E2-01 Biosynthetic pathways for xanthones from *Calophyllum thwaitesii*

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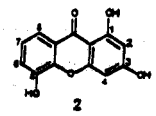
Calophyllum species of family Clusiaceae (Guttiferae) are a well-known source of phenolic secondary metabolites, and xanthones are very common among them. In the last 2 decades a considerable number of prenylated and geranylated xanthones have been reported from the *Calophyllum* species. The presence of these phenyl and geranyl side chains in the xanthone nucleus is of chemotaxonomic importance. Seven prenylated xanthones have been reported from *C.thwaitesii* and their possible biosynthetic pathways will be discussed. It has been reported that 2'-6 oxidative coupling of the initial precursor benzophenone (**1**) gives the 1,3,5-trioxygenated xanthone (**2**) while 6'-6 oxidative coupling leads to 1,3,7-trioxygenatedxanthone (**3**). The major xanthones of *C.thwaitesii* are thwaitesixanthone (**4**) calothwaitesixanthone (**5**) and 6-deoxy-y-mangostin (**6**). The above and 3 other xanthones dimethylcalabaxanthone (**7**) 11,12-dihydrothwaitesixanthone (**8**) and batukinaxanthone (**9**) have 1,3,7-trioxygenation pattern. Therefore in *C.thwaitesii*, 6'-6 oxidative coupling of benzophenone must be the most favourable biosynthetic pathway. Since trapezifolixanthone (10) is the only xanthone isolated from this plant with a 1,3,5-trioxygenated pattern, this minor constituent might have been formed *via* 2'-6 oxidative coupling of (**1**). Therefore 2'-6 oxidative coupling of benzophenone may be less favourable in *C.thwaitesii*. So far no methylated xanthone has been isolated from *C.thwaitesii*, and this further confirms the absence of methylating enzymes in this species, thus favouring the oxidative coupling to give pyrano ring systems.



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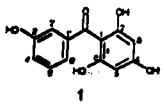

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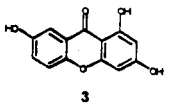

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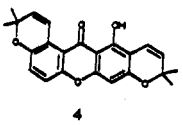

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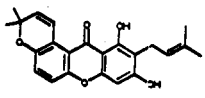

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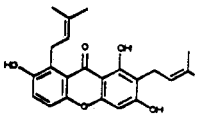

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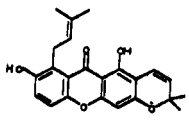

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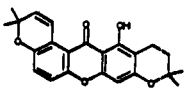

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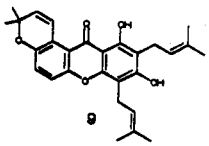

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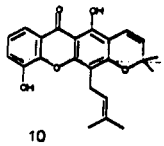

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