CONCLUSIONES

Conclusiones

1.- Se observó un notable grado de variabilidad genética en las poblaciones porcinas estudiadas a pesar de tratarse de poblaciones altamente seleccionadas. En este sentido los valores *PIC* de los microsatélites analizados oscilaron entre 0.3 y 0.6 con unos valores medios de 0.54 y 0.57 en las poblaciones Pietrain y Large White respectivamente.

2.- Con el método de análisis de los datos utilizado (Factor de Bayes) se observó que algunos de los QTLs de los cromosomas 2, 3, 4, 7, 8, 10 y 13 previamente descritos en cruces divergentes, estaban presentes en los cromosomas 2, 3, 4 y 7 en la población Large White, detectándose además la presencia de QTLs en las regiones control 1 y 9. Además se observó en la población Pietrain la presencia de QTL en los cromosomas 7 y 8. En resumen se observó que los QTL descritos en cruces divergentes están presentes en poblaciones comerciales, sin embargo no segregan por igual entre las distintas razas.

3.- Los QTLs detectados en la población Large White corresponden a los siguientes caracteres: Peso del jamón (cromosomas 1, 2 y 4), peso de la paletilla y peso del chuletero (cromosoma 2), peso del costillar (cromosomas 1, 2, 3 y 4), peso de la panceta (cromosomas 1, 3 y 4), profundidad de grasa subcutánea medida con Fat-O-Meater (cromosomas 1, 2, 3 y 4), profundidad en mm de grasa subcutánea al nivel de la primera vértebra dorsal (cromosomas 2 y 7), profundidad en mm de la grasa subcutánea al nivel de la primera vértebra lumbar (cromosomas 3 y 4), pH a las 24 horas postmortem en el músculo *longissimus dorsi* (cromosomas 3 y 4), pH a las 24 horas postmortem en el músculo *semimembranoso* (cromosomas 2, 3, 4, 8 y 9)

4.- En la población Pietrain se ha detectado un QTL para pH a las 24 horas postmortem en el músculo *longissimus dorsi* (cromosoma 7) y para peso de la panceta derecha (cromosoma 8).

5.- La detección de QTLs se ve afectada de forma significativa por el método estadístico de análisis utilizado. Así gran parte de los QTLs descritos en este trabajo no son detectados por métodos basados en regresión múltiple o componentes de varianza o viceversa.

6.- El análisis del gen receptor de rianodina en las poblaciones Pietrain y Large White del presente estudio, mostró que los animales con genotipo nn presentan un mayor peso del costillar y panceta, menor contenido de grasa dorsal y una mayor disminución de pH postmortem que los animales con el genotipo Nn. Las mismas diferencias se observan entre los animales con genotipo Nn con respecto a los de genotipo NN.

7.- El análisis de asociación del gen *H-FABP* reveló la existencia de diferencias significativas entre los distintos genotipos para los caracteres de grasa dorsal, longitud de canal y pH. Sin embargo estas asociaciones no se presentan por igual entre las distintas razas.

8.- El análisis de asociación del gen receptor de leptina (*LEPR*) reveló la existencia de diferencias significativas entre sus distintos genotipos con un menor pH a las 24 horas postmortem, sin embargo esta asociación solamente se presentó en la población Large White.

9.- La secuenciación del cDNA del gen de la piruvato carboxilasa (*PC*)reveló una alta similitud nucleotídica con otras especies de mamíferos, y que además es polimórfica.

10.- El mapeo mediante panel de células somáticas híbridas irradiadas reveló que el gen *PC* porcino está localizado en el cromosoma 2 en el brazo P entre los microsatélites SW 2623 (9.8 cM) y el SW 256 (19 cM).

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