1) Dominance doesn't matter -- with Hardy-Weinberg, you're just looking at alleles coming together in combinations at random (basically, at the proportions expected by their relative frequencies), and then coming apart and doing the same in the next generation. It doesn't consider "phenotype" at all and may be applied even to regions of the genome that are not genes.

2) This is a bit of a tough one at first, but it's mathematically simple. We're comparing frequency of aa (q^2) to Aa (2pq). If they're the same, then we're saying $q^2=2pq$.
We can divide both sides by q, and get q = 2p.
Importantly, q = 1-p (since there are only two alleles).
So, substituting, we get 1-p = 2p. Solving that, 1=3p, and thus p = 0.333.

3) Observed genotype frequencies:
BB: 750/1000 = 0.75 Alleles: B: 0.75 + 1/2 (0.1) = 0.8
Bb: 100/1000 = 0.10 b: 0.15 + 1/2 (0.1) = 0.2
bb: 150/1000 = 0.15

HW expected frequencies: BB: $p^2 = 0.8^2 = 0.64$
Bb: $2pq = 2(0.8)(0.2) = 0.32$
bb: $q^2 = 0.2^2 = 0.04$

Not at Hardy-Weinberg

4) % heterozygous observed < % heterozygous expected, so yes, this is in the direction predicted by a Wahlund effect.

5) F_{ST} = (HW expected heterozygous - observed heterzygous) / HW expected heterozygous

= (0.32 - 0.10)/ 0.32 = 0.22/0.32 = 0.6875

6) NO, gene flow would homogenize these allele frequencies. These are dramatically different -- much more than among most human populations.

7) 0.6875. Calculation is exactly the same.

8) Some things to think about. First, inbreeding itself doesn't cause problems (it just sorts how the allele are distributed into genotypes), but it does expose rare recessive mutations which can cause problems. That level of inbreeding has been shown in dogs to be associated with some severe problems. The answer is not a simple yes or no. Basically, such inbreeding is likely to create a situation wherein recessive mutations already present in the population are exposed, and diseases are then manifested.