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ALIGNMENT OF THE CHICKEN LINKAGE MAP WITH BAC CONTIGS

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The long term goal of our research is to align the chicken genetic linkage map, defined primarily by segregation of microsatellite and other DNA-based markers, with the anticipated BAC contig physical map of the chicken genome now being generated and eventually with the full genome sequence. Most results to date derive from hybridization to filter-spotted arrays containing about 39,000 BAC clones (one-third of our complete library). As an initial test, PCR-amplified DNA fragments of 31 markers from 10 linkage groups were labeled and hybridized in pools. Positive BAC colonies were confirmed by individual probe hybridization to BAC clone Southern blots and/or PCR amplification with primers derived from the marker sequence, generating 79 confirmed BAC alignments for this collection of probes. To increase throughput, we are now using pooled OVERGO hybridization probes. The primary advantage of OVERGO probes is that the sequence of all members of each pool can be adjusted to have similar melting temperatures. A 6x6x6 matrix of 216 probes based on markers on chromosomes 1 and 2 has been employed. Three-dimensional (18 pools) or four-dimensional (24 pools) hybridization is being used. Results focused on chromosomes 1, 2 and 17 will be presented. Additional screens using a 60,000 BAC subset of the total 115,000 BAC library are planned for other chicken linkage groups.

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