



**Between the Lines of Genetic Code: Chapter Nine.
Genetic Vectors Approach in a Study of Fine
Structure of Interaction Between Risk Haplotype
of HTR2A and ... Epitope Alleles in Rheumatoid
Arthritis**

Igor Sandalov, Leonid Padyukov

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We introduce new quantitative characteristics of the population using an analogy to the system of multi-spin molecules: the disease fields, which may depend on interactions, and the susceptibility to disease as derivative of genetic vector's (GV's) frequency of cases with respect to these fields. The genetic vector's approach (GVA) is applied to statistical analysis of the interaction of two SNP haplotype of HTR2A and shared epitope (SE) alleles in relation to development of rheumatoid arthritis (RA). The analysis is performed for two independent cohorts, EIRA and NARAC, and based on the evaluation of double- and triple genotype–genotype versus SE alleles correlations. The Gibbs-like parametrization of GV frequencies makes analysis transparent and easy interpretable. We find that the main contribution into association to RA comes from GVs containing double SE. GVA may resolve an opposite role in risk/protection from different pairs of genetic variations and reveal an association to RA whereas the univariate analysis does not show significant association.

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