Immunoprevention of dysplastic nevi in mice
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Melanoma, an aggressive malignancy of melanocytes, is responsible for more deaths than any other skin cancer. Despite the fact that there is a long lag period before pre-malignant dysplastic nevi (DN) transform into melanomas, there has been little progress on developing methods for melanoma prevention. When mice were pretreated with Abs to PD-L1 prior to topical administration with a regimen that produces dysplastic nevi (treatment of C3H/HeN mice with topical DMBA and TPA), significantly fewer dysplastic nevi developed at 25 weeks compared to animals given with isotype control Abs. Treatment with Abs was associated with a significant increase in CD4+ T-cells that produced IL-17 (0.4% vs. 0.78%) and IFN-γ (0.98 vs. 2.47%) compared to animals that had been pretreated with isotype controls. There was also a decrease in CD11b+, Gr1+ (5.28% vs. 1.84%) and CD24+CD25+Foxp3+ (6.93 vs. 3.16) cells. These findings indicate that treatment with Abs was an effective for immunoprevention of dysplastic nevi in individuals who are at risk for melanoma.

Melanoma and the protective role of phosphorylated α-syn(pSer129) to prevent malignant degeneration
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The misfolding and prion-like propagation of the protein α-synuclein (α-Syn) is the leading molecular signature in Parkinson’s disease (PD). It has a protective role in the growth in experimental models. Phosphorylated α-Syn(pSer129) is associated with enhanced nuclear localization. Hypothesis: Nuclear pSer129 plays a physiologic role of genomic protection in skin cells. Reduced DNA binding induces severe transcriptional deregulation leading to uncontrolled proliferation in melanoma. Objective: To demonstrate the reduced presence of pSer129 in the nuclei of melanoma cells. Methodology: Twenty skin biopsies for pathological analysis were immunostained for pSer129. The positivity of the nuclei was quantified using a mathematical algorithm in 40X photomicrographs. Biopsies included four each of Stages 2, 3, and 4 (Clark’s/Anatomical) Level melanomas and eight melanomas in situ (lentigo maligna). Each was stained with Mart-1 and HMB45 and in some p16. Ages ranged from 26-80 years old. Results: Biopsies from early stage melanoma in situ showed a remarkable loss of pSer129 immunopositivity in nuclei as compared with non-affected adjacent skin cells and later stage melanoma cells. Conclusion: The phosphorylated form of α-Syn accumulates in the nucleus of healthy cells. Although melanoma cells express high levels of α-Syn, mostly in the cytoplasm, the disappearance of pSer129 from the cell nuclei is closely related to the beginning of malignant degeneration. These results support a protective role of pSer129 of gene expression in skin cells.

Genome-wide scans identify genetic variants associated with facial aging traits quantified by deep learning methods
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We describe the occurrence and progression of facial aging as being driven by genetic factors. Previous studies have identified a number of genetic variants associated with facial aging traits. Quantification of facial aging traits using deep learning methods allows the identification of regions with strong associations with facial aging traits. In this study, we developed a deep learning framework to precisely measure 4 facial aging phenotypes (lacrimal sulcus, pigmentation spots, wrinkle forehead, and wrinkle under eyes). We then derived the phenotypes in 7,347 Han Chinese from two independent cohorts: Jilin cohort (N=5,016) and the National Survey of Physical Traits cohort (NSPT, N=2,311). A genome-wide scan in the Jilin cohort identified eight genomic regions showing genome-wide significant association with facial aging, including four previously unreported loci (i.e. 10q23.1, 9q22.13, 13q14.2 and 22q12.2) and four previously known genes: PPP2RC18, BNC2, Msd12 and MC1R. All the eight loci were successfully replicated in the NSPT cohort at nominal significance. Meta-analysis of all samples further enhanced the significance level of the novel associations on 10q23.1, 9q22.13, and 22q12.2 (P=3.65×10^{-10}, 2.82×10^{-10} and 5.08×10^{-10}, respectively). Our conclusion, out study identified five new risk factors for facial aging traits using deep learning-based measurement in Han Chinese.