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BAC CONTIG MAPPING OF THE CHICKEN GENOME

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The chicken is intensively being studied for genes affecting polygenic traits (quantitative trait loci or QTL) which drive the international efforts towards detailed physical and linkage mapping in chicken. To obtain a more detailed chicken-human comparative map, chicken BAC clones were isolated for 314 markers located at 10 cM intervals on the chicken linkage map. These BAC clones provide an excellent resource for FISH experiments in different bird species to perform comparative mapping. Sample sequencing of these BAC clones has also been used to identify chicken genes with homologues in human in order to improve the chicken-human comparative map. Furthermore, for five micro-chromosomes and part of chromosome 8, physical BAC contig maps are under construction by chromosome walking. In total more than 2600 BAC clones have been isolated so far. Fingerprinting of the complete BAC library is in progress in order to generate a BAC contig map of the complete chicken genome. This resource will lay the foundation towards the complete nucleotide sequence of the chicken genome, which is anticipated to aid in the identification of conserved regulatory elements in

vertebrates. Finally, an ACEDB based database has been implemented to hold all the chicken mapping data (ChickAce), which is available through our chicken genome mapping web site (http://www.zod.wau.nl/vf/).

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