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## RN gene polymorphisms effect in a family based-structure scheme in French purebred pig populations

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The study was based on performance recording (with 23 meat quality traits) in progeny testing station of half-sib families composed of 50 offspring (castrates and females) from purebred sires. The aim of this scheme was to estimate, in French purebred pig populations, the effect of polymorphisms. Data will be presented for 1,740 genotyped animals belonging to 4 groups of breeds: LW (3 Large-White type populations), LF (French Landrace), D (3 Duroc populations) and CH (4 Chinese-European lines). Eight polymorphisms in RN (PRKAG3) gene were analyzed: R200Q, V199I, G52S, K131R, P134L, T30N, V41I, L53P. No polymorphism was found for R200Q and L53P. Six haplotypes were defined with the remaining mutations. Effect of haplotypes was estimated with MIXED procedure (SAS software) with sex and slaughter date as fixed effects, mother and father as random effects and carcass weight as covariate. Most significant results were observed for pHSM(semi-membraneous pH 24 h post mortem) and MQI (Meat Quality Index combining pHSM, Minolta L\* and water holding capacity both on gluteus superficialis) in LW, LF, and D, for drip loss in LW and LF and for color traits (Minolta L\*, a\*, b\*) in LW, LF and CH. Results will be illustrated focusing on 2 meat quality traits (MQI, and drip loss) and 2 haplotypes. Haplotypic frequencies estimated on parents are 26% and 10% in LW, 64% and 20% in LF, 40% and 47% in D and 12% and 21% in CH for haplotype 1 and 2 respectively. Haplotype 1 is favorable for the 2 considered traits. Regarding combinations of haplotypes, 11 is significantly better than 16 in LW, LF and D and even more than 66 in D. Estimated effects between 11 and 16 are between 0.2 and 0.8 phenotypic standard deviation; the highest being observed in LW. In D, differences between 11 and 66 animals are estimated to be 0.9 phenotypic standard deviation for MQI.