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**Abstract**

Class A regressive multiple logistic segregation models with a sibling covariate were used to investigate the underlying determinants of asthma and respiratory allergy (defined from specific IgE levels to inhaled allergens) in the randomly recruited Caucasian families from the Genetic Analysis Workshop 12 asthma data sets--Perth, Busselton, and Southampton. For asthma, both a purely multifactorial model and a major gene (dominant or recessive) model with multifactorial effects fitted the data. For respiratory allergy, a dominant, dominant with multifactorial effects and a purely multifactorial model all fitted the data. However, homogeneity of the three studies was rejected for both traits indicating that the three populations are significantly different and should be analyzed separately. This finding has implications for the meta-analysis of asthma linkage studies.