of individuals genotyped at the locus; *Na*, number of alleles detected; *Ho*, observed heterozygosity; *He*, expected heterozygosity, HWE, Hardy-Weinberg equilibrium; No, not statistically supported; Yes, statistically supported. 1analyses using MICRO-CHECKER v.2.2.3; 2analyses using ARLEQUIN v.3.5.1.3.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Locus name/  GenBank acc. no. | n | Na | Ho | He | null alleles1 | deviation from HWE2 |
| LIM5  FJ652579 | 222 | 7 | 0.324 | 0.354 | No | No |
| LIM6  FJ652593 | 218 | 4 | 0.142 | 0.133 | No | No |
| LIM8  FJ652580 | 221 | 7 | 0.466 | 0.513 | No | No |
| LIM12a  FJ652583 | 218 | 4 | 0.431 | 0.446 | No | No |
| LIM12b  FJ652584 | 221 | 4 | 0.231 | 0.227 | No | No |
| LIM25  FJ652588 | 220 | 2 | 0.359 | 0.323 | No | No |
| LIM30  FJ652590 | 219 | 11 | 0.840 | 0.849 | No | No |
| LIM32  FJ652591 | 220 | 8 | 0.668 | 0.751 | No | No |
| C046  KT967115 | 218 | 8 | 0.789 | 0.798 | No | No |
| C994  KT967116 | 219 | 3 | 0.183 | 0.186 | No | No |
| C856  KT967117 | 219 | 10 | 0.836 | 0.803 | No | No |
| C586  KT967118 | 222 | 4 | 0.212 | 0.253 | No | No |
| C734  KT967119 | 218 | 4 | 0.248 | 0.274 | No | No |
| C008  KT967120 | 220 | 6 | 0.582 | 0.555 | No | No |
| C348  KT967121 | 220 | 9 | 0.541 | 0.604 | No | No |
| C501  KT967122 | 218 | 5 | 0.486 | 0.493 | No | No |
| C367  KT967123 | 219 | 5 | 0.333 | 0.352 | No | No |
| C772  KT967124 | 221 | 3 | 0.041 | 0.040 | No | No |
| C822  KT967125 | 222 | 5 | 0.320 | 0.343 | No | No |
| C697  KT967126 | 217 | 11 | 0.733 | 0.760 | No | No |
| C355  KT967128 | 218 | 8 | 0.610 | 0.628 | No | No |
| C980  KT967129 | 219 | 4 | 0.242 | 0.219 | No | No |
| C444  KT967131 | 220 | 9 | 0.727 | 0.758 | No | No |
| C893  KT967132 | 188 | 5 | 0.426 | 0.422 | No | No |
| C463  KT967133 | 220 | 5 | 0.227 | 0.244 | No | No |
| C129  KT967134 | 220 | 8 | 0.609 | 0.664 | No | No |
| C311B  KT967135 | 220 | 5 | 0.718 | 0.718 | No | No |

**Supplementary Table 2** PCR primer pairs (n = 27) used for amplification of godwit microsatellite loci. Names of the loci are indicated with those from Verkuil *et al.* (2009) prefixed ‘LIM’ and those from this work prefixed ‘C’. GenBank accession numbers for representative allelic sequences at each locus are listed. Underlined primer sequencers are (i) forward primers, M13(-21) universal primer 5’ tag sequence and (ii) reverse primers, PIG-tail to promote addition of 3’ As.

|  |  |  |
| --- | --- | --- |
| Locus/GenBank  Accession nº | Primer sequence (5’-3’) | Repeat motif/ nº repeats |
| LIM5  FJ652579 | F: TGTAAAACGACGGCCAGTACTGCTGCTTCCAAATGACA  R: GTTTTCTCCCCTCCATCTGAAAAG | (GA)10AA(GA)2 |
| LIM6  FJ652593 | F: TGTAAAACGACGGCCAGTTATTCAGCAGAACACACGCAC  R: GTTTACTGGTATTCTTTAACCCCGACTG | (AC)5GC(AC)6 |
| LIM8  FJ652580 | F: TGTAAAACGACGGCCAGTCTGAAGTGATCAGGCAAGGTG  R: GTTTTGTGGAGGAAGGAGGCTTG | (CA)12 |
| LIM12a  FJ652583 | F: TGTAAAACGACGGCCAGT GGTTCTCTTTGGGCTGTCTG  R: GTTT AGGAAACTCATCTGGGGTCTG | (CA) 10 |
| LIM12b  FJ652584 | F: TGTAAAACGACGGCCAGTGCCAAAATATTTGACAGACCCCAG  R: GTTT GAGTTTCCCAGCACTTTGCCC | (CA) 11 |
| LIM25  FJ652588 | F: TGTAAAACGACGGCCAGTTGACACCAGACAGTGTTGCAT  R: GTTTCCGACTTTATTTGGTTTTCCAG | (CA)4AAAA(CA)8 |
| LIM30  FJ652590 | F: TGTAAAACGACGGCCAGTACCTTAGTACATGGGGAACAG  R: GTTTTGAAGGCATATCTGGGGATGTC | (CA)10 |
| LIM32  FJ652591 | F: TGTAAAACGACGGCCAGTTCAGACGTCGATCACCTGAG  R: GTTTTGAAACTATAAATCCTGCGGG | (CA)9CC(CA)6 |
| C046  KT967115 | F: TGTAAAACGACGGCCAGTGTGCTCAGAGATAGGCAAACC  R: GTTTCTGAAGTGAAAAGAGCGGGG | (TATC)9 |
| C994  KT967116 | F: TGTAAAACGACGGCCAGTTTGATGAGAATCCTACCCCTG  R: GTTTGCGTCACAGTATGAACCCAC | (TTTG)8 |
| C856  KT967117 | F: TGTAAAACGACGGCCAGTTGTGAACCAGGGTGCTACTC  R: GTTTTTTAAGGTGGCCAAAGCAGG | (TAT)12 |
| C586  KT967118 | F: TGTAAAACGACGGCCAGTGCACTCTCAGTCCACAATGC  R: GTTTACACCTGCCAGTAAGAAACAG | (ATTT)7 |
| C734  KT967119 | F: TGTAAAACGACGGCCAGTACTTACAGTGCTTCTCTTGGC  R: GTTTTAGCCTGGGTTTTTCCTGTG | (GTTT)8 |
| C008  KT967120 | F: TGTAAAACGACGGCCAGTCAGGCTTCCCCAAAATGTCC  R: GTTTGGAACTGGCAGCTTAATGGC | (AAT)7 |
| C348  KT967121 | F: TGTAAAACGACGGCCAGTCTGGACGGACATGGAGTCTG  R: GTTTCACAACAACTGAGTAGGGGC | (TG)13 |
| C501  KT967122 | F: TGTAAAACGACGGCCAGTTTGCTGACTCCTGAGACCAC  R: GTTTTGCCAGTTCTCACCCCATAC | (TTCA)7 |
| C367  KT967123 | F: TGTAAAACGACGGCCAGTAACTGTTGCGTAGTGTTCGG  R: GTTTTTAGCAGGGCCCAAAGAAAC | (GAAG)7 |
| C772  KT967124 | F: TGTAAAACGACGGCCAGTTGCAGAGACCCCTAAAGCTG  R: GTTTTTTGGCCCTTTACATTCGGC | (CAT)7 |
| C822  KT967125 | F: TGTAAAACGACGGCCAGTTGCCCCCTAAGATACACTGC  R: GTTTTCACGCCCCTGTGACTAATG | (TTG)8 |
| C697  KT967126 | F: TGTAAAACGACGGCCAGTTCCATGAGGCAAATGCCAAG  R: GTTTGGGATGTGTAGCTGGGGTAG | (GATA)8 |
| C355  KT967128 | F: TGTAAAACGACGGCCAGTCATTCTCCTTCGGGCTTTGC  R: GTTTGTTTGTCAGGTGCTTCCTCG | (AAC)8 |
| C980  KT967129 | F: TGTAAAACGACGGCCAGTGTCCATGCAAAGCCCATCAG  R: GTTTTCTTCCAGTTCAGTCTTGGC | (ATT)8 |
| C444  KT967131 | F: TGTAAAACGACGGCCAGTAGCTGGGAAGATGTGCCTG  R: GTTTGCACAGGGGAAGGTGAAATG | (GAAG)9 |
| C893  KT967132 | F: TGTAAAACGACGGCCAGTTCCATCTTTAGTCCCCTGCC  R: GTTTTGCTCTCTGAGGTGAATGCC | (AT)13 |
| C463  KT967133 | F: TGTAAAACGACGGCCAGTTCTCCCAGTGTCTGTTTCCG  R: GTTTGAGGAGCAGTTTTACGTGCG | (GGA)8 |
| C129  KT967134 | F: TGTAAAACGACGGCCAGTCAAGTGGAGCTGTTCCCTCC  R: GTTTAACATTTCTCCTCCCCGCTC | (AGAA)10 |
| C311B  KT967135 | F: TGTAAAACGACGGCCAGTCCCTGCTCACCTAACAGACC  R: GTTTCACGCTGCATGGAAGGATG | (TTG)7 |

**Supplementary Figure 1** Lack ofspatialgenetic structure in bar-tailed godwits across the three study sites. The plot shows the probability of individual godwits (n = 237) belonging to each of three assumed genetic clusters, analysed in STRUCTURE v.2.3.4. Vertical bars indicate the admixture proportion of individuals [0;1] assuming *K* = 3.

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1. **Resighting frequencies used in the determination of migration date.**

**Supplementary Figure 2** Histograms of the number of records used to establish last dates of godwits in Auckland and Otago. Data span 2014–2016 for Auckland and 2013–2016 for Auckland. Data represent 260 records of 172 birds in Auckland and 247 records of 127 birds in Otago; multiple values from the same individuals were averaged for analysis.

