Evaluation of Chemokine (CK) and CK-Receptor Variants as Modifiers of Risk for Developing Multiple Cutaneous Melanoma

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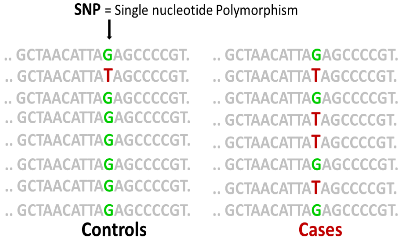
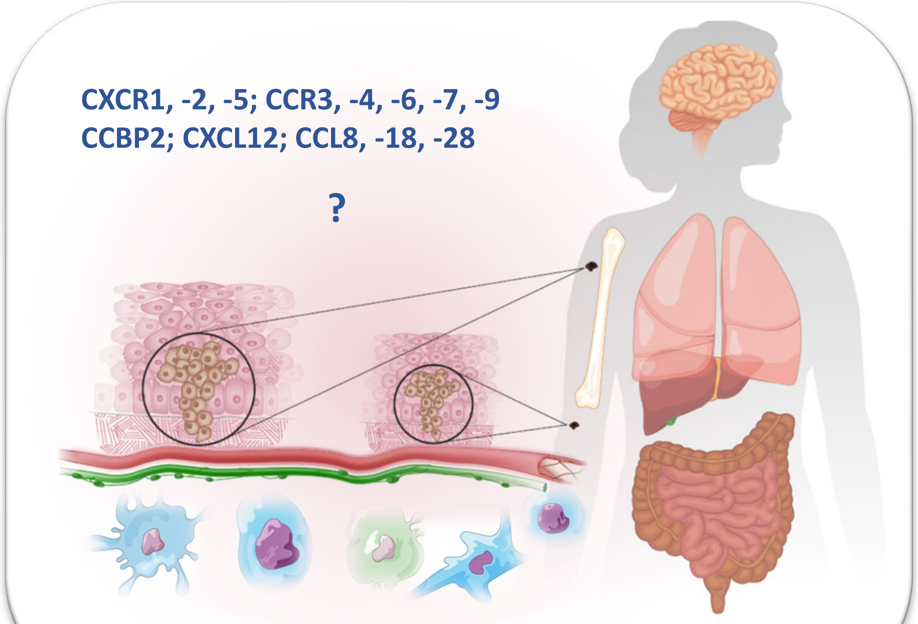
- N-**2,469** patients with incident single primary melanoma (SMP)
- N-**1,206** patients with incident multiple primary melanoma (MPM)

Genes, Environment, and Melanoma (GEM) Study

- **Genotyping candidate markers: 215 SNPs in 55 genes, using Illumina & MassArray.**
- **Statistical analysis: logistic regression to calculate odds ratios for multiple melanoma, adjusted for age, sex, age*sex, study center.**

- **22 SNPs (13 genes) significantly associated with melanoma risk ($p<0.05$)**
- **Range of the per allele effects: 11- 40%.**





CXCR1, -2, -5; CCR3, -4, -6, -7, -9
CCBP2; CXCL12; CCL8, -18, -28

Work in Progress: analyses & interpretation

- Haplotype analyses (inferred): 19 SNPs in 7 blocks
- Evaluation of functional relevance based on evidence and *in silico* predictions (*e.g.,* effect on GEx) for:
  - Significant SNPs
  - SNPs in high linkage disequilibrium (LD)