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Human Skin Color As A Model Phenotype For Testing Human Coding Polymorphisms In Zebrafish



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Genome-wide studies of complex traits and diseases yields candidate polymorphisms associated with phenotype, but functional testing in model organisms is necessary to establish causation. The growing number of candidate genes and polymorphisms found through SNP chip and whole genome sequence analysis has created a pressing need for systematic experimental approaches for assessing phenotypic impact. We are testing the hypothesis that a convergence of human data focusing on phenotypic extremes, and experimental animal data can be used to accelerate phenotypic testing of candidate polymorphisms. We are using an easy-to-score phenotype, skin color, as a model for studying other multigenic phenotypes. Several genes that are responsible for the lighter skin color in Europeans as compared to Africans has been discovered, but our knowledge of global skin color remains incomplete without the identification of the primary polymorphisms responsible for the lighter skin of East Asians and/or Amerindians. Towards the identification of candidate polymorphisms involved in determining the lighter skin color of East Asians and Amerindians, we collected samples from a population admixed for Amerindian and African ancestry.