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Extensive parent-of-origin genetic effects on fetal growth

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Background

Epigenetic effects have recently been recognized as playing a very significant role in several normal and pathological phenotypes. Imprinting, the silencing of either the paternally or maternally inherited allele, is one of the most pervasive and consistent epigenetic mechanisms across species and individuals. The majority of imprinted loci are involved in fetal growth regulation, and several defects in the epigenetic regulation of these genes are associated with extremes of fetal growth.

Materials and methods

We surveyed 62 SNPs across 17 genes (Table 1) in a cohort of African-American mother-newborn pairs selected using

Table 1: SNPs Genotyped

INSIG2	rs7566605	**GRB10**	rs2074778	**H19**	rs2839703	**GNAS**	rs965808
IGFBP2	rs9341090		rs2282931		rs217727		rs1800902
	rs3770473		rs6945597		rs2067051		rs6123832
	rs9341178		rs7791286		rs2251375		rs6026576
GHRL	rs35684	**LEP**	rs10249476		rs4929984		rs6092704
	rs4684677		rs12535708	**IGF2**	rs680		rs2057291
	rs696217		rs7799039		rs3213233		rs7121
	rs26802		rs2167270		rs734351		rs234621
GHSR	rs509035		rs10954173	**IGF2AS**	rs1003483	**Ancestry**	rs2814778
	rs572169		rs3828942		rs3741206	**Informative**	rs11903376
	rs512692	**CPA4**	rs6942830		rs3741205		rs17614025
ADIPO	rs266729		rs1038627		rs3741204		rs7732591
	rs182052		rs3800775		rs1004446		rs9321552
EDN1	rs2070698	**MEST**	rs1005171	**INS**	rs3842756		rs1426492
	rs2070699	**GAD2**	rs2839670		rs3842748		rs12677824
	rs5369		rs2236418		rs689		rs803733
	rs5370	**TCF7L2**	rs7903146		rs3842738		rs161272
ENPP1	rs1044498		rs10885406				rs680273
	rs7754561						rs3825663
							rs735480

stringent inclusion/exclusion criteria intended to enrich for the genetic component of fetal growth regulation. All association analyses were adjusted for admixture using a suite of ancestry informative SNP markers. By inferring haplotypes within the imprinted loci in mothers and newborns, we could unambiguously infer the parental origin of haplotypes and associated alleles in the majority of newborns.

Results and conclusion

We found very significant parent-of-origin effects in the insulin, H19 and GNAS genes that were completely consistent with their known patterns of imprinting. In the case of the insulin polymorphisms, a consistent trend was also observed for newborn IGF-II levels with respect to parental origin of haplotypes.

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