

According to our literature analysis, if a sampling were undertaken in Columbian montane habitats, we would expect to find species from the following species groups: *repleta*, *cardini*, *guarani*, *inmigrans*, *pallidipenis*, *tripunctata*, *melanogaster*, *obscura*, *saltans*, and *willistoni*. Other species groups we expect to find from the *virilis-repleta* radiation, but not present in the stock center, are: *annulimana*, *bromeliae*, *canalinae*, *dreyfusi*, *flavopilosa*, *funebri*, *mesophragmatica*, and *virilis*. Similarly, from the *inmigrans-tripunctata* radiation we expect to find *calloptera* and *rubifrons*. There are also species groups that were only found in one source of information but can probably be found in Colombia: *casatanea*, *xantopallescens*, *macroptera*, *quinaria*, *onycophora*, and *sticta*.

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### **Genetic markers of the *Va/Ba* balanced lethal strain of *Drosophila subobscura*.**

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The *Va/Ba* strain, constructed by Sperlich *et al.* (1977), is the only balanced lethal strain in *D. subobscura*. It allows the production of homozygous O chromosomes and has been a useful tool not only to analyse chromosomal viabilities but also to obtain homokaryotypic lines (Mestres and Serra, 2008). Besides the morphological dominant mutations *Va* (*Varicose*) and *Ba* (*Bare*), other genetic markers have been characterized in this strain, some of them by our group and not described previously. Here we present a list of these markers.

Table 1.

	Va chromosome	Ba chromosome
Inversions:	O <sub>VIII+210+3+4</sub>	O <sub>st</sub>
Morphological markers:	Va chromosome alleles	Ba chromosome alleles
<i>Va</i> ( <i>Varicose</i> ): dominant	<i>Va</i>	<i>Va</i> <sup>+</sup>
<i>Ba</i> ( <i>Bare</i> ): dominant	<i>Ba</i> <sup>+</sup>	<i>Ba</i>
<i>ch</i> ( <i>cherry</i> ): recessive	<i>ch</i>	<i>ch</i> <sup>+</sup>
<i>cu</i> ( <i>curled</i> ): recessive	<i>cu</i>	<i>cu</i> <sup>+</sup>
Allozyme markers:	Va chromosome alleles	Ba chromosome alleles
<i>AcpH</i>	1.00	1.00
<i>AO</i>	1.00	1.00
<i>Lap</i>	1.00	1.11
<i>ME</i>	1.00	1.00
<i>Pept-1</i>	0.40	1.00
<i>Xdh</i>	1.00	1.00
Nucleotide sequences	Va chromosome GeneBank accession number:	Ba chromosome GeneBank accession number:
<i>Odh</i>	AJ496721	EF467328
Microsatellite loci <sup>*</sup> :	Va chromosome alleles	Ba chromosome alleles
dsub01	263	261
dsub02	230	230
dsub04	197	198
dsub12	272	256
dsub25	260	246
dsub26	442	454
dsub29	258	251
dsub34	117	101
dsub38	417	417
dsub47	146	144
dsub51	398	400
dsub71	258	261

\* Primers are described in Pascual *et al.* (2000), Pegueroles *et al.* (2010). Chromosomal location of the microsatellite loci is described in Santos *et al.* (2010).

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