5. CONCLUSIONES

Las conclusiones que se pueden extraer del presente trabajo son:

1. La región de 1,944 Mb que rodea al locus *Adh* en *D. melanogaster* (elemento B) está representada en 6 posiciones cromosómicas distintas en las especies *D. repleta* y *D. buzzatii*. Los genes *Adh* y *Adhr* están incluidos en un segmento conservado de 366 kb. Sin embargo, el hecho de que un segmento esté conservado no excluye que en su interior se hayan producido microrreordenaciones que no pueden ser detectadas con la técnica de hibridación *in situ*.

2. La hibridación de 160 clones procedentes de la especie *D. melanogaster* en las especies *D. repleta* y *D. buzzatii* confirma una vez más las homologías cromosómicas establecidas en el género *Drosophila* y la gran reorganización del contenido genético de los elementos cromosómicos debida a la fijación de inversiones paracéntricas. Sólo 2 clones, el gen *Lsp1alpha* y el cósmido 174F6, no hibridaron en el elemento cromosómico esperado y representan probablemente eventos de transposición. La estima de la tasa de transposición en el género *Drosophila* es de $4{,}9 \times 10^{-5}$ por gen y por millón de años. Esta cifra es una subestima ya que no incluye genes repetidos en tándem, que a menudo muestran transposición, ni transposiciones intracromosómicas.

3. La tasa de fijación de inversiones (± SD) durante la divergencia de las especies *D. melanogaster* y *D. repleta* es de 118 ± 17 para el elemento A; 30 ± 13 para el elemento B; y 56 ± 8 para el elemento D. La densidad de puntos de rotura varía hasta cuatro veces entre los elementos A, B, D y E. El elemento A es el que muestra la mayor densidad (10,83) aunque también existen diferencias entre las densidades de los tres autosomas analizados: el elemento E presenta la densidad más elevada (8,14), el elemento D una densidad intermedia (4,63) y el elemento B la densidad más baja (2,57). Estos resultados concuerdan con los obtenidos al comparar especies del grupo *virilis*, en las que el elemento A evoluciona más rápido que el E que a su vez evoluciona más rápido que el D sugiriendo que este patrón podría ser relativamente general.

4. Debido a los múltiples efectos de las inversiones parece poco probable que un único factor pueda explicar la variación en la tasa de evolución de los diferentes elementos cromosómicos observada en el género *Drosophila*. Es más probable que varios factores, entre ellos cantidad de DNA repetitivo, tasa de recombinación o densidad génica contribuyan a esta variación.

5. La estima para la tasa de fijación de inversiones en todo el genoma durante la divergencia de las especies *D. melanogaster* y *D. repleta* es de 393, es decir, 0,053 puntos de rotura fijados por Mb y por Ma. Esta estima es comparable a las obtenidas para otras especies del género *Drosophila* pero superior a la tasa estimada en varias especies de mamíferos y plantas. Esta mayor tasa evolutiva del género *Drosophila* podría ser debida a un tiempo de generación más corto y un menor efecto detrimental de las inversiones sobre la fertilidad en estas especies. Sólo la estima obtenida a partir de la comparación de las secuencias de dos especies de levadura es comparable a la estima para las especies del género *Drosophila*.

6. Se han identificado 9 segmentos cromosómicos conservados en el elemento A, 6 en la región *Adh* del elemento B y 13 en el elemento D. No hay evidencias de restricciones funcionales que puedan explicar la conservación de estos segmentos cromosómicos. Solo 1 segmento en el elemento A y 1 en el elemento D tienen un tamaño superior al esperado de acuerdo con la hipótesis de que los segmentos conservados son el resultado de la fijación de un número limitado de reordenaciones con puntos de rotura al azar desde la divergencia de las especies comparadas. Sin embargo, debido a que estos dos segmentos incluyen tan solo 2 marcadores es probable que dentro de ellos se hayan producido reorganizaciones que no han sido detectadas.

7. La conservación de tres complejos génicos en las especies *D. repleta* y *D. buzzatii*, complejo *achaete-scute*, complejo *iroquois* y complejo *knirps-knirps-related*, que en *D. melanogaster* muestran expresión corregulada sugiere que la selección natural puede jugar un papel en algunos casos para mantener juntos genes funcionalmente relacionados.

8. Los resultados obtenidos en el presente trabajo apuntan hacia una organización modular del genoma en las especies del género *Drosophila*. El genoma de *Drosophila* se puede considerar un mosaico de módulos independientes que pueden cambiar de localización cromosómica, la mayoría de veces dentro del mismo elemento cromosómico y solo ocasionalmente entre elementos, sin que estos cambios tengan consecuencias para su función.

9. La comparación de la organización molecular del cromosoma X en las especie *D. repleta* y *D. buzzatii* indica que los puntos de rotura de las inversiones Xb y Xc fijadas entre estas dos especies han sido mal asignados. De acuerdo a los resultados obtenidos en el presente trabajo las inversiones Xb y Xc no estarían dispuesta en tándem sino que serian inversiones solapantes. Los puntos de rotura de estas inversiones se han localizado en F1c-G1e y F1a-F2i.

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